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(54) Titre : COMPOSITIONS PERMETTANT DE MODULER L'EXPRESSION DE TAU
(54) Title: COMPOSITIONS FOR MODULATING TAU EXPRESSION

(57) Abrégé/Abstract:

Disclosed herein are antisense compounds and methods for decreasing Tau mRNA and protein expression. Such methods, compounds, and compositions are useful to treat, prevent, or ameliorate Tau-associated diseases, disorders, and conditions.



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(54) **Title:** COMPOSITIONS FOR MODULATING TAU EXPRESSION

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



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COMPOSITIONS FOR MODULATING TAU EXPRESSION

5 **Sequence Listing**

The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled BIOL0227WOSEQ_ST25.txt created July 17, 2014, which is 916 Kb in size.

Field

10 Provided are compositions and methods for reducing expression of Tau mRNA and protein in an animal. Such methods are useful to treat, prevent, or ameliorate neurodegenerative diseases, including Tauopathies, Alzheimer's Disease, Fronto-temporal Dementia (FTD), FTDP-17, Progressive Supranuclear Palsy (PSP), Chronic Traumatic Encephalopathy (CTE), Corticobasal Ganglionic Degeneration (CBD), Epilepsy, and Dravet's Syndrome by inhibiting expression of Tau in an animal.

15

Background

The primary function of Tau is to bind to and stabilize microtubules, which are important structural components of the cytoskeleton involved in mitosis, cytokinesis, and vesicular transport. Tau is found in multiple tissues, but is particularly abundant in axons of neurons. In humans, there are six isoforms of Tau
20 that are generated by alternative splicing of exons 2, 3, and 10. Splicing of exons 2 and 3 at the N-terminus of the protein leads to inclusion of zero, one, or two 29 amino acid acidic domains and is termed 0N, 1N, or 2N Tau respectively. The influence of these domains on Tau function is not fully clear, though may play a role in interactions with the plasma membrane. Inclusion of exon 10 at the C-terminus leads to inclusion of the microtubule binding domain encoded by exon 10. Since there are 3 microtubule binding domains elsewhere
25 in Tau, this Tau isoform (with exon 10 included) is termed 4R Tau, where 'R' refers to the number of repeats of microtubule binding domains. Tau without exon 10 is termed 3R Tau. Since more microtubule binding domains (4R compared with 3R) increases the binding to microtubules, 4R Tau presumably significantly increases microtubule binding and assembly. The ratio of 3R/4R Tau is developmentally regulated, with fetal tissues expressing exclusively 3R Tau and adult human tissues expressing approximately equal levels of
30 3R/4R Tau. Deviations from the normal ratio of 3R/4R Tau are characteristic of neurodegenerative FTD Tauopathies. It is not known how changing the 3R/4R Tau ratio at a later stage in the adult animal will affect Tau pathogenesis.

Serine-threonine directed phosphorylation regulates the microtubule binding ability of Tau. Hyperphosphorylation promotes detachment of Tau from microtubules. Other post translational modifications of Tau have been described; however the significance of these is unclear. Phosphorylation of Tau is also developmentally regulated with higher phosphorylation in fetal tissues and much lower phosphorylation in the adult. One characteristic of neurodegenerative disorders is aberrantly increased Tau phosphorylation.

The microtubule network is involved in many important processes within the cell including structural integrity needed for maintaining morphology of cells and operating transport machinery. Since binding of Tau to microtubules stabilizes microtubules, Tau is likely to be a key mediator of some of these processes and disruption of normal Tau in neurodegenerative diseases may disrupt some of these key cellular processes.

One of the early indicators that Tau may be important in neurodegenerative syndromes was the recognition that Tau is a key component of neurofibrillary inclusions in Alzheimer's disease. In fact, neurofibrillary inclusions are aggregates of hyperphosphorylated Tau protein. Along with amyloid beta containing plaques, neurofibrillary inclusions are a hallmark of Alzheimer's disease and correlate significantly with cognitive impairment. 95% of Tau accumulations in AD are found in neuronal processes and is termed neuritic dystrophy. The process(es) whereby this microtubule associated protein becomes disengaged from microtubules and forms accumulations of proteins and how this relates to neuronal toxicity is not well understood.

Neuronal Tau inclusions are a pathological characteristic of not only Alzheimer's disease, but also a subset of Frontotemporal dementia (FTD), PSP, and CBD. The link between Tau and neurodegeneration was solidified by the discovery that mutations in the Tau gene cause a subset of FTD. These genetic data have also highlighted the importance of the 3R:4R ratio of Tau. Many of the Tau mutations that cause FTD lead to a change in Tau splicing which leads to preferential inclusion of exon 10, and thus to increased 4R Tau. The overall Tau levels are normal. Whether the Tau isoform change or the amino acid change or both cause neurodegeneration remains unknown. Recent data suggest that PSP may also be associated with an increased 4R:3R Tau ratio.

To help understand the influence of Tau ratios on neurodegeneration, a mouse model based on one of the splicing Tau mutations (N279K) has been generated using a minigene that includes the Tau promoter and the flanking intronic sequences of exon 10. As in humans, these mice demonstrate increased levels of 4R Tau compared with transgenics expressing WT Tau and develop behavioral and motor abnormalities as well as accumulations of aggregated Tau in the brain and spinal cord.

The protein "Tau" has been associated with multiple diseases of the brain including Alzheimer's disease, frontotemporal dementia, progressive supranuclear palsy, corticobasal ganglionic degeneration,

dementia pugilistica, parkinsonism linked to chromosome, Lytico-Bodig disease, tangle-predominant dementia, ganglioglioma, gangliocytoma, meningioangiomas, subacute sclerosing panencephalitis, lead encephalopathy, tuberous sclerosis, Hallervorden-Spatz disease, Pick's disease, argyrophilic grain disease, corticobasal degeneration or frontotemporal lobar degeneration and others. Tau-associated disorders such as

5 AD are the most common cause of dementia in the elderly. AD affects an estimated 15 million people worldwide and 40% of the population above 85 years of age. AD is characterized by two pathological hallmarks: Tau neurofibrillary inclusions (NFT) and amyloid- β (A β) plaques.

There is currently a lack of acceptable options for treating such neurodegenerative diseases. It is therefore an object herein to provide methods for the treatment of such diseases.

Summary

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

15 oligonucleotides.

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

Also provided are methods, compounds, and compositions useful for preventing, treating, and ameliorating diseases, disorders, and conditions. In certain embodiments, such Tau related diseases, disorders, and conditions are neurodegenerative diseases. In certain embodiments, such neurodegenerative diseases, disorders, and conditions include Tauopathies, Alzheimer's Disease, Fronto-temporal Dementia (FTD), FTDP-17, Progressive Supranuclear Palsy (PSP), Chronic Traumatic Encephalopathy (CTE),

25 Corticobasal Ganglionic Degeneration (CBD), Epilepsy, and Dravet's Syndrome

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 neurodegenerative disorder include growing older, having a personal or family history, or genetic predisposition. Certain symptoms and outcomes associated with development of a neurodegenerative disorder include but are not limited to: presence of

30 hyperphosphorylated Tau, presence of neurofibrillary inclusions, reduction of neurological function, reduced memory, reduced motor function, reduced motor coordination, and confusion.

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

The present disclosure provides the following non-limiting numbered embodiments:

Embodiment 1: A compound, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and having a nucleobase sequence comprising at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, or at least 20 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 20-2443 and SEQ ID NOs: 2478-2483.

Embodiment 2: A compound, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and having a nucleobase sequence comprising at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, or at least 20 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 2444-2477 and SEQ ID NOs: 2484-2565.

Embodiment 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 any of the nucleobase sequences of SEQ ID NOs: 20-2565.

Embodiment 4: 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 135783-135980 of SEQ ID NO: 1.

Embodiment 5: 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 135853-135872 of SEQ ID NO: 1.

Embodiment 6: 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 135783-135929 of SEQ ID NO: 1.

Embodiment 7: 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 135783-135914 of SEQ ID NO: 1.

Embodiment 8: The compound of embodiments 4-7, 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

5 SEQ ID NO: 1.

Embodiment 9: The compound of any preceding embodiment, consisting of a single-stranded modified oligonucleotide.

Embodiment 10: The compound of any preceding embodiment, wherein at least one internucleoside linkage is a modified internucleoside linkage.

10 Embodiment 11: The compound of embodiment 10, wherein at least one modified internucleoside linkage is a phosphorothioate internucleoside linkage.

Embodiment 12: The compound of embodiment 10, wherein each modified internucleoside linkage is a phosphorothioate internucleoside linkage.

15 Embodiment 13: The compound of any preceding embodiment, wherein at least one internucleoside linkage is a phosphodiester internucleoside linkage.

Embodiment 14: The compound of any preceding embodiment, wherein at least one internucleoside linkage is a phosphorothioate linkage and at least one internucleoside linkage is a phosphodiester linkage.

20 Embodiment 15: The compound of any preceding embodiment, wherein at least one nucleoside comprises a modified nucleobase.

Embodiment 16: The compound of embodiment 15, wherein the modified nucleobase is a 5-methylcytosine.

Embodiment 17: The compound of any preceding embodiment, wherein at least one nucleoside of the modified oligonucleotide comprises a modified sugar.

25 Embodiment 18: The compound of embodiment 17, wherein the at least one modified sugar is a bicyclic sugar.

Embodiment 19: The compound of embodiment 18, wherein the bicyclic sugar comprises a chemical link between the 2' and 4' position of the sugar 4'-CH₂-N(R)-O-2' bridge wherein R is, independently, H, C1-C12 alkyl, or a protecting group.

30 Embodiment 20: The compound of embodiment 18, wherein the bicyclic sugar comprises a 4'-CH₂-N(R)-O-2' bridge wherein R is, independently, H, C1-C12 alkyl, or a protecting group.

Embodiment 21: The compound of embodiment 17, wherein at least one modified sugar comprises a 2'-O-methoxyethyl group.

Embodiment 22: The compound of embodiment 17, wherein the modified sugar comprises a 2'-O(CH₂)₂-OCH₃ group.

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

a gap segment consisting of 10 linked deoxynucleosides;

a 5' wing segment consisting of 5 linked nucleosides; and

a 3' wing segment consisting of 5 linked nucleosides;

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

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

a gap segment consisting of 9 linked deoxynucleosides;

15 a 5' wing segment consisting of 5 linked nucleosides; and

a 3' wing segment consisting of 5 linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

Embodiment 25: The compound of any preceding embodiment, wherein the modified oligonucleotide
20 comprises:

a gap segment consisting of 7 linked deoxynucleosides;

a 5' wing segment consisting of 5 linked nucleosides; and

a 3' wing segment consisting of 6 linked nucleosides;

25 wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

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

a gap segment consisting of 8 linked deoxynucleosides;

a 5' wing segment consisting of 5 linked nucleosides; and

a 3' wing segment consisting of 5 linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

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

a gap segment consisting of 8 linked deoxynucleosides;

a 5' wing segment consisting of 4 linked nucleosides; and

a 3' wing segment consisting of 6 linked nucleosides;

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

Embodiment 28: The compound of any preceding embodiment, wherein the modified oligonucleotide comprises:

a gap segment consisting of 8 linked deoxynucleosides;

a 5' wing segment consisting of 6 linked nucleosides; and

15 a 3' wing segment consisting of 4 linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

Embodiment 29: The compound of any preceding embodiment, wherein the modified oligonucleotide consists of 20 linked nucleosides.

20 Embodiment 30: The compound of any preceding embodiment, wherein the modified oligonucleotide consists of 19 linked nucleosides.

Embodiment 31: The compound of any preceding embodiment, wherein the modified oligonucleotide consists of 18 linked nucleosides.

25 Embodiment 32: A composition comprising the compound of any preceding embodiment or salt thereof and at least one of a pharmaceutically acceptable carrier or diluent.

Embodiment 33: A method comprising administering to an animal the compound or composition of any preceding embodiment.

Embodiment 34: The method of embodiment 33, wherein the animal is a human.

30 Embodiment 35: The method of embodiment 33, wherein administering the compound prevents, treats, ameliorates, or slows progression of a tau associated disease, disorder or condition.

Embodiment 36: The method of embodiment 35, wherein the disease, disorder or condition is a Tauopathy, Alzheimer's Disease, Fronto-temporal Dementia (FTD), FTDP-17, Progressive Supranuclear Palsy (PSP), Chronic Traumatic Encephalopathy (CTE), Corticobasal Ganglionic Degeneration (CBD), Epilepsy, or Dravet's Syndrome.

5 Embodiment 37: Use of the compound or composition of any preceding embodiment for the manufacture of a medicament for treating a neurodegenerative disorder.

Embodiment 38: A compound consisting of ISIS 613099.

10 Embodiment 39: A compound consisting of ISIS 613361.

Embodiment 40: A compound consisting of ISIS 613370.

15 Embodiment 41: A compound consisting of ISIS 623782.

Embodiment 42: A compound consisting of ISIS 623996.

Embodiment 43: A composition comprising the compound of any of embodiments 38 – 42, or salt thereof, and at least one of a pharmaceutically acceptable carrier or diluent.

20 Embodiment 44: A method comprising administering to an animal the compound or composition of any of embodiments 38 - 43.

Embodiment 45: The method of embodiment 44, wherein the animal is a human.

Embodiment 46: The method of embodiment 44, wherein administering the compound prevents, treats, ameliorates, or slows progression of a tau associated disease, disorder or condition.

25 Embodiment 47: The method of embodiment 46, wherein the disease, disorder or condition is a Tauopathy, Alzheimer's Disease, Fronto-temporal Dementia (FTD), FTDP-17, Progressive Supranuclear Palsy (PSP), Chronic Traumatic Encephalopathy (CTE), Corticobasal Ganglionic Degeneration (CBD), Epilepsy, or Dravet's Syndrome.

30 Embodiment 48: Use of the compound or composition of any of embodiments 38 – 43 for the manufacture of a medicament for treating a neurodegenerative disorder.

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,
35 the use of the singular includes the plural unless specifically stated otherwise. As used herein, the use of "or" means "and/or" unless stated otherwise. Additionally, as used herein, the use of "and" means "and/or" unless

stated otherwise. Furthermore, the use of the term “including” as well as other forms, such as “includes” and “included”, is not limiting. Also, terms such as “element” or “component” encompass both elements and components comprising one unit and elements and components that comprise more than one subunit, unless specifically stated otherwise.

5 The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

Definitions

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

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

15 “2’-O-methoxyethyl” (also 2’-MOE and 2’-OCH₂CH₂-OCH₃ and MOE) refers to an O-methoxy-ethyl modification of the 2’ position of a furanose ring. A 2’-O-methoxyethyl modified sugar is a modified sugar.

 “2’-MOE nucleoside” (also 2’-O-methoxyethyl nucleoside) means a nucleoside comprising a 2’-MOE modified sugar moiety.

20 “2’-substituted nucleoside” means a nucleoside comprising a substituent at the 2’-position of the furanose ring other than H or OH. In certain embodiments, 2’ substituted nucleosides include nucleosides with bicyclic sugar modifications.

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

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

30 “Administered concomitantly” refers to the co-administration of two pharmaceutical agents in any manner in which the pharmacological effects of both are manifest in the patient at the same time. Concomitant administration does not require that both pharmaceutical agents be administered in a single pharmaceutical composition, in the same dosage form, or by the same route of administration. The effects of both pharmaceutical agents need not manifest themselves at the same time. The effects need only be overlapping for a period of time and need not be coextensive.

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

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

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

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

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

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

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

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

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

“Base complementarity” refers to the capacity for the precise base pairing of nucleobases of an 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 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'.

5 “Constrained ethyl nucleoside” (also cEt 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.

10 “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.

20 “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.

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

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

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

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

“Efficacy” means the ability to produce a desired effect.

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

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

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

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

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

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

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

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

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

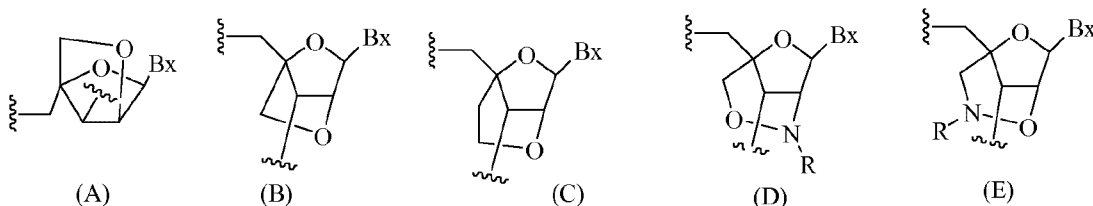
“Inhibiting Tau” means reducing the level or expression of a Tau mRNA and/or protein. In certain
5 embodiments, Tau mRNA and/or protein levels are inhibited in the presence of an antisense compound targeting Tau, including an antisense oligonucleotide targeting Tau, as compared to expression of Tau mRNA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

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

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

“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-
15 Methyleneoxy (4'-CH₂-O-2') LNA, (B) β -D-Methyleneoxy (4'-CH₂-O-2') LNA, (C) Ethyleneoxy (4'-(CH₂)₂-O-2') LNA, (D) Aminoxy (4'-CH₂-O-N(R)-2') LNA and (E) Oxyamino (4'-CH₂-N(R)-O-2') LNA, as depicted below.



As used herein, LNA compounds include, but are not limited to, compounds having at least one
20 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 $-[C(R_1)(R_2)]_n-$, $-C(R_1)=C(R_2)-$, $-C(R_1)=N-$, $-C(=NR_1)-$, $-C(=O)-$, $-C(=S)-$, $-O-$, $-Si(R_1)_2-$, $-S(=O)_x-$ and $-N(R_1)-$; wherein: x is 0, 1, or 2; n is 1, 2, 3, or 4; each R_1 and R_2 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,
25 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
30 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: $-[C(R_1)(R_2)]_n-$, $-[C(R_1)(R_2)]_n-O-$, $-C(R_1R_2)-N(R_1)-O-$ or $-C(R_1R_2)-O-N(R_1)-$.

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

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

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

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

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

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

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

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

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

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

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

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

5 “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
10 bonding with a nucleobase at a certain position of a target nucleic acid, then the position of hydrogen bonding between the oligonucleotide and the target nucleic acid is considered to be complementary at that nucleobase pair.

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

15 “Nucleoside” means a nucleobase linked to a sugar.

“Nucleoside mimetic” includes those structures used to replace the sugar or the sugar and the base and not necessarily the linkage at one or more positions of an oligomeric compound such as for example nucleoside mimetics having morpholino, cyclohexenyl, cyclohexyl, tetrahydropyranyl, bicyclo, or tricyclo sugar mimetics, *e.g.*, non furanose sugar units. Nucleotide mimetic includes those structures used to replace
20 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
25 tetrahydropyranyl ring system. “Mimetic” refers to groups that are substituted for a sugar, a nucleobase, and/or internucleoside linkage. Generally, a mimetic is used in place of the sugar or sugar-internucleoside linkage combination, and the nucleobase is maintained for hybridization to a selected target.

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

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

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

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

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

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

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

10 “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.

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

15 “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.

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

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

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

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

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

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

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

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

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

5 “Shortened” or “truncated” versions of antisense oligonucleotides taught herein have one, two or more nucleosides deleted.

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

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

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

“Slows progression” means decrease in the development of the said disease.

15 “Specifically hybridizable” 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
20 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
25 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.

30 “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.

“Tau” means mammalian microtubule-associated protein tau (MAPT), including human microtubule-associated protein tau (MAPT).

35 “Tau associated disease” means any disease associated with any Tau nucleic acid or expression product thereof. Such diseases may include a neurodegenerative disease. Such neurodegenerative diseases

may include Tauopathies, Alzheimer's Disease, Fronto-temporal Dementia (FTD), FTDP-17, Progressive Supranuclear Palsy (PSP), Chronic Traumatic Encephalopathy (CTE), Corticobasal Ganglionic Degeneration (CBD), Epilepsy, and Dravet's Syndrome.

"Tau mRNA" means any messenger RNA expression product of a DNA sequence encoding Tau.

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

"Tau protein" means the polypeptide expression product of a Tau nucleic acid.

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

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

15 "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).

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

Certain Embodiments

25 Certain embodiments provide methods, compounds, and compositions for inhibiting Tau mRNA and protein expression. Certain embodiments provide methods, compounds, and composition for decreasing Tau mRNA and protein levels.

Certain embodiments provide antisense compounds targeted to a Tau nucleic acid. In certain embodiments, the Tau nucleic acid is the sequence set forth in GENBANK Accession No. GENBANK Accession No. NT_010783.15 truncated from nucleotides 9240000 to 9381000 (incorporated herein as SEQ ID NO: 1), GENBANK Accession No. NM_001123066.3 (incorporated herein as SEQ ID NO: 2), GENBANK Accession No. NM_016841.4, a variant mRNA sequence which skips exons 3, 4, 6, 8, 10, and 12 (incorporated herein as SEQ ID NO: 3), GENBANK Accession No. NT_010783.14 truncated from nucleotides 2624000 to 2761000 (incorporated herein as SEQ ID NO: 4), GENBANK Accession No. DR002467.1 (incorporated herein as SEQ ID NO: 5), GENBANK Accession No. NM_001203251.1 (incorporated herein as SEQ ID NO: 6), and GENBANK Accession No. NM_016835.4 (incorporated herein as SEQ ID NO: 7).

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Certain embodiments provide methods for the treatment, prevention, or amelioration of diseases, disorders, and conditions associated with Tau in an individual in need thereof. Also contemplated are methods for the preparation of a medicament for the treatment, prevention, or amelioration of a disease, disorder, or condition associated with Tau. Tau associated diseases, disorders, and conditions include neurodegenerative diseases. In certain embodiments, tau associated diseases include Tauopathies, Alzheimer's Disease, Fronto-temporal Dementia (FTD), FTDP-17, Progressive Supranuclear Palsy (PSP), Chronic Traumatic Encephalopathy (CTE), Corticobasal Ganglionic Degeneration (CBD), Epilepsy, or Dravet's Syndrome.

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: 20-2443 and SEQ ID NOs: 2478-2483.

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: 2444-2477 and SEQ ID NOs: 2484-2565.

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: 20-2565.

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 135783-135980 of SEQ ID NO: 1.

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 135853-135872 of SEQ ID NO: 1.

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 135783-135929 of SEQ

ID NO: 1.

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 135783-135914 of SEQ ID NO: 1.

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: 1.

In certain embodiments, the compound is 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 is a phosphorothioate internucleoside linkage.

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

In certain embodiments, at least one internucleoside linkage is a phosphodiester internucleoside linkage.

In certain embodiments, at least one internucleoside linkage is a phosphorothioate linkage and at least one internucleoside linkage is a phosphodiester linkage.

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

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

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

In certain embodiments, at least one modified sugar is a bicyclic sugar.

In certain embodiments, the bicyclic sugar comprises a chemical link between the 2' and 4' position of the sugar 4'-CH₂-N(R)-O-2' bridge wherein R is, independently, H, C1-C12 alkyl, or a protecting group.

In certain embodiments, the bicyclic sugar comprises a 4'-CH₂-N(R)-O-2' bridge wherein R is, independently, H, C1-C12 alkyl, or a protecting group.

In certain embodiments, at least one modified sugar comprises a 2'-O-methoxyethyl group.

In certain embodiments, the modified sugar comprises a 2'-O(CH₂)₂-OCH₃ group.

In certain embodiments, 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.

In certain embodiments, the modified oligonucleotide comprises:

a gap segment consisting of 9 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 comprises:

10 a gap segment consisting of 7 linked deoxynucleosides;

a 5' wing segment consisting of 5 linked nucleosides; and

a 3' wing segment consisting of 6 linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

15 In certain embodiments, the modified oligonucleotide comprises:

a gap segment consisting of 8 linked deoxynucleosides;

a 5' wing segment consisting of 5 linked nucleosides; and

a 3' wing segment consisting of 5 linked nucleosides;

20 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 comprises:

a gap segment consisting of 8 linked deoxynucleosides;

a 5' wing segment consisting of 4 linked nucleosides; and

a 3' wing segment consisting of 6 linked nucleosides;

25 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 comprises:

a gap segment consisting of 8 linked deoxynucleosides;

a 5' wing segment consisting of 6 linked nucleosides; and

30 a 3' wing segment consisting of 4 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.

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

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

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

Certain embodiments provide methods comprising administering to an animal any compound or composition described herein.

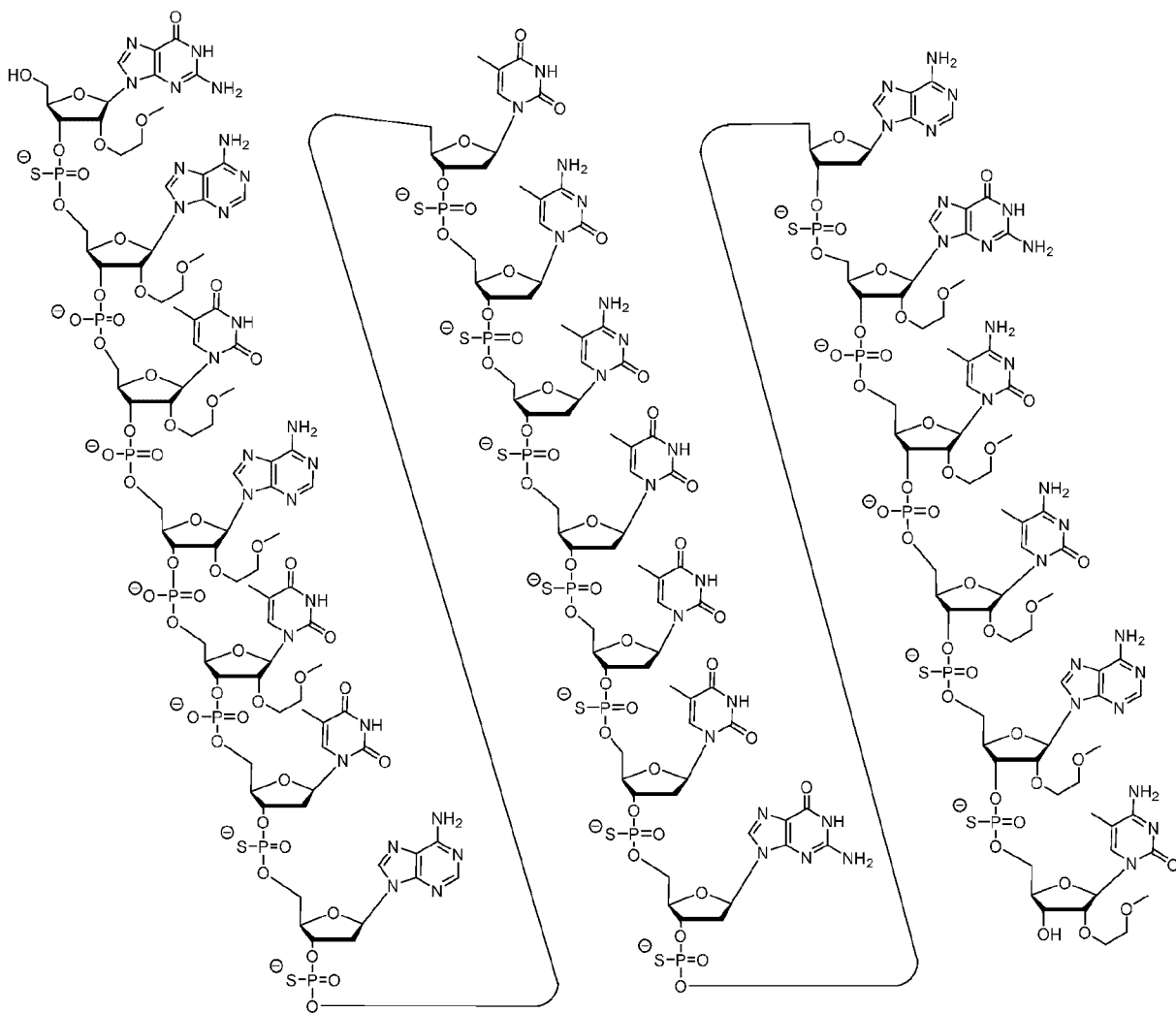
5 In certain embodiments, the animal is a human.

In certain embodiments, administering the compound prevents, treats, ameliorates, or slows progression of a tau associated disease, disorder or condition.

10 In certain embodiments, the disease, disorder or condition is a Tauopathy, Alzheimer's Disease, Fronto-temporal Dementia (FTD), FTDP-17, Progressive Supranuclear Palsy (PSP), Chronic Traumatic Encephalopathy (CTE), Corticobasal Ganglionic Degeneration (CBD), Epilepsy, or Dravet's Syndrome.

Certain embodiments provide use of any of the compounds or compositions of described herein for the manufacture of a medicament for treating a neurodegenerative disorder.

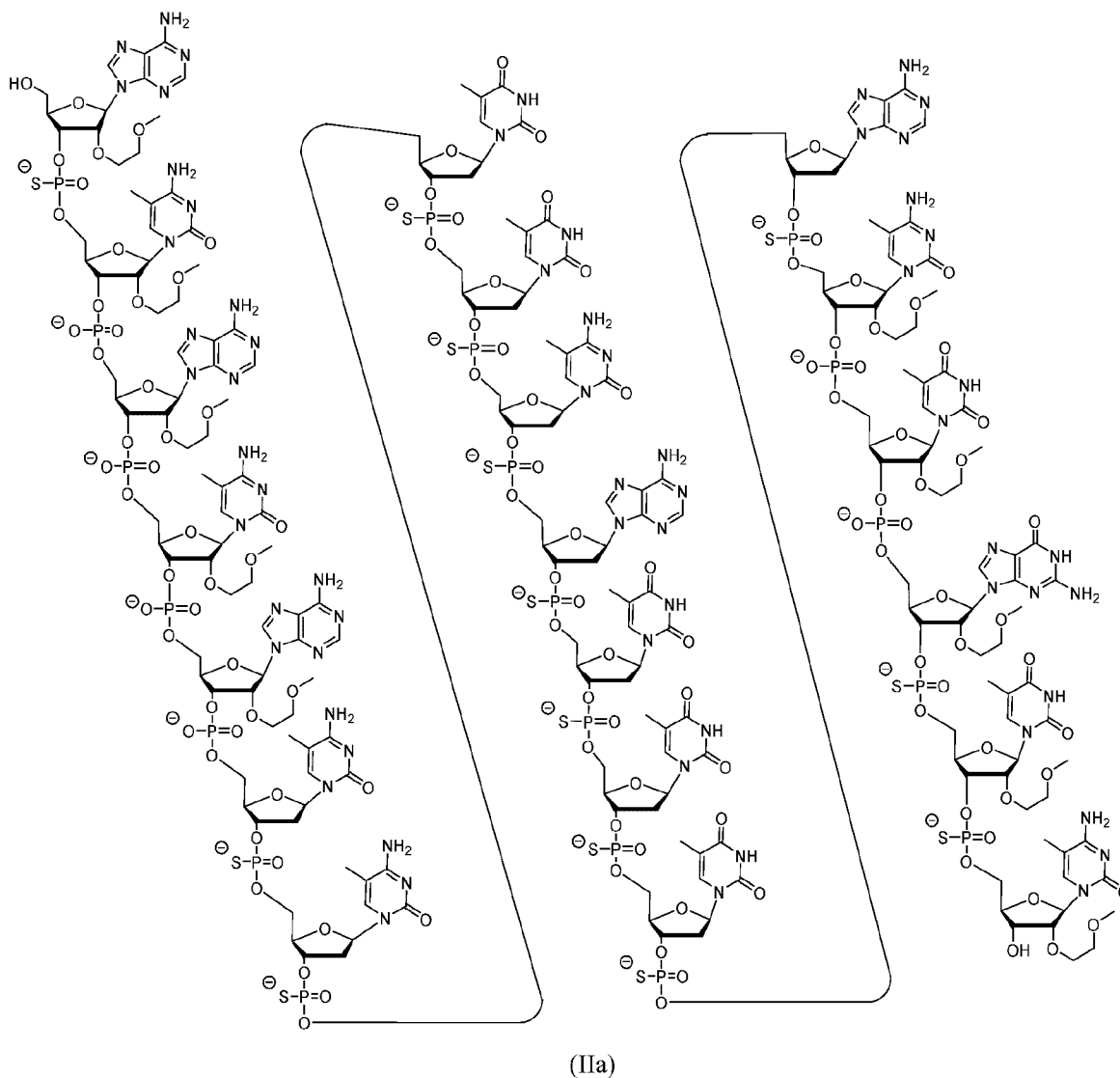
Certain embodiments provide compounds according to the following formula (Ia):



(Ia)

, or a pharmaceutically acceptable salt thereof. In certain embodiments, provided are pharmaceutical compositions comprising the compound having the formula (Ia).

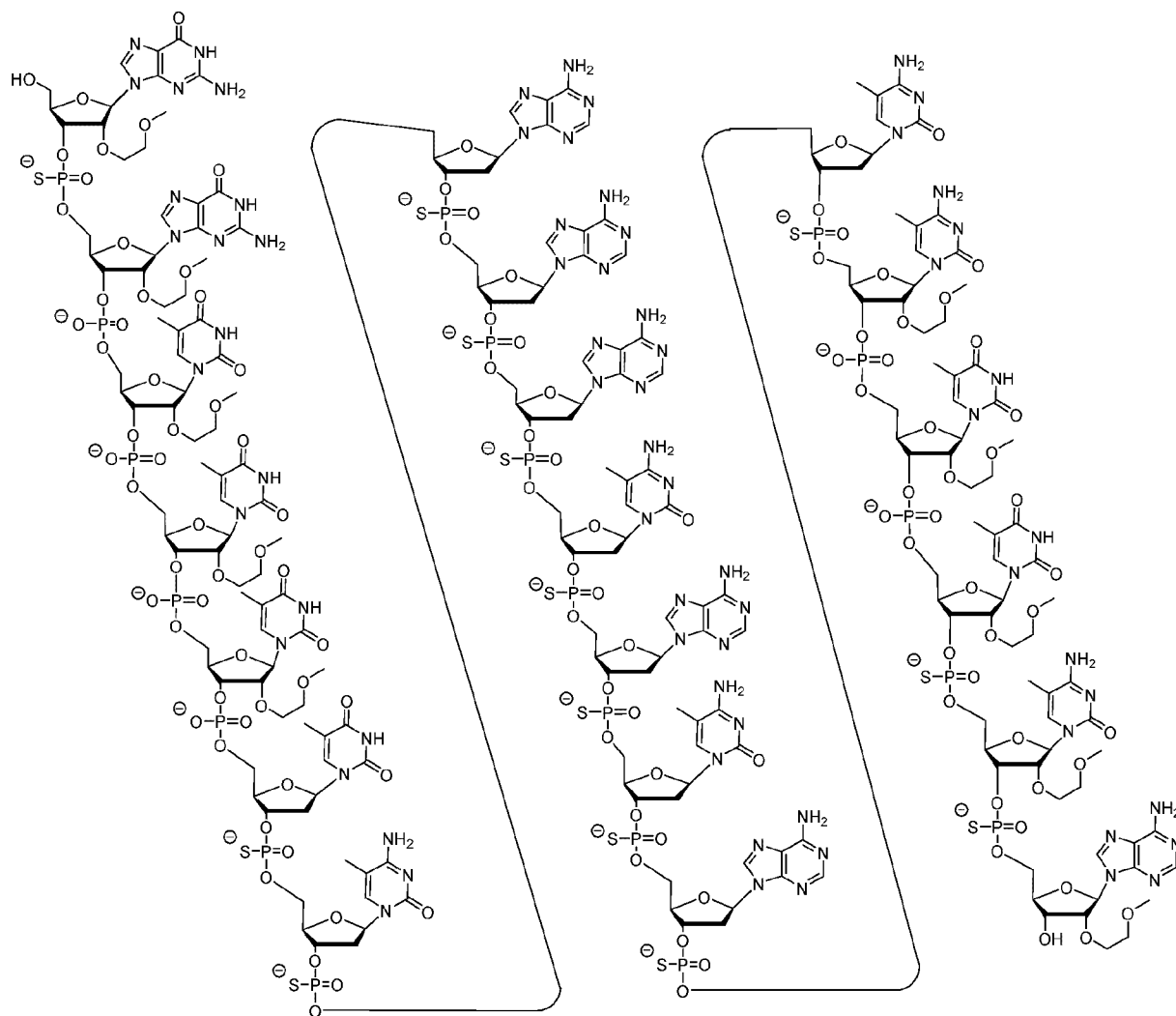
Certain embodiments provide compounds according to the following formula (IIa):



5

, or a pharmaceutically acceptable salt thereof. In certain embodiments, provided are pharmaceutical compositions comprising the compound having the formula (IIa).

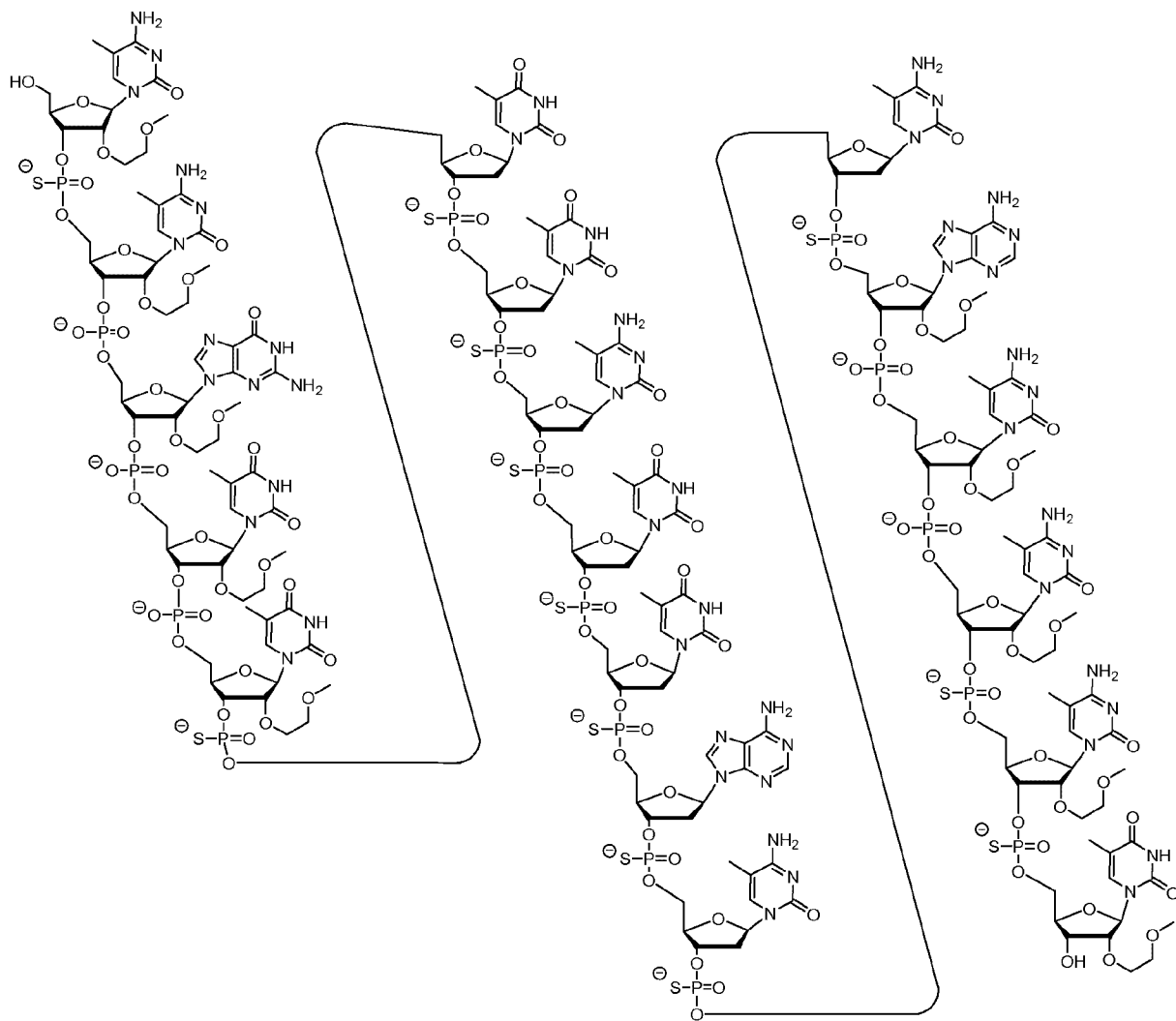
Certain embodiments provide compounds according to the following formula (IIIa):



(IIIa)

, or a pharmaceutically acceptable salt thereof. In certain embodiments, provided are
 5 pharmaceutical compositions comprising the compound having the formula (IIIa).

Certain embodiments provide compounds according to the following formula (IVa):

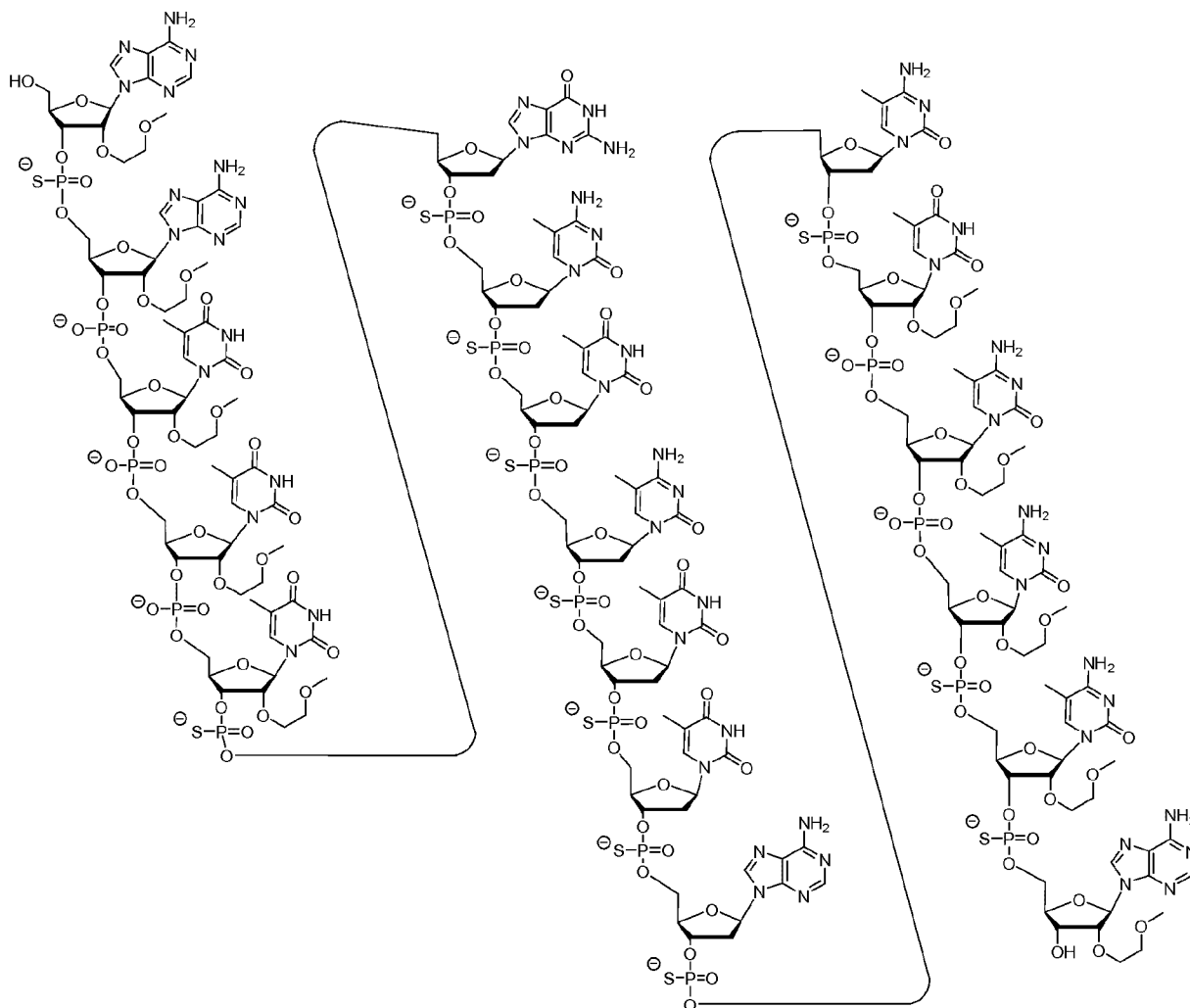


(IVa)

, or a pharmaceutically acceptable salt thereof. In certain embodiments, provided are pharmaceutical compositions comprising the compound having the formula (IVa).

5

Certain embodiments provide compounds according to the following formula (Va):



(Va)

, or a pharmaceutically acceptable salt thereof. In certain embodiments, provided are
 5 pharmaceutical compositions comprising the compound having the formula (Va).

Antisense Compounds

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

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

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

In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 12 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 13 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 14 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 15 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 16 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 17 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 18 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 19 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 20 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 21 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 22 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 23 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 24 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 25 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 26 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 27 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 28 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 29 subunits in length. In certain embodiments, an antisense compound targeted to a Tau nucleic acid is 30 subunits in length. In certain embodiments, the antisense compound targeted to a Tau 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 Tau 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 Tau 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*.

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

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

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

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

In certain embodiments, gapmers provided herein include, for example 18-mers having a motif of 4-8-6.

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

In certain embodiments, gapmers provided herein include, for example 18-mers having a motif of 5-7-6.

Target Nucleic Acids, Target Regions and Nucleotide Sequences

Nucleotide sequences that encode Tau include, without limitation, the following: GENBANK Accession No. NT_010783.15 truncated from nucleotides 9240000 to 9381000 (incorporated herein as SEQ ID NO: 1), GENBANK Accession No. NM_001123066.3 (incorporated herein as SEQ ID NO: 2), GENBANK Accession No. NM_016841.4, a variant mRNA sequence which skips exons 3, 4, 6, 8, 10, and 12 (incorporated herein as SEQ ID NO: 3), GENBANK Accession No. NT_010783.14 truncated from nucleotides 2624000 to 2761000 (incorporated herein as SEQ ID NO: 4), GENBANK Accession No. DR002467.1 (incorporated herein as SEQ ID NO: 5), GENBANK Accession No. NM_001203251.1 (incorporated herein as SEQ ID NO: 6), and GENBANK Accession No. NM_016835.4 (incorporated herein as SEQ ID NO: 7).

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

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

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

A target region may contain one or more target segments. Multiple target segments within a target region may be overlapping. Alternatively, they may be non-overlapping. In certain embodiments, target segments within a target region are separated by no more than about 300 nucleotides. In certain 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 nucleic acid, or is a range defined by any two of the preceeding values. In certain embodiments, target segments within a target region are separated by no more than, or no more than about, 5 nucleotides on the target nucleic acid. In certain embodiments, target segments are contiguous. Contemplated are target regions defined by a range having a starting nucleic acid that is any of the 5' target sites or 3' target sites listed herein.

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

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

There may be variation in activity (e.g., as defined by percent reduction of target nucleic acid levels) of the antisense compounds within an active target region. In certain embodiments, reductions in Tau mRNA levels are indicative of inhibition of Tau expression. Reductions in levels of a Tau protein are also indicative of inhibition of target mRNA expression. Reduction of percent of cells staining positive for hyperphosphorylated Tau are indicative of inhibition of Tau expression. Further, phenotypic changes are indicative of inhibition of Tau expression. Improvement in neurological function is indicative of inhibition of Tau expression. Improved memory and motor function are indicative of inhibition of Tau expression. Reduction of neurofibrillary inclusions is indicative of inhibition of Tau expression.

Hybridization

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

Non-complementary nucleobases between an antisense compound and a Tau 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 Tau nucleic acid such that intervening or adjacent segments are not involved in the hybridization event (e.g., a loop structure, mismatch or hairpin structure).

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

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

In certain embodiments, the antisense compounds provided herein, or specified portions thereof, are fully complementary (*i.e.*, 100% complementary) to a target nucleic acid, or specified portion thereof. For example, an antisense compound may be fully complementary to a Tau 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, such as a Tau nucleic acid, or specified portion thereof.

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

The antisense compounds provided herein also include those which are complementary to a portion of a target nucleic acid. As used herein, “portion” refers to a defined number of contiguous (i.e. linked) nucleobases within a region or segment of a target nucleic acid. A “portion” can also refer to a defined number of contiguous nucleobases of an antisense compound. In certain embodiments, the antisense compounds, are complementary to at least an 8 nucleobase portion of a target segment. In certain embodiments, the antisense compounds are complementary to at least a 9 nucleobase portion of a target segment. In certain embodiments, the antisense compounds are complementary to at least a 10 nucleobase portion of a target segment. In certain embodiments, the antisense compounds, are complementary to at least an 11 nucleobase portion of a target segment. In certain embodiments, the antisense compounds, are complementary to at least a 12 nucleobase portion of a target segment. In certain embodiments, the antisense compounds, are complementary to at least a 13 nucleobase portion of a target segment. In certain embodiments, the antisense compounds, are complementary to at least a 14 nucleobase portion of a target segment. In certain embodiments, the antisense compounds, are complementary to at least a 15 nucleobase portion of a target segment. Also contemplated are antisense compounds that are complementary to at least a

9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more nucleobase portion of a target segment, or a range defined by any two of these values.

Identity

5 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
10 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.

15 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,
20 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.

30 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
35 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.

5 *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
10 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
15 of preparation of phosphorous-containing and non-phosphorous-containing linkages are well known.

In certain embodiments, antisense compounds targeted to a Tau nucleic acid comprise one or more modified internucleoside linkages. In certain embodiments, the modified internucleoside linkages are interspersed throughout the antisense compound. In certain embodiments, the modified internucleoside linkages are phosphorothioate linkages. In certain embodiments, each internucleoside linkage of an antisense
20 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
25 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
30 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
35 Published on 11/22/07 wherein LNA is substituted with for example a 5'-methyl or a 5'-vinyl group).

Examples of nucleosides having modified sugar moieties include without limitation nucleosides comprising 5'-vinyl, 5'-methyl (*R* or *S*), 4'-S, 2'-F, 2'-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(R_l)-(CH₂)₂-N(R_m)(R_n), where each R_l, R_m and R_n is, independently, H or 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 bicyclic nucleosides, include but are not limited to one of the formulae: 4'-(CH₂)-O-2' (LNA); 4'-(CH₂)-S-2'; 4'-(CH₂)₂-O-2' (ENA); 4'-CH(CH₃)-O-2' 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 published International Application WO/2009/006478, published January 8, 2009); 4'-CH₂-N(OCH₃)-2' (and analogs thereof see published International Application WO/2008/150729, published 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 published International Application WO 2008/154401, published on December 8, 2008).

Further reports related to bicyclic nucleosides can also be found in published literature (see for example: 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.*, *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; U.S. Patent Serial Nos. 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 comprises 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;

5 n is 1, 2, 3, or 4;

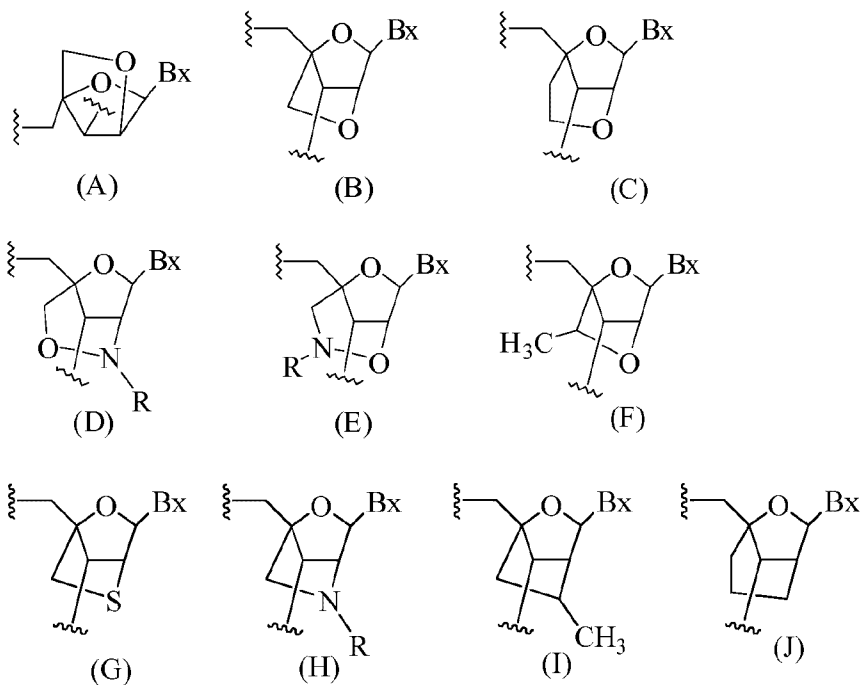
each R_a and R_b is, independently, H, a protecting group, hydroxyl, C_1 - C_{12} alkyl, substituted C_1 - C_{12} alkyl, C_2 - C_{12} alkenyl, substituted C_2 - C_{12} alkenyl, C_2 - C_{12} alkynyl, substituted C_2 - C_{12} alkynyl, C_5 - C_{20} aryl, substituted C_5 - C_{20} aryl, heterocycle radical, substituted heterocycle radical, heteroaryl, substituted heteroaryl, C_5 - C_7 alicyclic radical, substituted C_5 - C_7 alicyclic radical, halogen, OJ_1 , NJ_1J_2 , SJ_1 , N_3 , $COOJ_1$, acyl ($C(=O)$ -H), substituted acyl, CN, sulfonyl ($S(=O)_2-J_1$), or sulfoxyl ($S(=O)-J_1$); and

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

15 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.

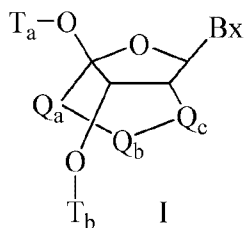
In certain embodiments, bicyclic nucleosides are further defined by isomeric configuration. For
 20 example, a nucleoside comprising a 4'-2' methylene-oxy bridge, may be in the α -L configuration or in the β -D configuration. Previously, α -L-methyleneoxy (4'- CH_2 -O-2') BNA's have been incorporated 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
 25 (4'- CH_2 -O-2') BNA, (B) β -D-methyleneoxy (4'- CH_2 -O-2') BNA, (C) ethyleneoxy (4'-(CH_2)₂-O-2') BNA, (D) aminooxy (4'- CH_2 -O-N(R)-2') BNA, (E) oxyamino (4'- CH_2 -N(R)-O-2') BNA, and (F) methyl(methyleneoxy) (4'-CH(CH_3)-O-2') BNA, (G) methylene-thio (4'- CH_2 -S-2') BNA, (H) methylene-amino (4'- CH_2 -N(R)-2') BNA, (I) methyl carbocyclic (4'- CH_2 -CH(CH_3)-2') BNA, and (J) propylene carbocyclic (4'-(CH_2)₃-2') BNA as depicted below.



5 wherein Bx is the base moiety and R is independently H, a protecting group or C₁-C₁₂ alkyl.

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



wherein:

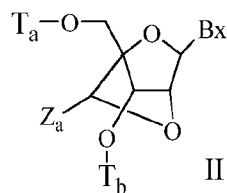
10 Bx is a heterocyclic base moiety;

-Q_a-Q_b-Q_c- is -CH₂-N(R_c)-CH₂-, -C(=O)-N(R_c)-CH₂-, -CH₂-O-N(R_c)-, -CH₂-N(R_c)-O- or -N(R_c)-O-CH₂;

R_c is C₁-C₁₂ alkyl or an amino protecting group; and

15 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:



wherein:

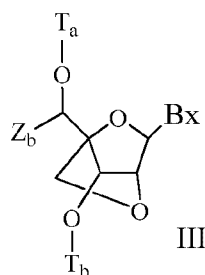
Bx is a heterocyclic base moiety;

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

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

10 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 .

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



15

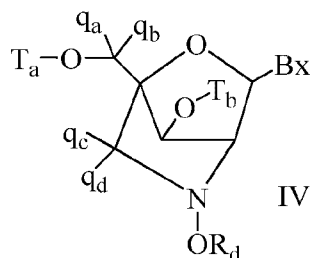
wherein:

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 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:



wherein:

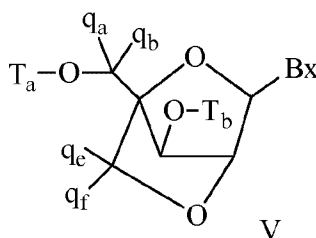
Bx is a heterocyclic base moiety;

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;

5 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;

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



wherein:

Bx is a heterocyclic base moiety;

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

q_a, q_b, q_c and q_d 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,

20 N(H)C(=NH)NJ_jJ_k, N(H)C(=O)NJ_jJ_k or N(H)C(=S)NJ_jJ_k;

or q_c and q_d together are =C(q_g)(q_h);

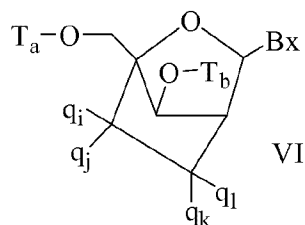
q_g and q_h are each, independently, H, halogen, C₁-C₁₂ alkyl or substituted C₁-C₁₂ alkyl.

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
25 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.

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
30 (Wengel *et al.*, WO 99/14226). Furthermore, synthesis of 2'-amino-BNA, a novel conformationally restricted high-affinity oligonucleotide analog has been described in the art (Singh *et al.*, *J. Org. Chem.*,

1998, 63, 10035-10039). In addition, 2'-amino- and 2'-methylamino-BNA's have been prepared and the thermal stability of their duplexes with complementary RNA and DNA strands has been previously reported.

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



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 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, N(H)C(=NH)NJ_jJ_k, N(H)C(=O)NJ_jJ_k or N(H)C(=S)NJ_jJ_k; and

15 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).

20

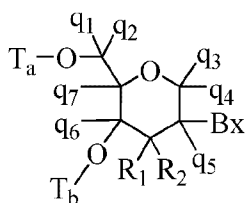
As used herein, "4'-2' bicyclic nucleoside" or "4' to 2' bicyclic nucleoside" refers to a bicyclic nucleoside comprising a furanose ring comprising a bridge connecting two carbon atoms of the furanose ring connects the 2' carbon atom and the 4' carbon atom of the sugar ring.

25 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.

30 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, 841-854), fluoro HNA (F-HNA) or those compounds 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 H and R₂ is methoxyethoxy.

As used herein, "2'-modified" or "2'-substituted" refers to a nucleoside comprising a sugar comprising a substituent at the 2' position other than H or OH. 2'-modified nucleosides, include, but are not limited to, bicyclic nucleosides wherein the bridge connecting two carbon atoms of the sugar ring connects the 2' carbon and another carbon of the sugar ring; and nucleosides with non-bridging 2'-substituents, such as allyl, amino, azido, thio, O-allyl, O-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.

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

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.

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 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 (see for example review article: Leumann, *Bioorg. Med. Chem.*, 2002, 10, 841-854).

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.

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

In certain embodiments, antisense compounds comprise one or more nucleosides having modified sugar moieties. In certain embodiments, the modified sugar moiety is 2'-MOE. In certain embodiments, the 2'-MOE modified nucleosides are arranged in a gapmer motif. In certain embodiments, the modified sugar moiety is a bicyclic nucleoside having a (4'-CH(CH₃)-O-2') bridging group. In certain embodiments, the (4'-CH(CH₃)-O-2') modified nucleosides are arranged throughout the wings of a gapmer motif.

Compositions and Methods for Formulating Pharmaceutical Compositions

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

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

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

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

Conjugated Antisense Compounds

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

Antisense compounds can also be modified to have one or more stabilizing groups that are generally attached to one or both termini of antisense compounds to enhance properties such as, for example, nuclease stability. Included in stabilizing groups are cap structures. These terminal modifications protect the antisense compound having terminal nucleic acid from exonuclease degradation, and can help in delivery and/or localization within a cell. The cap can be present at the 5'-terminus (5'-cap), or at the 3'-terminus (3'-cap), or can be present on both termini. Cap structures are well known in the art and include, for example,

inverted deoxy abasic caps. Further 3' and 5'-stabilizing groups that can be used to cap one or both ends of an antisense compound to impart nuclease stability include those disclosed in WO 03/004602 published on January 16, 2003.

5 *Cell culture and antisense compounds treatment*

The effects of antisense compounds on the level, activity or expression of Tau 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
10 commercially available reagents (e.g. Invitrogen Life Technologies, Carlsbad, CA). Illustrative cell types include, but are not limited to, HepG2 cells, Hep3B cells, and primary hepatocytes.

In vitro testing of antisense oligonucleotides

Described herein are methods for treatment of cells with antisense oligonucleotides, which can be
15 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 (Invitrogen, Carlsbad, CA). Antisense oligonucleotides may
20 be mixed with LIPOFECTIN in OPTI-MEM 1 (Invitrogen, 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 (Invitrogen, Carlsbad, CA). Antisense oligonucleotide is mixed with LIPOFECTAMINE
25 in OPTI-MEM 1 reduced serum medium (Invitrogen, 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.

30 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 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
35 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 from 625 to 20,000 nM when transfected using electroporation.

RNA Isolation

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

Analysis of inhibition of target levels or expression

10 Inhibition of levels or expression of a Tau nucleic acid can be assayed in a variety of ways known in the art. For example, target nucleic acid levels can be quantitated by, e.g., Northern blot analysis, competitive polymerase chain reaction (PCR), or 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
15 commercially available ABI PRISM 7600, 7700, or 7900 Sequence Detection System, available from PE-Applied Biosystems, Foster City, CA and used according to manufacturer's instructions.

Quantitative Real-Time PCR Analysis of Target RNA Levels

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

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

Gene (or RNA) target quantities obtained by real time PCR are normalized using either the expression level of a gene whose expression is constant, such as cyclophilin A, or by quantifying total RNA using RIBOGREEN (Invitrogen, Inc. Carlsbad, CA). Cyclophilin A expression is quantified by real time
30 PCR, by being run simultaneously with the target, multiplexing, or separately. Total RNA is quantified using RIBOGREEN RNA quantification reagent (Invitrogen, Inc. Eugene, OR). Methods of RNA 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 Tau nucleic acid. Methods for designing real-
35 time PCR probes and primers are well known in the art, and may include the use of software such as PRIMER EXPRESS Software (Applied Biosystems, Foster City, CA).

Analysis of Protein Levels

Antisense inhibition of Tau nucleic acids can be assessed by measuring Tau protein levels. Protein levels of Tau can be evaluated or quantitated in a variety of ways well known in the art, such as

5 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
10 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 Tau and produce phenotypic changes, such as, improved cognition and motor
15 function. In certain embodiments, cognition is measured by novel object recognition and nestlet building activity. In certain embodiments, motor function is measured by walking initiation analysis, rotarod, grip strength, pole climb, open field performance, balance beam, hindpaw footprint testing in the animal. In certain embodiments, antisense compounds, for example, antisense oligonucleotides, are tested in animals to assess their ability to reduce hyperphosphorylated tau and neurofibrillary tangles. In certain embodiments,
20 antisense compounds, for example, antisense oligonucleotides, are tested to assess their ability to prevent, and/or reduce severity of, seizures in a pentylenetetrazol (PTZ) induced seizure model.

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
25 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 CNS tissue or CSF and changes in Tau nucleic acid expression are measured.

Certain Indications

In certain embodiments, provided herein are methods, compounds, and compositions of treating an individual comprising administering one or more pharmaceutical compositions described herein. In certain embodiments, the individual has a neurodegenerative disease. In certain embodiments, the individual is at risk for developing a neurodegenerative disease, including, but not limited to, a Tauopathy, Alzheimer's
35 Disease, Fronto-temporal Dementia (FTD), FTDP-17, Progressive Supranuclear Palsy (PSP), Chronic Traumatic Encephalopathy (CTE), Corticobasal Ganglionic Degeneration (CBD), Epilepsy, and Dravet's

Syndrome. In certain embodiments, the individual has been identified as having a Tau associated disease. In certain embodiments, provided herein are methods for prophylactically reducing Tau 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 Tau nucleic acid.

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

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

In certain embodiments, pharmaceutical compositions comprising an antisense compound targeted to
20 Tau are used for the preparation of a medicament for treating a patient suffering or susceptible to a neurodegenerative disease including a Tauopathy, Alzheimer's Disease, Fronto-temporal Dementia (FTD), FTDP-17, Progressive Supranuclear Palsy (PSP), Chronic Traumatic Encephalopathy (CTE), Corticobasal Ganglionic Degeneration (CBD), Epilepsy, and Dravet's Syndrome.

25 *Certain Hotspot Regions*

1. Nucleobases 135783-135980 of SEQ ID NO: 1

In certain embodiments, antisense oligonucleotides are designed to target nucleobases 135783-135980 of SEQ ID NO: 1 (GENBANK Accession No. GENBANK Accession No. NT_010783.15 truncated from nucleotides 9240000 to 9381000). In certain embodiments, nucleobases 135783-135980 are a hotspot
30 region. In certain embodiments, nucleobases 135783-135980 are targeted by antisense oligonucleotides. In certain embodiments, the antisense oligonucleotides are 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, 5-9-5 MOE gapmers, 5-7-6 MOE gapmers, and 5-8-5 MOE gapmers. In certain
35 embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphorothioate internucleoside linkages. In certain embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphodiester internucleoside linkages. In certain embodiments, the nucleosides of the antisense

oligonucleotides are linked by phosphorothioate and phosphodiester internucleotide linkages (e.g., the antisense oligonucleotides have “mixed backbones”).

In certain embodiments, nucleobases 135783-135980 are targeted by the following ISIS numbers: 424879, 424880, 548937, 613114-613120, 622096-622150, 623988-623996, 664511-664542, and 664661-664819.

In certain embodiments, nucleobases 135783-135980 are targeted by the following SEQ ID NOs: 56, 57, 248, 462-467, 1668-1698, 2025-2048, 2301-2309, 2331- 2443, and 2478-2483.

In certain embodiments, antisense oligonucleotides targeting nucleobases 135783-135980 achieve at least 12%, at least 13%, at least 14%, at least 15%, at least 16%, at least 17%, at least 18%, at least 19%, 20%, at least 21%, at least 22%, at least 23%, at least 24%, at least 25%, at least 26%, at least 27%, at least 28%, at least 29%, 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%, or at least 93% reduction of Tau mRNA and/or protein levels in vitro and/or in vivo.

2. Nucleobases 135853-135872 of SEQ ID NO: 1

In certain embodiments, antisense oligonucleotides are designed to target nucleobases 135853-135872 of SEQ ID NO: 1 (GENBANK Accession No. GENBANK Accession No. NT_010783.15 truncated from nucleotides 9240000 to 9381000). In certain embodiments, nucleobases 135853-135872 are a hotspot region. In certain embodiments, nucleobases 135853-135872 are targeted by antisense oligonucleotides. In certain embodiments, the antisense oligonucleotides are 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, 5-9-5 MOE gapmers, 5-7-6 MOE gapmers, or 5-8-5 MOE gapmers. In certain embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphorothioate internucleoside linkages. In certain embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphodiester internucleoside linkages. In certain embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphorothioate and phosphodiester internucleotide linkages (e.g., the antisense oligonucleotides have “mixed backbones”).

In certain embodiments, nucleobases 135853-135872 are targeted by the following ISIS numbers: 424879, 424880, 613117, 613118, 622114-622125, 623993-623996, 664522-664542, 664676-664713, 664729-664766, and 664783-664819.

In certain embodiments, nucleobases 135853-135872 are targeted by the following SEQ ID NOs: 56, 57, 248, 464-465, 1668-1673, 2039-2048, 2306-2309, 2345-2443, and 2478-2483.

In certain embodiments, antisense oligonucleotides targeting nucleobases 135853-135872 achieve 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%, or at least 87% reduction of Tau mRNA and/or protein levels in vitro and/or in vivo.

3. Nucleobases 135783-135929 of SEQ ID NO: 1

In certain embodiments, antisense oligonucleotides are designed to target nucleobases 135783-135929 of SEQ ID NO: 1 (GENBANK Accession No. GENE135783.1 truncated from nucleotides 9240000 to 9381000). In certain embodiments, nucleobases 135783-135929 are a hotspot region. In certain embodiments, nucleobases 135783-135929 are targeted by antisense oligonucleotides. In certain embodiments, the antisense oligonucleotides are 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, 5-9-5 MOE gapmers, 5-7-6 MOE gapmers, or 5-8-5 MOE gapmers. In certain embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphorothioate internucleoside linkages. In certain embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphodiester internucleoside linkages. In certain embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphorothioate and phosphodiester internucleotide linkages (e.g., the antisense oligonucleotides have "mixed backbones").

In certain embodiments, nucleobases 135783-135929 are targeted by the following ISIS numbers: 424879, 424880, 548937, 613114-613119, 622096-622138, 623988-623996, 664511-664542, and 664661-664819.

In certain embodiments, nucleobases 135783-135929 are targeted by the following SEQ ID NOs: 56, 57, 248, 462-466, 1668-1686, 2025-2048, 2301-2309, 2331-2443, and 2478-2483.

In certain embodiments, antisense oligonucleotides targeting nucleobases 135783-135929 achieve at least 12%, at least 13%, at least 14%, at least 15%, at least 16%, at least 17%, at least 18%, at least 19%, 20%, at least 21%, at least 22%, at least 23%, at least 24%, at least 25%, at least 26%, at least 27%, at least 28%, at least 29%, 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%, or at least 93% reduction of Tau mRNA and/or protein levels in vitro and/or in vivo.

4. Nucleobases 135783-135914 of SEQ ID NO: 1

In certain embodiments, antisense oligonucleotides are designed to target nucleobases 135783-135914 of SEQ ID NO: 1 (GENBANK Accession No. GENE135783.1 truncated from nucleotides 9240000 to 9381000). In certain embodiments, nucleobases 135783-135914 are a hotspot region. In certain embodiments, nucleobases 135783-135914 are targeted by antisense oligonucleotides. In certain embodiments, the antisense oligonucleotides are 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, 5-9-5 MOE gapmers, 5-7-6 MOE gapmers, or 5-8-5 MOE gapmers. In certain embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphorothioate internucleoside linkages. In certain embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphodiester internucleoside linkages. In certain embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphorothioate and phosphodiester internucleotide linkages (e.g., the antisense oligonucleotides have “mixed backbones”).

In certain embodiments, nucleobases 135783-135914 are targeted by the following ISIS numbers: 424879, 424880, 548937, 613114-613119, 622096-622133, 623988-623996, 664511-664542, 664661-664819.

In certain embodiments, nucleobases 135783-135914 are targeted by the following SEQ ID NOs: 56, 57, 248, 462-466, 1668-1681, 2025-2048, 2301-2309, 2331-2443, and 2478-2483.

In certain embodiments, nucleobases 135783-135914 are targeted by the following ISIS numbers: 424879, 424880, 548937, 613114-613119, 622096- 622133, and 623988- 623996.

In certain embodiments, nucleobases 135783-135914 are targeted by the following SEQ ID NOs: 56, 57, 248, 462-466, 1668-1681, 2025-2048, and 2301-2309.

In certain embodiments, antisense oligonucleotides targeting nucleobases 135783-135914 achieve at least 12%, at least 13%, at least 14%, at least 15%, at least 16%, at least 17%, at least 18%, at least 19%, 20%, at least 21%, at least 22%, at least 23%, at least 24%, at least 25%, at least 26%, at least 27%, at least 28%, at least 29%, 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%, or at least 93% reduction of Tau mRNA and/or protein levels in vitro and/or in vivo.

5 **EXAMPLES**

Non-limiting disclosure

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.

10

Example 1: Antisense inhibition of human Tau in HepG2 cells by MOE gapmers

Antisense oligonucleotides were designed targeting a tau nucleic acid and were tested for their effects on tau mRNA in vitro. Cultured HepG2 cells were transfected using Lipofectin reagent with 100 nM antisense oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and tau mRNA levels were measured by quantitative real-time PCR. Human primer probe set
15 RTS3104 (forward sequence AAGATTGGGTCCCTGGACAAT, designated herein as SEQ ID NO: 10; reverse sequence AGCTTGTGGGTTTCAATCTTTTATT, designated herein as SEQ ID NO: 11; probe sequence CACCCACGTCCCTGGCGGA, designated herein as SEQ ID NO: 12) was used to measure mRNA levels. Tau mRNA levels were adjusted according to total RNA content, as measured by
20 RIBOGREEN®. Results are presented as percent inhibition of tau, relative to untreated control cells.

The newly designed 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 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
25 2'-MOE modification. The internucleoside linkages throughout each gapmer are phosphorothioate linkages. All cytosine residues throughout each gapmer are 5-methylcytosines. "Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. "Stop site" indicates the 3'-most nucleoside to which the gapmer is targeted human gene sequence. Each gapmer listed in Table 1 below is targeted to either the human tau genomic sequence, designated herein as SEQ ID NO: 1 (GENBANK
30 Accession No. NT_010783.15 truncated from nucleotides 9240000 to 9381000) or to the human tau mRNA sequence, designated herein as SEQ ID NO: 2 (GENBANK Accession No. NM_001123066.3). 'n/a' indicates that the oligonucleotide does not target the gene sequence with 100% complementarity. The

sequences listed in Table 2 do not target either SEQ ID NO: 1 or 2 with 100% complementarity, but instead target SEQ ID NO: 3 (GENBANK Accession No. NM_016841.4, a variant mRNA sequence which skips exons 3, 4, 6, 8, 10, and 12) or SEQ ID NO: 4 (GENBANK Accession No. NT_010783.14 truncated from nucleotides 2624000 to 2761000).

5

Table 1

Inhibition of Tau mRNA by 5-10-5 MOE gapmers targeting SEQ ID NOs: 1 and 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
424863	n/a	n/a	TTGTAGACTATTTGCACACT	59	2240	2259	20
433519	28769	28788	CACAGGCAGATGCGAACCCT	57	n/a	n/a	21
433520	47181	47200	TGGTGGAGACAAGACATTCT	57	n/a	n/a	22
433521	71387	71406	CCATCCCCTAATAGTTAGCA	29	n/a	n/a	23
433522	72861	72880	CATGAGGCTTGGGATCTGAA	49	n/a	n/a	24
433474	73879	73898	GTGATCTTCCATCACTTCGA	61	345	364	25
433523	73980	73999	GTCCACTAACCTTTCAGGCC	63	n/a	n/a	26
433518	83423	83442	AGCATCAGAGGTTTCAGAGC	46	501	520	27
424852	83437	83456	GTTGGAGTGCTCTTAGCATC	58	515	534	28
433513	85934	85953	GGCAGCCTGCTTGCCGGGAG	68	573	592	29
433524	87927	87946	GAGGATTTTCCTTGAGAGAG	53	n/a	n/a	30
433525	89950	89969	GTTCACTGACCTTGGGTCAC	38	n/a	n/a	31
433526	91248	91267	ATGATTTCTAGAGGTCATGC	61	n/a	n/a	32
433514	95121	95140	AGAGGAAATCCACAGGGAGG	43	1120	1139	33
433515	95372	95391	TTCAGAGGGCTCTGGAAGGT	58	1371	1390	34
433527	95790	95809	ACACCATGAGGGCACCCGTC	65	n/a	n/a	35
433528	98549	98568	ACCATGCGAGCTGATAAAAT	46	n/a	n/a	36
433516	101406	101425	AAGGTTTTAGCAGAGGAACG	50	1514	1533	37
433517	101507	101526	AGGAAGGTGGCTCTGGGCAC	73	1615	1634	38
433476	103087	103106	CCAGAGCTGGGTGGTGTCTT	60	n/a	n/a	39
433477	108040	108059	GGTGGAGTACGGACCACTGC	71	2006	2025	40
433478	108054	108073	AAGACGGCGACTTGGGTGGA	65	2020	2039	41
424857	108148	108167	TGGTGCTTCAGGTTCTCAGT	54	2114	2133	42
433529	121819	121838	TTATCTGCACCTTTGGTAGC	29	n/a	n/a	43
424859	121828	121847	TCTTATTAATTATCTGCACC	50	2149	2168	44
424860	121838	121857	AGATCCAGCTTCTTATTAAT	36	2159	2178	45
424861	121846	121865	CGTTGCTAAGATCCAGCTTC	48	2167	2186	46
424862	121865	121884	GAGCCACACTTGGACTGGAC	79	2186	2205	47
433530	122497	122516	GGTGGCGCAGGCTAAGCATA	52	n/a	n/a	48
424864	125798	125817	GAGCCACACTTGGAGGTCAC	63	2279	2298	49
433531	125834	125853	ACAGGGCTACCTGGTTTATG	53	n/a	n/a	50
424866	130141	130160	ATTTTACTTCCACCTGGCCA	70	2329	2348	51

433479	130188	130207	GGACCCAATCTTCGACTGGA	70	2376	2395	52
424926	135467	135486	GTGGGTTTCAATCTGCAAGA	39	n/a	n/a	53
424869	135475	135494	GTCAGCTTGTGGGTTTCAAT	74	2438	2457	54
433480	135673	135692	GATCACAAACCTGCTTGGC	60	2636	2655	55
424879	135848	135867	TGATTTTGAAGTCCCGAGCC	64	2811	2830	56
424880	135853	135872	ATCACTGATTTTGAAGTCCC	54	2816	2835	57
433481	136033	136052	CAGAAGCAGCTTTCAGAGCC	38	2996	3015	58
433482	136118	136137	AAATCCTTTGTTGCTGCCAC	37	3081	3100	59
424882	136425	136444	CCCACAGGCTGCCCTGCAGA	57	3388	3407	60
433483	136491	136510	GGAGGTCATCCACGAAGTGC	67	3454	3473	61
433484	136577	136596	GGAAGCCCCTCAACTCAGGC	28	3540	3559	62
433485	136655	136674	GGTCTGCAAAGTGCCAAAA	49	3618	3637	63
424883	136675	136694	TGGTTAGCCCTAAAGTCCCA	54	3638	3657	64
433486	136686	136705	ACAAAGAGAAGTGGTTAGCC	39	3649	3668	65
424884	136703	136722	AAGAGGCACAAGTCCTTACA	40	3666	3685	66
433487	136748	136767	CAGAGATGCCAGTGGCCCAG	70	3711	3730	67
433488	137083	137102	GGAACCGAATCAGATCATGA	54	4046	4065	68
433489	137387	137406	TGGAGGGCTGATACTATGCA	45	4350	4369	69
433490	137430	137449	AAAAGAACCATTTCGAAGGG	41	4393	4412	70
433491	137540	137559	ATCCAACTACAACCTCAACAG	17	4503	4522	71
424894	137579	137598	ATCATAGTCACTCTGGTGAA	56	4542	4561	72
433492	137694	137713	GCCACACGAGTCCCAGTGTG	45	4657	4676	73
433493	137731	137750	AAAACCTTGGGAGGCCCCAGC	50	4694	4713	74
433494	138173	138192	GATCCAGGACAGGCAATTCA	58	5136	5155	75
433495	138205	138224	TCCTCAGGCAGGCAGCTTGG	49	5168	5187	76
433496	138303	138322	TTCTCATGGCAGCAGATGGA	51	5266	5285	77
433497	138338	138357	TTAGGCAGCAATGTTTTGCA	18	5301	5320	78
433498	138503	138522	AGAGTTCTGGGCCCAGAGAC	73	5466	5485	79
433499	138675	138694	AGGAAGAGGAACCGAGGTGC	59	5638	5657	80
433500	138774	138793	TCTTAGGCTGGCCCCAAGAG	36	5737	5756	81
433501	138812	138831	TCAATTTATCTGCCAGCACT	28	5775	5794	82
433502	138845	138864	TCCTCATTTAAGATCACAAAG	36	5808	5827	83
433503	138983	139002	ATGGAAGTATTGATAAAGTG	47	5946	5965	84
433504	139003	139022	CACCACTGAAGTCAATTTAA	23	5966	5985	85
433505	139112	139131	AGTTTAAGTGCTGCACCCCA	52	6075	6094	86
433506	139137	139156	GAAATCATGAAAAGGGTTAC	25	6100	6119	87
433507	139154	139173	CTCTAGCAAATGTGGTTGAA	42	6117	6136	88
433508	139229	139248	AGCCAGCTGCCTGGGAAAGC	70	6192	6211	89
433509	139359	139378	TAGAGGGAAGGATGCCAAGG	56	6322	6341	90
433510	139406	139425	GTGTGTCTGGAGCCAGTGTG	49	6369	6388	91
424910	139675	139694	GAAATCATGGGACTTGCAAG	52	6638	6657	92
433512	139729	139748	AAAGCTAAGCTAAGATGATT	31	6692	6711	93
424913	139797	139816	TTACAGCAACAGTCAGTGTA	42	6760	6779	94

Table 2

Inhibition of Tau mRNA by 5-10-5 MOE gapmers targeting SEQ ID NOs: 3 and 4

ISIS NO	Target SEQ ID NO	Target Start Site	Sequence	% inhibition	SEQ ID NO
424917	3	968	TTGTAGACTATTTGCACCTT	51	95
433475	3	443	TCTTCAGCTTTCAGGCCAGC	68	96
433511	4	135519	AGAAGTTTTATGAAGCCGCA	13	97

5 Example 2: Dose-dependent antisense inhibition of human tau in HepG2 cells by 5-10-5 MOE gapmers

Gapmers from studies described above exhibiting significant *in vitro* inhibition of Tau mRNA were selected and tested at various doses in HepG2 cells. Cells were plated at a density of 10,000 cells per well and transfected using Lipofectin reagent with 12.5 nM, 25.0 nM, 50.0 nM, 100.0 nM, or 200.0 nM concentrations of antisense oligonucleotide, as specified in the Table below. After a treatment period of approximately 16 hours, RNA was isolated from the cells and Tau mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3104 was used to measure mRNA levels. Tau mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of tau, relative to untreated control cells. Tau mRNA levels were significantly reduced in a dose-dependent manner in antisense oligonucleotide treated cells.

Table 3

ISIS No	12.5 nM	25.0 nM	50.0 nM	100.0 nM	200.0 nM
424862	17	24	41	64	84
424866	14	25	47	63	84
433498	27	42	61	79	82
433508	25	31	53	66	83
433517	25	34	57	72	78
433487	18	30	38	60	76
433477	23	31	51	71	80
433475	18	33	57	71	85
433513	24	30	50	71	77
433483	23	28	41	58	74
433527	19	32	46	60	77

Example 3: Antisense inhibition of human Tau in SH-SY5Y cells by 5-10-5 MOE gapmers

Additional antisense oligonucleotides were designed targeting a Tau nucleic acid and were tested for their effects on Tau mRNA in vitro. 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. Cultured SH-SY5Y cells were transfected using electroporation with 7,000 nM antisense oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and Tau mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3104 was used to measure mRNA levels. Tau mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of Tau, relative to untreated control cells.

The newly designed 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 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'-MOE modification. The internucleoside linkages throughout each gapmer are phosphorothioate linkages. All cytosine residues throughout each gapmer are 5-methylecytosines. "Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. "Stop site" indicates the 3'-most nucleoside to which the gapmer is targeted human gene sequence. Each gapmer listed in the Tables below is targeted to either the human Tau genomic sequence, designated herein as SEQ ID NO: 1 (GENBANK Accession No. NT_010783.15 truncated from nucleotides 9240000 to 9381000) or to the human Tau mRNA sequence, designated herein as SEQ ID NO: 2 (GENBANK Accession No. NM_001123066.3). 'n/a' indicates that the antisense oligonucleotide does not target that particular gene sequence with 100% complementarity.

Table 4

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
548786	73867	73886	CACTTCGAACTCCTGGCGGG	73	333	352	98
548787	73869	73888	ATCACTTCGAACTCCTGGCG	64	335	354	99
548788	73871	73890	CCATCACTTCGAACTCCTGG	78	337	356	100
548789	73873	73892	TTCCATCACTTCGAACTCCT	49	339	358	101
548790	73875	73894	TCTTCCATCACTTCGAACTC	33	341	360	102
548791	73877	73896	GATCTTCCATCACTTCGAAC	54	343	362	103
433474	73879	73898	GTGATCTTCCATCACTTCGA	86	345	364	25
548792	73906	73925	CCTGTCCCCCAACCCGTACG	38	372	391	104

548793	73908	73927	TTCCTGTCCCCCAACCCGTA	58	374	393	105
548794	73910	73929	CTTTCCTGTCCCCCAACCCG	55	376	395	106
548795	73912	73931	ATCTTTCCTGTCCCCCAACC	14	378	397	107
548796	73914	73933	TGATCTTTCCTGTCCCCCAA	59	380	399	108
548797	73916	73935	CCTGATCTTTCCTGTCCCC	67	382	401	109
548798	73918	73937	CCCCTGATCTTTCCTGTCCC	67	384	403	110
548799	73920	73939	CCCCCTGATCTTTCCTGTC	33	386	405	111
548800	73922	73941	AGCCCCCTGATCTTTCCTG	45	388	407	112
548801	73924	73943	GTAGCCCCCTGATCTTTC	62	390	409	113
548802	73926	73945	GTGTAGCCCCCTGATCTTT	42	392	411	114
548803	73928	73947	TGGTGTAGCCCCCTGATCT	58	394	413	115
548804	73930	73949	CATGGTGTAGCCCCCTGAT	62	396	415	116
548805	73932	73951	TGCATGGTGTAGCCCCCTG	82	398	417	117
548806	73934	73953	GGTGCATGGTGTAGCCCCC	79	400	419	118
548807	73936	73955	TTGGTGCATGGTGTAGCCCC	58	402	421	119
548808	73938	73957	TCTTGGTGCATGGTGTAGCC	60	404	423	120
548809	73940	73959	GGTCTTGGTGCATGGTGTAG	67	406	425	121
548810	73945	73964	CTCTTGGTCTTGGTGCATGG	61	411	430	122
548811	73958	73977	CGTCCGTGTCACCCTCTTGG	73	424	443	123
548812	98559	98578	GCTTTTACTGACCATGCGAG	68	1449	1468	124
548813	98561	98580	TTGCTTTTACTGACCATGCG	64	1451	1470	125
548814	98563	98582	CTTTGCTTTTACTGACCATG	40	1453	1472	126
548815	98565	98584	GTCTTTGCTTTTACTGACCA	60	1455	1474	127
548816	98567	98586	CCGTCTTTGCTTTTACTGAC	50	1457	1476	128
548817	98569	98588	TCCCGTCTTTGCTTTTACTG	46	1459	1478	129
548818	98571	98590	AGTCCCGTCTTTGCTTTTAC	41	1461	1480	130
548819	98573	98592	CCAGTCCCGTCTTTGCTTTT	37	1463	1482	131
548820	98577	98596	GCTTCCAGTCCCGTCTTTGC	43	1467	1486	132
548821	98579	98598	TCGCTTCCAGTCCCGTCTTT	35	1469	1488	133
548822	98581	98600	CATCGCTTCCAGTCCCGTCT	73	1471	1490	134
548823	98583	98602	GTCATCGCTTCCAGTCCCGT	63	1473	1492	135
548824	98585	98604	TTGTCATCGCTTCCAGTCCC	50	1475	1494	136
548825	98587	98606	TTTTGTCATCGCTTCCAGTC	46	1477	1496	137
548826	103023	103042	GGCCCTTCTGGCCTGGAGGG	64	1747	1766	138
548827	103025	103044	CTGGCCCTTCTGGCCTGGAG	29	1749	1768	139
548828	103027	103046	GCCTGGCCCTTCTGGCCTGG	40	1751	1770	140
548829	103029	103048	TGGCCTGGCCCTTCTGGCCT	12	1753	1772	141
548830	103031	103050	GTTGGCCTGGCCCTTCTGGC	53	1755	1774	142
548831	103052	103071	TTTTGCTGGAATCCTGGTGG	20	1776	1795	143
548832	103054	103073	GTTTTTGCTGGAATCCTGGT	29	1778	1797	144
548833	103056	103075	GGGTTTTTGCTGGAATCCTG	51	1780	1799	145
548834	103075	103094	GGTGTCTTTGGAGCGGGCGG	44	1799	1818	146
548835	103077	103096	GTGGTGTCTTTGGAGCGGGC	30	1801	1820	147

548836	103079	103098	GGGTGGTGTCTTTGGAGCGG	38	1803	1822	148
548837	103081	103100	CTGGGTGGTGTCTTTGGAGC	29	1805	1824	149
548838	103083	103102	AGCTGGGTGGTGTCTTTGGA	37	1807	1826	150
548839	103085	103104	AGAGCTGGGTGGTGTCTTTG	0	1809	1828	151
548840	107921	107940	ATCCCCTGATTTTGGAGGTT	27	1887	1906	152
548841	107923	107942	CGATCCCCTGATTTTGGAGG	65	1889	1908	153
548842	107925	107944	TGCGATCCCCTGATTTTGGGA	53	1891	1910	154
548843	107927	107946	GCTGCGATCCCCTGATTTTG	23	1893	1912	155
548844	107929	107948	CCGCTGCGATCCCCTGATTT	32	1895	1914	156
548845	107931	107950	AGCCGCTGCGATCCCCTGAT	51	1897	1916	157
548846	107933	107952	GTAGCCGCTGCGATCCCCTG	14	1899	1918	158
548847	107968	107987	CGGCTGCCGGGAGTGCCTGG	33	1934	1953	159
548848	107970	107989	AGCGGCTGCCGGGAGTGCCT	52	1936	1955	160
548849	107972	107991	GGAGCGGCTGCCGGGAGTGC	44	1938	1957	161
548850	108047	108066	CGACTTGGGTGGAGTACGGA	10	2013	2032	162
548851	108049	108068	GGCGACTTGGGTGGAGTACG	29	2015	2034	163
548852	108051	108070	ACGGCGACTTGGGTGGAGTA	39	2017	2036	164
548853	108053	108072	AGACGGCGACTTGGGTGGAG	6	2019	2038	165
548854	108055	108074	GAAGACGGCGACTTGGGTGG	0	2021	2040	166
548855	108057	108076	CGGAAGACGGCGACTTGGGT	40	2023	2042	167
548856	108059	108078	GGCGGAAGACGGCGACTTGG	38	2025	2044	168
548857	108061	108080	TTGGCGGAAGACGGCGACTT	41	2027	2046	169
548858	108063	108082	TCTTGGCGGAAGACGGCGAC	35	2029	2048	170
548859	108065	108084	GCTCTTGGCGGAAGACGGCG	54	2031	2050	171
548860	108067	108086	CGGCTCTTGGCGGAAGACGG	58	2033	2052	172
548861	108069	108088	GGCGGCTCTTGGCGGAAGAC	55	2035	2054	173
433498	138503	138522	AGAGTTCTGGGCCAGAGAC	53	5466	5485	79

Table 5

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
548885	n/a	n/a	GGGAGATTCTTTCAGGCCAG	0	444	463	174
548893	n/a	n/a	GAGCTTTGAGTTGAGGGACC	0	1432	1451	175
548894	n/a	n/a	GACCATGCGAGCTTTGAGTT	13	1440	1459	176
548895	n/a	n/a	TACTGACCATGCGAGCTTTG	33	1444	1463	177
548881	6183	6202	ATAGTCGACAGAGGCGAGGA	43	283	302	178
548882	73840	73859	CATCCTGGTTCAAAGTTCAC	30	306	325	179
548883	73846	73865	CTCAGCCATCCTGGTTCAAA	39	312	331	180
548884	73847	73866	GCTCAGCCATCCTGGTTCAA	53	313	332	181
548886	83401	83420	GGTTCCTCAGATCCGTCCTC	53	479	498	182
548887	83438	83457	TGTTGGAGTGCTCTTAGCAT	33	516	535	183

548888	85939	85958	TGCGCGGCAGCCTGCTTGCC	32	578	597	184
548889	94699	94718	ACCACCTTACCACTTTCAGG	35	698	717	185
548890	94775	94794	GGGAGCCCCAGGCATGCCGG	45	774	793	186
548891	95125	95144	TTGGAGAGGAAATCCACAGG	13	1124	1143	187
548892	95131	95150	GAAACTTTGGAGAGGAAATC	0	1130	1149	188
548896	98557	98576	TTTTACTGACCATGCGAGCT	40	1447	1466	189
548897	101425	101444	AAGGCAAGGCCTATTTTCA	34	1533	1552	190
548898	101469	101488	TGGATCAGAGGGTCTGAGCT	40	1577	1596	191
548899	101501	101520	GTGGCTCTGGGCACACAGCA	63	1609	1628	192
548900	108037	108056	GGAGTACGGACCACTGCCAC	37	2003	2022	193
433477	108040	108059	GGTGGAGTACGGACCACTGC	21	2006	2025	40
548862	108071	108090	CAGGCGGCTCTTGGCGGAAG	24	2037	2056	194
548863	108073	108092	TGCAGGCGGCTCTTGGCGGA	34	2039	2058	195
548864	108075	108094	TCTGCAGGCGGCTCTTGGCG	40	2041	2060	196
548865	108129	108148	TGGAGCCGATCTTGGACTTG	23	2095	2114	197
548866	108131	108150	AGTGGAGCCGATCTTGGACT	4	2097	2116	198
548901	108134	108153	CTCAGTGGAGCCGATCTTGG	28	2100	2119	199
548902	108136	108155	TTCTCAGTGGAGCCGATCTT	9	2102	2121	200
548903	108155	108174	TCCCGGCTGGTGCTTCAGGT	33	2121	2140	201
548904	121675	121694	TTTCGGACTTGGCAGAGGCA	50	n/a	n/a	202
548905	121728	121747	GAGTGACATGCGCCACCCTG	65	n/a	n/a	203
548906	121736	121755	CTTTCGATGAGTGACATGCG	19	n/a	n/a	204
548907	121794	121813	AAAAGGATGAGTGACACGCC	58	n/a	n/a	205
548908	121916	121935	GTGAAGGTACTCACACTGCC	34	n/a	n/a	206
548909	121917	121936	TGTGAAGGTACTCACACTGC	21	n/a	n/a	207
548910	121992	122011	CTATGCAGTGTCTCGCAAGT	39	n/a	n/a	208
548911	122001	122020	GGATTTATTCTATGCAGTGT	38	n/a	n/a	209
548912	122002	122021	AGGATTTATTCTATGCAGTG	37	n/a	n/a	210
548913	122015	122034	TGAGAGCCCAAGAAGGATTT	15	n/a	n/a	211
548914	122022	122041	CAGATCCTGAGAGCCCAAGA	33	n/a	n/a	212
548915	122025	122044	AGCCAGATCCTGAGAGCCCA	55	n/a	n/a	213
548916	122137	122156	GGACCCAGAAATGCTGGGAC	18	n/a	n/a	214
548917	125555	125574	AAATGTGTTGTCGAAATTCT	0	n/a	n/a	215
548918	125568	125587	AGTCAGGGTGGAAAAATGTG	0	n/a	n/a	216
548919	125578	125597	AGCACATCCTAGTCAGGGTG	39	n/a	n/a	217
548920	125587	125606	GCCATGAGGAGCACATCCTA	45	n/a	n/a	218
548921	125600	125619	GTGGTTCCCAGCTGCCATGA	38	n/a	n/a	219
548922	125603	125622	ACAGTGGTTCCCAGCTGCCA	38	n/a	n/a	220
548923	125619	125638	CCCAGGCCCTTATTGGACAG	19	n/a	n/a	221
548867	125778	125797	CTTGCTCAGGTCAACTGGTT	45	2259	2278	222
548925	125812	125831	GGATGTTGCCTAATGAGCCA	35	2293	2312	223
548926	130194	130213	GTCCAGGGACCCAATCTTCG	87	2382	2401	224
548927	130196	130215	TTGTCCAGGGACCCAATCTT	48	2384	2403	225

548928	135478	135497	AAGGTCAGCTTGTGGGTTTC	52	2441	2460	226
548868	135518	135537	CTCCGCCCGTGGTCTGTCT	37	2481	2500	227
548869	135520	135539	ATCTCCGCCCGTGGTCTGT	25	2483	2502	228
548870	135522	135541	CGATCTCCGCCCGTGGTCT	48	2485	2504	229
548871	135524	135543	CACGATCTCCGCCCGTGGT	38	2487	2506	230
548872	135526	135545	TACACGATCTCCGCCCGTG	33	2489	2508	231
548873	135528	135547	TGTACACGATCTCCGCCCG	22	2491	2510	232
548874	135530	135549	CTTGTACACGATCTCCGCC	38	2493	2512	233
548875	135532	135551	GACTTGTACACGATCTCCGC	13	2495	2514	234
548876	135534	135553	GCGACTTGTACACGATCTCC	40	2497	2516	235
548877	135536	135555	TGGCGACTTGTACACGATCT	33	2499	2518	236
548878	135538	135557	ACTGGCGACTTGTACACGAT	25	2501	2520	237
548879	135540	135559	CCACTGGCGACTTGTACACG	19	2503	2522	238
548929	135546	135565	CAGACACCACTGGCGACTTG	33	2509	2528	239
548930	135593	135612	GCTGCCGGTGGAGGAGACAT	29	2556	2575	240
548931	135594	135613	TGCTGCCGGTGGAGGAGACA	19	2557	2576	241
548932	135600	135619	TGTCGATGCTGCCGGTGGAG	20	2563	2582	242
548933	135601	135620	ATGTCGATGCTGCCGGTGGGA	20	2564	2583	243
548934	135610	135629	GAGTCTACCATGTCGATGCT	23	2573	2592	244
548880	135654	135673	CCAGGGAGGCAGACACCTCG	28	2617	2636	245
548935	135662	135681	CTGCTTGGCCAGGGAGGCAG	14	2625	2644	246
548936	135674	135693	TGATCACAACCCTGCTTGG	25	2637	2656	247
548937	135786	135805	CCGAAGTGCAGAGAGCAGCT	66	2749	2768	248
433498	138503	138522	AGAGTTCTGGGCCAGAGAC	34	5466	5485	79

Example 4: Dose-dependent antisense inhibition of human Tau in SH-SY5Y cells by 5-10-5 MOE gapmers

Gapmers from studies described above exhibiting significant *in vitro* inhibition of Tau mRNA were selected and tested at various doses in SH-SY-5Y cells. Cells were plated at a density of 20,000 cells per well and transfected using electroporation with 1.25 μ M, 2.50 μ M, 5.00 μ M, 10.00 μ M, and 20.00 μ M concentrations of antisense oligonucleotide, as specified in the Table below. After a treatment period of approximately 16 hours, RNA was isolated from the cells and Tau mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3104 was used to measure mRNA levels. Tau mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN[®]. Results are presented as percent inhibition of Tau, relative to untreated control cells. Tau mRNA levels were significantly reduced in a dose-dependent manner in antisense oligonucleotide treated cells.

Table 6

ISIS No	1.25 μ M	2.50 μ M	5.00 μ M	10.00 μ M	20.00 μ M
433474	29	54	74	83	88
433477	0	0	11	33	59
433498	0	10	30	53	71
548786	9	29	51	66	82
548787	19	27	61	85	87
548788	31	31	54	72	94
548805	19	48	62	81	96
548806	25	50	75	80	95
548811	21	42	60	74	94
548812	47	39	64	77	91
548822	0	32	52	62	91
548899	19	50	69	87	93
548905	11	32	57	80	95
548907	14	28	44	80	91
548937	24	43	66	82	91

Example 5: Antisense inhibition of human Tau in SH-SY5Y cells by 5-10-5 MOE gapmers

Additional antisense oligonucleotides were designed targeting a Tau nucleic acid and were tested for their effects on Tau mRNA in vitro. Cultured SH-SY5Y cells were plated at a density of 20,000 cells per well and were transfected using electroporation with 6,000 nM antisense oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and Tau mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3104 was used to measure mRNA levels. Tau mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of tau, relative to untreated control cells.

The newly designed 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'-MOE modification. The internucleoside linkages throughout each gapmer are phosphorothioate linkages. All cytosine residues throughout each gapmer are 5-methylcytosines. "Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. "Stop site" indicates the 3'-most nucleoside to which the gapmer is targeted human gene sequence. Each gapmer listed in the Tables below is targeted to the human tau genomic sequence, designated herein as SEQ ID NO: 1 (GENBANK Accession No. NT_010783.15 truncated from nucleotides 9240000 to 9381000).

Table 7

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	SEQ ID NO
433474	73879	73898	GTGATCTTCCATCACTTCGA	63	25
559166	26760	26779	TGCTTACACACCACACACAC	0	249
	26944	26963			
559167	26761	26780	ATGCTTACACACCACACACA	4	250
	26945	26964			
559168	26762	26781	CATGCTTACACACCACACAC	0	251
	26946	26965			
559169	81022	81041	TACAGATATATGATTGGATG	0	252
	81125	81144			
559170	81023	81042	GTACAGATATATGATTGGAT	0	253
	81126	81145			
559171	81024	81043	TGTACAGATATATGATTGGA	0	254
	81127	81146			
559172	81025	81044	ATGTACAGATATATGATTGG	0	255
	81128	81147			
559173	81026	81045	TATGTACAGATATATGATTG	0	256
	81129	81148			
559174	81027	81046	TTATGTACAGATATATGATT	0	257
	81130	81149			
559175	81028	81047	ATTATGTACAGATATATGAT	0	258
	81131	81150			
559176	81029	81048	GATTATGTACAGATATATGA	0	259
	81132	81151			
559177	81030	81049	GGATTATGTACAGATATATG	0	260
	81133	81152			
559178	81031	81050	TGGATTATGTACAGATATAT	0	261
	81134	81153			
559179	81032	81051	ATGGATTATGTACAGATATA	0	262
	81135	81154			
559180	81033	81052	AATGGATTATGTACAGATAT	0	263
	81136	81155			
559181	81034	81053	GAATGGATTATGTACAGATA	0	264
	81137	81156			
559182	81035	81054	AGAATGGATTATGTACAGAT	0	265
	81138	81157			
559183	81036	81055	AAGAATGGATTATGTACAGA	0	266
	81139	81158			
559184	81037	81056	GAAGAATGGATTATGTACAG	0	267
	81140	81159			
559185	81038	81057	GGAAGAATGGATTATGTACA	0	268

	81141	81160			
559186	81039	81058	GGGAAGAATGGATTATGTAC	0	269
	81142	81161			
559187	81040	81059	AGGGAAGAATGGATTATGTA	0	270
	81143	81162			
559188	81041	81060	GAGGGAAGAATGGATTATGT	0	271
	81144	81163			
559189	81042	81061	CGAGGGAAGAATGGATTATG	0	272
	81145	81164			
559190	81043	81062	CCGAGGGAAGAATGGATTAT	33	273
	81146	81165			
559191	81044	81063	ACCGAGGGAAGAATGGATTA	12	274
	81147	81166			
559192	81045	81064	AACCGAGGGAAGAATGGATT	1	275
	81148	81167			
559193	81046	81065	GAACCGAGGGAAGAATGGAT	0	276
	81149	81168			
559194	81047	81066	TGAACCGAGGGAAGAATGGA	0	277
	81150	81169			
559195	81048	81067	ATGAACCGAGGGAAGAATGG	0	278
	81151	81170			
559196	81049	81068	GATGAACCGAGGGAAGAATG	0	279
	81152	81171			
559197	81050	81069	GGATGAACCGAGGGAAGAAT	0	280
	81153	81172			
559198	81051	81070	TGGATGAACCGAGGGAAGAA	0	281
	81154	81173			
559199	81052	81071	ATGGATGAACCGAGGGAAGA	0	282
	81155	81174			
559200	81053	81072	GATGGATGAACCGAGGGAAG	0	283
	81156	81175			
559201	81054	81073	GGATGGATGAACCGAGGGAA	1	284
	81157	81176			
559202	81055	81074	TGGATGGATGAACCGAGGGA	0	285
	81158	81177			
559203	81056	81075	ATGGATGGATGAACCGAGGG	0	286
	81159	81178			
559204	81057	81076	GATGGATGGATGAACCGAGG	0	287
	81160	81179			
559205	81058	81077	GGATGGATGGATGAACCGAG	0	288
	81161	81180			
559206	81096	81115	AAGGATGAAGGAAGGGATGG	0	289
	81199	81218			

559207	81097	81116	GAAGGATGAAGGAAGGGATG	0	290
	81200	81219			
559208	81098	81117	GGAAGGATGAAGGAAGGGAT	0	291
	81201	81220			
559209	81100	81119	TAGGAAGGATGAAGGAAGGG	0	292
	81203	81222			
559210	81101	81120	ATAGGAAGGATGAAGGAAGG	0	293
	81204	81223			
559211	81102	81121	GATAGGAAGGATGAAGGAAG	0	294
	81205	81224			
559212	81103	81122	TGATAGGAAGGATGAAGGAA	0	295
	81206	81225			
559213	81104	81123	ATGATAGGAAGGATGAAGGA	0	296
	81207	81226			
559214	81105	81124	GATGATAGGAAGGATGAAGG	0	297
	81208	81227			
559215	81106	81125	GGATGATAGGAAGGATGAAG	0	298
	81209	81228			
559216	81107	81126	TGGATGATAGGAAGGATGAA	0	299
	81210	81229			
559217	81108	81127	ATGGATGATAGGAAGGATGA	0	300
	81211	81230			
559218	81109	81128	GATGGATGATAGGAAGGATG	0	301
	81212	81231			
559219	81110	81129	GGATGGATGATAGGAAGGAT	0	302
	81213	81232			
559220	81111	81130	TGGATGGATGATAGGAAGGA	0	303
	81214	81233			
559221	81112	81131	TTGGATGGATGATAGGAAGG	0	304
	81215	81234			
559222	81113	81132	ATTGGATGGATGATAGGAAG	0	305
	81216	81235			
559223	81114	81133	GATTGGATGGATGATAGGAA	0	306
	81217	81236			
559224	81115	81134	TGATTGGATGGATGATAGGA	0	307
	81218	81237			
559225	81116	81135	ATGATTGGATGGATGATAGG	0	308
	81219	81238			
559226	81117	81136	TATGATTGGATGGATGATAG	0	309
	81220	81239			
559227	80890	80909	AGATATGGGTGGATGGATGG	0	310
	81472	81491			
559228	80891	80910	AAGATATGGGTGGATGGATG	0	311

	81473	81492			
559229	80892	80911	GAAGATATGGGTGGATGGAT	0	312
	81474	81493			
559230	98881	98900	ACACACCTTCATTTACTGTC	79	313
	98918	98937			
559231	98882	98901	AACACACCTTCATTTACTGT	56	314
	98919	98938			
559232	98883	98902	AAACACACCTTCATTTACTG	59	315
	98920	98939			
559233	98884	98903	CAAACACACCTTCATTTACT	51	316
	98921	98940			
559234	98885	98904	TCAAACACACCTTCATTTAC	25	317
	98922	98941			
559235	98887	98906	TTTCAAACACACCTTCATTT	25	318
	98924	98943			
559236	98888	98907	TTTTCAAACACACCTTCATT	14	319
	98925	98944			
559237	98889	98908	GTTTTCAAACACACCTTCAT	42	320
	98926	98945			
559238	98890	98909	GGTTTTCAAACACACCTTCA	79	321
	98927	98946			
559239	98891	98910	TGGTTTTCAAACACACCTTC	87	322
	98928	98947			
559240	111795	111814	GAAAACAGAGAAAAGCACAA	12	323
	111819	111838			
559241	119594	119613	AGAAGTGATATCATATCCTA	63	324
	119905	119924			
559242	119595	119614	AAGAAGTGATATCATATCCT	74	325
	119906	119925			

Example 6: Dose-dependent antisense inhibition of human tau in SH-SY5Y cells by 5-10-5 MOE gapmers

- 5 Gapmers from studies described above exhibiting significant *in vitro* inhibition of Tau mRNA were selected and tested at various doses in SH-SY-5Y cells. Cells were plated at a density of 20,000 cells per well and transfected using electroporation with 0.625 μ M, 1.25 μ M, 2.500 μ M, 5.00 μ M, 10.00 μ M, and 20.00 μ M concentrations of antisense oligonucleotide, as specified in the Table below. After a treatment period of approximately 16 hours, RNA was isolated from the
- 10 cells and Tau mRNA levels were measured by quantitative real-time PCR. Human primer probe set

RTS3104 was used to measure mRNA levels. Tau mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of Tau, relative to untreated control cells. Tau mRNA levels were significantly reduced in a dose-dependent manner in antisense oligonucleotide treated cells.

5

Table 8

ISIS No	0.625 μM	1.25 μM	2.50 μM	5.00 μM	10.00 μM	20.00 μM
433474	17	39	53	73	81	88
559230	30	50	67	81	92	94
559231	0	16	26	44	63	83
559232	10	12	23	30	62	79
559233	5	10	21	38	62	81
559237	0	16	27	31	58	88
559238	25	18	72	77	86	86
559239	26	47	64	80	88	93
559241	0	18	34	61	74	95
559242	13	20	23	47	71	83

Example 7: Antisense inhibition of human Tau in SH-SY5Y cells by MOE gapmers with Phosphorothioate and Phosphodiester Internucleoside Linkages

Antisense oligonucleotides were designed targeting a tau nucleic acid and were tested for their effects on tau mRNA in vitro. 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. Cultured SH-SY5Y cells were transfected using electroporation with 8,000 nM antisense oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and tau mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3104 was used to measure mRNA levels. Tau mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of tau, relative to untreated control cells.

The newly designed 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'-MOE modification. The internucleoside linkages throughout each gapmer are either phosphorothioate linkages or phosphodiester linkages. All cytosine residues throughout each gapmer are 5-methylcytosines. The 'Chemistry' column describes the internucleoside linkages of each oligonucleotide. 's' indicates phosphorothioate linkage and 'o' indicates phosphodiester linkage. "Start site" indicates the 5'-most

nucleoside to which the gapmer is targeted in the human gene sequence. "Stop site" indicates the 3'-most nucleoside to which the gapmer is targeted human gene sequence.

Each gapmer listed in the Tables below is targeted to either the human Tau genomic sequence, designated herein as SEQ ID NO: 1 (GENBANK Accession No. NT_010783.15 truncated from nucleotides 9240000 to 9381000), human Tau mRNA sequences, designated herein as SEQ ID NO: 2 (GENBANK Accession No. NM_001123066.3) or SEQ ID NO: 3 (GENBANK Accession No. NM_016841.4). Several oligonucleotides, presented in Tables 10, 12, and 16, target variant mRNA sequences, designated herein as SEQ ID NO: 5 (GENBANK Accession No. DR002467.1), SEQ ID NO: 6 (GENBANK Accession No. NM_001203251.1) or SEQ ID NO: 7 (GENBANK Accession No. NM_016835.4). The oligonucleotides are presented in the various tables according to the main gene sequence that they target with 100% complementarity. 'n/a' indicates that the antisense oligonucleotide does not target that particular gene sequence with 100% complementarity.

Table 9
Inhibition of Tau mRNA by 5-10-5 MOE gapmers with phosphorothioate and phosphodiester internucleoside linkages targeting SEQ ID NOs: 1 and 3

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	SEQ ID NO: 3 Start Site	SEQ ID NO: 3 Stop Site	Linkage chemistry	SEQ ID NO
433475	n/a	n/a	TCTTCAGCTTTCAGGCCAGC	41	443	462	ssssssssssssssssssss	96
613242	n/a	n/a	CTTCAGCTTTCAGGCCAGCG	54	442	461	soooooossssssssooss	326
613243	n/a	n/a	TCTTCAGCTTTCAGGCCAGC	43	443	462	soooooossssssssooss	96
613244	n/a	n/a	CCATGCGAGCTTGGGTCACG	64	511	530	soooooossssssssooss	327
613245	n/a	n/a	CAGCCCCCTTGGCTTTTTTG	30	565	584	soooooossssssssooss	328
613247	n/a	n/a	TTGCACCTTCCCGCCTCCCG	53	957	976	soooooossssssssooss	329
613240	5897	5916	TGCCGCTCGGCCGTCCGGCG	9	n/a	n/a	soooooossssssssooss	330
613249	6292	6311	GCCCGGCGCACGAAGCCCCA	80	n/a	n/a	soooooossssssssooss	331
613250	7099	7118	AGAAAGAAATCCGCCCGAG	45	n/a	n/a	soooooossssssssooss	332
613251	11709	11728	ATAATGGAATACTTATTGCA	54	n/a	n/a	soooooossssssssooss	333
613252	11819	11838	GCAGGAGCATGGCACCTGGA	79	n/a	n/a	soooooossssssssooss	334
613253	12081	12100	ACTCGCTGACATGGTGTTTG	87	n/a	n/a	soooooossssssssooss	335
613254	13386	13405	GATGACTCCACAATGTAAAC	75	n/a	n/a	soooooossssssssooss	336
613255	16760	16779	CCTATAGGATTATCCAGGAA	88	n/a	n/a	soooooossssssssooss	337
613256	16987	17006	CATTTCTCATCAGCCATCGA	81	n/a	n/a	soooooossssssssooss	338
613257	17428	17447	ACCAAAGACTTCAGATCAGC	88	n/a	n/a	soooooossssssssooss	339
613412	73879	73898	GTGATCTTCCATCACTTCGA	82	345	364	soooooossssssssooss	25
613246	103087	103106	CCAGAGCTGGGTGGTGTCTT	51	686	705	soooooossssssssooss	39
613181	138046	138065	AGCTTCTGGGAGCTGCAGAT	80	3737	3756	soooooossssssssooss	340
613182	138083	138102	AGAGGAACCCAGTCTGAGGG	49	3774	3793	soooooossssssssooss	341

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613183	138116	138135	AGGCTGCGCTGCCCCTCCAG	68	3807	3826	S0000SSSSSSSSSS00SS	342
613184	138149	138168	AATCCCTGCTGTGGTCCGAG	63	3840	3859	S0000SSSSSSSSSS00SS	343
613185	138182	138201	TCTAGAGCAGATCCAGGACA	53	3873	3892	S0000SSSSSSSSSS00SS	344
613186	138215	138234	AAGTCATCCTTCCTCAGGCA	63	3906	3925	S0000SSSSSSSSSS00SS	345
613187	138248	138267	CAAGGCTTTGGGAACAGTGT	78	3939	3958	S0000SSSSSSSSSS00SS	346
613188	138250	138269	GTCAAGGCTTTGGGAACAGT	84	3941	3960	S0000SSSSSSSSSS00SS	347
613189	138281	138300	TTGTGCAAGGTCAGCGGGCT	75	3972	3991	S0000SSSSSSSSSS00SS	348
613190	138314	138333	CGGCTTCCCTTTTCTCATGG	75	4005	4024	S0000SSSSSSSSSS00SS	349
613191	138347	138366	TGAGTTTCTTTAGGCAGCAA	82	4038	4057	S0000SSSSSSSSSS00SS	350
613192	138380	138399	AACCAGAAGTGGCAGAATTG	47	4071	4090	S0000SSSSSSSSSS00SS	351
613193	138413	138432	CAAGTCCCTCAGGGTTGCCT	78	4104	4123	S0000SSSSSSSSSS00SS	352
613194	138454	138473	CGAAGCTGCCAGCCCCAGGG	70	4145	4164	S0000SSSSSSSSSS00SS	353
613195	138487	138506	AGACTTCCTTTCAGGTAAAG	77	4178	4197	S0000SSSSSSSSSS00SS	354
613196	138503	138522	AGAGTTCTGGGCCAGAGAC	58	4194	4213	S0000SSSSSSSSSS00SS	79
613197	138520	138539	AGGGAGGCTCTTGGTGGAGA	35	4211	4230	S0000SSSSSSSSSS00SS	355
613198	138553	138572	ACTTAGGAGAATTGCTGGGA	75	4244	4263	S0000SSSSSSSSSS00SS	356
613199	138586	138605	CCCACATTTCTTCTCCTTC	72	4277	4296	S0000SSSSSSSSSS00SS	357
613200	138636	138655	ACTGTTGGCAGTAATGAGGG	71	4327	4346	S0000SSSSSSSSSS00SS	358
613201	138674	138693	GGAAGAGGAACCGAGGTGCG	61	4365	4384	S0000SSSSSSSSSS00SS	359
613202	138707	138726	CATGGTGCTGAAGAGCAGGG	71	4398	4417	S0000SSSSSSSSSS00SS	360
613203	138740	138759	GGGAGATCCCAGAGCCTTCC	53	4431	4450	S0000SSSSSSSSSS00SS	361
613204	138773	138792	CTTAGGCTGGCCCCAAGAGC	64	4464	4483	S0000SSSSSSSSSS00SS	362
613205	138806	138825	TATCTGCCAGCACTGATCAC	56	4497	4516	S0000SSSSSSSSSS00SS	363
613206	138839	138858	TTTAAGATCACAAGCCAGCG	62	4530	4549	S0000SSSSSSSSSS00SS	364
613207	138872	138891	GAGGAGTGCCAGCCCTGGG	54	4563	4582	S0000SSSSSSSSSS00SS	365
613208	138905	138924	CTGGCTCTGCAGGTGGGAGA	44	4596	4615	S0000SSSSSSSSSS00SS	366
613209	138938	138957	TACAGTATATCCTATCTAGC	57	4629	4648	S0000SSSSSSSSSS00SS	367
613210	138971	138990	ATAAAGTGAGTCAGCAGCTT	71	4662	4681	S0000SSSSSSSSSS00SS	368
613211	139004	139023	TCACCACTGAAGTCAATTTA	72	4695	4714	S0000SSSSSSSSSS00SS	369
613212	139037	139056	AGCACAACAAGCAATAGCAA	80	4728	4747	S0000SSSSSSSSSS00SS	370
613213	139070	139089	ACTATCTTACACATTCCTCC	48	4761	4780	S0000SSSSSSSSSS00SS	371
613214	139103	139122	GCTGCACCCCAAGATCTCCC	79	4794	4813	S0000SSSSSSSSSS00SS	372
613215	139136	139155	AAATCATGAAAAGGGTTACG	61	4827	4846	S0000SSSSSSSSSS00SS	373
613216	139169	139188	GTGGCTGCTCCCTCCCTCTA	60	4860	4879	S0000SSSSSSSSSS00SS	374
613217	139188	139207	CCCAAGGGCCTCTAACTCCG	64	4879	4898	S0000SSSSSSSSSS00SS	375
613218	139202	139221	TGGAAAAGAGAAACCCCAAG	56	4893	4912	S0000SSSSSSSSSS00SS	376
613219	139229	139248	AGCCAGCTGCCTGGGAAAGC	63	4920	4939	S0000SSSSSSSSSS00SS	89
613220	139235	139254	TGAACTAGCCAGCTGCCTGG	46	4926	4945	S0000SSSSSSSSSS00SS	377
613221	139268	139287	TATTCCTACGCCTGCACCTG	54	4959	4978	S0000SSSSSSSSSS00SS	378
613222	139301	139320	AGAGGGCAGCAGGCCAAAGC	48	4992	5011	S0000SSSSSSSSSS00SS	379
613223	139337	139356	TTAGGGAGGCATGATTGTGG	55	5028	5047	S0000SSSSSSSSSS00SS	380
613224	139368	139387	CCAACGGCTTAGAGGGAAGG	61	5059	5078	S0000SSSSSSSSSS00SS	381
613225	139370	139389	TGCCAACGGCTTAGAGGGAA	65	5061	5080	S0000SSSSSSSSSS00SS	382

613226	139403	139422	TGTCTGGAGCCAGTGTGAGA	56	5094	5113	s0000ssssssssss00ss	383
613227	139436	139455	CGAGTGATCTCAGCTCCAAA	79	5127	5146	s0000ssssssssss00ss	384
613228	139502	139521	TGATCACCTCTGCCCTCGCC	72	5193	5212	s0000ssssssssss00ss	385
613229	139535	139554	TGAAGCTGCAGGTCTGTAGA	57	5226	5245	s0000ssssssssss00ss	386
613230	139568	139587	CTTTTCAAAGCTGAAGAGAA	57	5259	5278	s0000ssssssssss00ss	387
613231	139601	139620	AGGTGAGGCTCTAGGCCAGT	76	5292	5311	s0000ssssssssss00ss	388
613232	139636	139655	CAACATGGCAAACATCATGGG	76	5327	5346	s0000ssssssssss00ss	389
613233	139669	139688	ATGGGACTTGCAAGTGCCAG	83	5360	5379	s0000ssssssssss00ss	390
613234	139702	139721	CCTCCCCCACCCTCAGAAT	15	5393	5412	s0000ssssssssss00ss	391
613235	139735	139754	AGACAGAAAGCTAAGCTAAG	50	5426	5445	s0000ssssssssss00ss	392
613236	139768	139787	TTAAACACACAATACACTA	46	5459	5478	s0000ssssssssss00ss	393
613237	139801	139820	ACTTTTACAGCAACAGTCAG	54	5492	5511	s0000ssssssssss00ss	394
613238	139834	139853	TTAATCAGAGTAATAACTT	12	5525	5544	s0000ssssssssss00ss	395

Table 10

Inhibition of Tau mRNA by 5-10-5 MOE gapmers with phosphorothioate and phosphodiester internucleoside linkages targeting SEQ ID NOs: 5 and 6

5

ISIS NO	Target SEQ ID NO	Target Start Site	Sequence	% inhibition	Linkage chemistry	SEQ ID NO
613239	5	3	TGCCCTTCGCGGTCCCTTCG	2	s0000ssssssssss00ss	396
613241	5	424	CTGTCCCCCAAACCCGTACG	56	s0000ssssssssss00ss	397
613248	6	524	GCTTCCGCTGTTGGAGTGCT	62	s0000ssssssssss00ss	398

Table 11

Inhibition of Tau mRNA by 5-10-5 MOE gapmers with phosphorothioate and phosphodiester internucleoside linkages targeting SEQ ID NOs: 1 and 3

10

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	SEQ ID NO: 3 Start Site	SEQ ID NO: 3 Stop Site	Linkage chemistry	SEQ ID NO
433475	n/a	n/a	TCTTCAGCTTTCAGGCCAGC	17	443	462	ssssssssssssssssss	96
613027	5901	5920	GCCCTGCCGCTCGGCCGTCC	29	1	20	s0000ssssssssss00ss	399
613028	5934	5953	TTCTCCTCCGCCACTAGTG	22	34	53	s0000ssssssssss00ss	400
613029	5987	6006	GAACGCGAGCCTCCCCAGGG	1	87	106	s0000ssssssssss00ss	401
613030	6020	6039	GAGGCCGCGGGCGGCGCAG	2	120	139	s0000ssssssssss00ss	402
613031	6053	6072	GAGGGCGCGCGCCGGCGAAG	0	153	172	s0000ssssssssss00ss	403
613032	6086	6105	TTGGTGCCGGAGCTGGTGGG	54	186	205	s0000ssssssssss00ss	404
613033	6119	6138	GGCAGAAGGTGGGCGGTGGC	74	219	238	s0000ssssssssss00ss	405
613034	6185	6204	TGATAGTCGACAGAGGCGAG	71	285	304	s0000ssssssssss00ss	406
613035	73867	73886	CACTTCGAACCTCTGGCGGG	67	333	352	s0000ssssssssss00ss	98

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613036	73869	73888	ATCACTTCGAACTCCTGGCG	72	335	354	S0000SSSSSSSSSS00SS	99
613037	73871	73890	CCATCACTTCGAACTCCTGG	69	337	356	S0000SSSSSSSSSS00SS	100
613412	73879	73898	GTGATCTTCCATCACTTCGA	72	345	364	S0000SSSSSSSSSS00SS	25
613038	73906	73925	CCTGTCCCCCAACCCGTACG	44	372	391	S0000SSSSSSSSSS00SS	104
613039	73932	73951	TGCATGGTGTAGCCCCCTG	80	398	417	S0000SSSSSSSSSS00SS	117
613040	73934	73953	GGTGCATGGTGTAGCCCCC	73	400	419	S0000SSSSSSSSSS00SS	118
613041	73939	73958	GTCTTGGTGCATGGTGTAGC	77	405	424	S0000SSSSSSSSSS00SS	407
613042	73958	73977	CGTCCGTGTCACCCTCTTGG	79	424	443	S0000SSSSSSSSSS00SS	123
613044	83397	83416	CCTCAGATCCGTCCTCAGTG	67	n/a	n/a	S0000SSSSSSSSSS00SS	408
613045	83430	83449	TGCTCTTAGCATCAGAGGTT	89	n/a	n/a	S0000SSSSSSSSSS00SS	409
613046	85902	85921	CTAAGGGTGTCTGTCACATCT	69	n/a	n/a	S0000SSSSSSSSSS00SS	410
613047	85934	85953	GGCAGCCTGCTTGCCGGGAG	51	n/a	n/a	S0000SSSSSSSSSS00SS	29
613048	85935	85954	CGGCAGCCTGCTTGCCGGGA	51	n/a	n/a	S0000SSSSSSSSSS00SS	411
613049	85968	85987	TGGTTCCTTCTGGGATCTCC	76	n/a	n/a	S0000SSSSSSSSSS00SS	412
613051	94719	94738	CTCGGAGGAAGCCTTCCTGG	53	n/a	n/a	S0000SSSSSSSSSS00SS	413
613052	94752	94771	TGAGCTGGTGGCTCAGACCT	41	n/a	n/a	S0000SSSSSSSSSS00SS	414
613053	94825	94844	CCTGTCCCCGAAGGTTGGCG	61	n/a	n/a	S0000SSSSSSSSSS00SS	415
613054	94875	94894	GGTGCTTGAGCAGCTCAGGG	70	n/a	n/a	S0000SSSSSSSSSS00SS	416
613055	94908	94927	GCGGCCCTCCTGGTGCAGG	47	n/a	n/a	S0000SSSSSSSSSS00SS	417
613056	94941	94960	CCGGCCTCTCTTTGCCCCCT	31	n/a	n/a	S0000SSSSSSSSSS00SS	418
613057	94974	94993	CGTCGCGGTCTTCATCCACC	42	n/a	n/a	S0000SSSSSSSSSS00SS	419
613058	95038	95057	GGCCGCCCATCTTGGGCTGG	0	n/a	n/a	S0000SSSSSSSSSS00SS	420
613059	95071	95090	ATGCTGGTGGCTTCTCTGGC	53	n/a	n/a	S0000SSSSSSSSSS00SS	421
613060	95098	95117	ATGGCACCTCCGCTGGGAA	39	n/a	n/a	S0000SSSSSSSSSS00SS	422
613061	95121	95140	AGAGGAAATCCACAGGGAGG	30	n/a	n/a	S0000SSSSSSSSSS00SS	33
613062	95154	95173	GCTCTGAGGCTGGGATCTCT	70	n/a	n/a	S0000SSSSSSSSSS00SS	423
613063	95187	95206	GCCCTTTGGCCCGCCCTACA	67	n/a	n/a	S0000SSSSSSSSSS00SS	424
613064	95235	95254	CGTTGGGTGTGATTTCCACG	61	n/a	n/a	S0000SSSSSSSSSS00SS	425
613065	95268	95287	AATGCTCCTCCGAGTGCGCC	85	n/a	n/a	S0000SSSSSSSSSS00SS	426
613066	95313	95332	CCTCTGGCCCCTCTCCAGGG	43	n/a	n/a	S0000SSSSSSSSSS00SS	427
613067	95346	95365	CTTTTGTGTCTCTCCCAA	42	n/a	n/a	S0000SSSSSSSSSS00SS	428
613068	95379	95398	GCTGCTTTTCAGAGGGCTCT	51	n/a	n/a	S0000SSSSSSSSSS00SS	429
613069	95412	95431	GGCTGACGGGCTTCCCCCGC	61	n/a	n/a	S0000SSSSSSSSSS00SS	430
613070	95429	95448	TTTGAGTTGAGGGACCCGGC	33	n/a	n/a	S0000SSSSSSSSSS00SS	431
613073	98559	98578	GCTTTTACTGACCATGCGAG	79	522	541	S0000SSSSSSSSSS00SS	124
613074	98581	98600	CATCGCTTCCAGTCCCGTCT	78	544	563	S0000SSSSSSSSSS00SS	134
613075	98587	98606	TTTTGTCATCGCTTCCAGTC	35	550	569	S0000SSSSSSSSSS00SS	137
613076	101406	101425	AAGGTTTTAGCAGAGGAACG	63	n/a	n/a	S0000SSSSSSSSSS00SS	37
613077	101457	101476	TCTGAGCTACCAGGAGTGGG	65	n/a	n/a	S0000SSSSSSSSSS00SS	432
613078	101491	101510	GCACACAGCAGGGCTGGAGG	68	n/a	n/a	S0000SSSSSSSSSS00SS	433
613079	101501	101520	GTGGCTCTGGGCACACAGCA	77	n/a	n/a	S0000SSSSSSSSSS00SS	192
613080	101507	101526	AGGAAGGTGGCTCTGGGCAC	69	n/a	n/a	S0000SSSSSSSSSS00SS	38
613081	101537	101556	GGGAAGTGACAGAAGAGACG	46	n/a	n/a	S0000SSSSSSSSSS00SS	434

613082	101570	101589	GTTTCATCTCCTTTGCTCCA	57	n/a	n/a	sooooooooooooo	435
613083	102995	103014	CCGCGGTGTGGCGATCTTCG	9	594	613	sooooooooooooo	436
613084	103028	103047	GGCCTGGCCCTTCTGGCCTG	14	627	646	sooooooooooooo	437
613085	103075	103094	GGTGTCTTTGGAGCGGGCGG	37	674	693	sooooooooooooo	146
613086	105445	105464	CTTCTCTGGACTTGCTTAGT	45	n/a	n/a	sooooooooooooo	438
613087	105475	105494	CTCTCAGATCTGGGCCCTGC	41	n/a	n/a	sooooooooooooo	439
613088	105478	105497	CCTCTCTCAGATCTGGGCC	49	n/a	n/a	sooooooooooooo	440
613089	107932	107951	TAGCCGCTGCGATCCCCTGA	19	719	738	sooooooooooooo	441
613090	107968	107987	CGGCTGCCGGGAGTGCCTGG	31	755	774	sooooooooooooo	159
613091	108021	108040	CCACCTTCTTGGGCTCCCGG	17	808	827	sooooooooooooo	442
613092	108040	108059	GGTGGAGTACGGACCACTGC	20	827	846	sooooooooooooo	40
613093	108054	108073	AAGACGGCGACTTGGGTGGA	0	841	860	sooooooooooooo	41
613094	108101	108120	CAGGTCTGGCATGGGCACGG	67	888	907	sooooooooooooo	443
613095	108134	108153	CTCAGTGGAGCCGATCTTGG	31	921	940	sooooooooooooo	199
613096	108167	108186	CACCTTCCCGCCTCCCGGCT	47	954	973	sooooooooooooo	444
613097	121845	121864	GTTGCTAAGATCCAGCTTCT	49	n/a	n/a	sooooooooooooo	445
613098	121865	121884	GAGCCACACTTGGACTGGAC	85	n/a	n/a	sooooooooooooo	47
613099	121878	121897	GATATTATCCTTTGAGCCAC	88	n/a	n/a	sooooooooooooo	446
613101	125784	125803	GGTCACCTTGCTCAGGTCAA	68	993	1012	sooooooooooooo	447
613102	125817	125836	ATGATGGATGTTGCCTAATG	14	1026	1045	sooooooooooooo	448
613103	130141	130160	ATTTTACTTCCACCTGGCCA	22	1057	1076	sooooooooooooo	51

Table 12

Inhibition of Tau mRNA by 5-10-5 MOE gapmers with phosphorothioate and phosphodiester internucleoside linkages targeting SEQ ID NOs: 6 and 7

5

ISIS NO	Target SEQ ID NO	Target Start Site	Sequence	% inhibition	Linkage chemistry	SEQ ID NO
613043	6	442	GAGATTCTTTCAGGCCAGCG	17	sooooooooooooo	449
613050	7	685	TTTCAGGCTCTTGGGTCACG	0	sooooooooooooo	450
613071	7	1430	GCTTTGAGTTGAGGGACCCG	23	sooooooooooooo	451
613072	7	1444	TACTGACCATGCGAGCTTTG	73	sooooooooooooo	177
613100	7	2178	TATTTGCACACTGCCGCCTC	13	sooooooooooooo	452

Table 13

Inhibition of Tau mRNA by 5-10-5 MOE gapmers with phosphorothioate and phosphodiester internucleoside linkages targeting SEQ ID NOs: 1 and 3

10

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	SEQ ID NO: 3 Start Site	SEQ ID NO: 3 Stop Site	Linkage chemistry	SEQ ID NO
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433475	n/a	n/a	TCTTCAGCTTTTCAGGCCAGC	23	443	462	ssssssssssssssssssss	96
613412	73879	73898	GTGATCTTCCATCACTTCGA	76	345	364	soooooossssssssooss	25
613104	130143	130162	AGATTTTACTTCCACCTGGC	59	1059	1078	soooooossssssssooss	453
613105	130176	130195	CGACTGGACTCTGTCCTTGA	47	1092	1111	soooooossssssssooss	454
613106	130225	130244	TATTTCTCCGCCAGGGACG	90	1141	1160	soooooossssssssooss	455
613107	135483	135502	CGCGGAAGGTCAGCTTGTGG	43	1174	1193	soooooossssssssooss	456
613108	135516	135535	CCGCCCCGTGGTCTGTCTTG	44	1207	1226	soooooossssssssooss	457
613109	135549	135568	CCCCAGACACCACTGGCGAC	36	1240	1259	soooooossssssssooss	458
613110	135590	135609	GCCGGTGGAGGAGACATTGC	51	1281	1300	soooooossssssssooss	459
613111	135654	135673	CCAGGGAGGCAGACACCTCG	61	1345	1364	soooooossssssssooss	245
613112	135697	135716	AATTATTGACCGCCCCAGGG	33	1388	1407	soooooossssssssooss	460
613113	135730	135749	TTTTTCCACACTCTCTCATT	41	1421	1440	soooooossssssssooss	461
613114	135783	135802	AACTGCGAGGAGCAGCTGGG	51	1474	1493	soooooossssssssooss	462
613115	135786	135805	CCGAAGTGCAGGAGCAGCT	78	1477	1496	soooooossssssssooss	248
613116	135816	135835	CAAAAGCAGGTTAAGTGATT	28	1507	1526	soooooossssssssooss	463
613117	135849	135868	CTGATTTTGAAGTCCCAGC	69	1540	1559	soooooossssssssooss	464
613118	135869	135888	ATTTGCTCTTACTCCCATCA	80	1560	1579	soooooossssssssooss	465
613119	135882	135901	TTGGAAAGATGAAATTTGCT	52	1573	1592	soooooossssssssooss	466
613120	135948	135967	TGTTGGATGTGGCCATGTTT	63	1639	1658	soooooossssssssooss	467
613121	136049	136068	GTCCCTTGAAATCCCCAGA	45	1740	1759	soooooossssssssooss	468
613122	136082	136101	CCACAACAGGGCCAGAGGTG	55	1773	1792	soooooossssssssooss	469
613123	136115	136134	TCCTTTGTTGCTGCCACTGC	59	1806	1825	soooooossssssssooss	470
613124	136148	136167	GCCTGTGGCTCCACGAACAC	72	1839	1858	soooooossssssssooss	471
613125	136181	136200	CCCCGTCACACTCACACAAG	43	1872	1891	soooooossssssssooss	472
613126	136214	136233	GGCCTCCCCCGTGGCCTCCC	37	1905	1924	soooooossssssssooss	473
613127	136247	136266	TGCTTCCTCTCCCCTCTGCC	41	1938	1957	soooooossssssssooss	474
613128	136295	136314	GATGTCTACTCTCCAGCACG	32	1986	2005	soooooossssssssooss	475
613129	136328	136347	ATAGGCCTTGGCTCTCCCAG	73	2019	2038	soooooossssssssooss	476
613130	136361	136380	AGGACAGGCGGCCGCTCAGA	46	2052	2071	soooooossssssssooss	477
613131	136394	136413	TGACCCACAGCAGGCCCCCA	14	2085	2104	soooooossssssssooss	478
613132	136427	136446	CTCCACAGGCTGCCCTGCA	46	2118	2137	soooooossssssssooss	479
613133	136460	136479	CAGCTTGCCTTCTCTTTTAA	58	2151	2170	soooooossssssssooss	480
613134	136491	136510	GGAGGTCATCCACGAAGTGC	45	2182	2201	soooooossssssssooss	61
613135	136493	136512	AAGGAGGTCATCCACGAAGT	41	2184	2203	soooooossssssssooss	481
613136	136515	136534	GACATCAAGGTCAGTCTTTT	80	2206	2225	soooooossssssssooss	482
613137	136541	136560	AGGGAGGAAGAGGCCAGCGC	60	2232	2251	soooooossssssssooss	483
613138	136574	136593	AGCCCTCAACTCAGGCCCC	53	2265	2284	soooooossssssssooss	484
613139	136607	136626	TCAATAAAACAGGGTTTCTG	38	2298	2317	soooooossssssssooss	485
613140	136640	136659	CAAAATCATGGCAGCAGTTC	26	2331	2350	soooooossssssssooss	486
613141	136673	136692	GTTAGCCCTAAAGTCCAGG	76	2364	2383	soooooossssssssooss	487
613142	136706	136725	CCCAAGAGGCACAAGTCCTT	57	2397	2416	soooooossssssssooss	488
613143	136739	136758	CAGTGGCCCAGGCTTGAAA	63	2430	2449	soooooossssssssooss	489
613144	136748	136767	CAGAGATGCCAGTGGCCCAG	43	2439	2458	soooooossssssssooss	67

613145	136772	136791	TGCCTCCCAGACCCCCACAC	23	2463	2482	S0000SSSSSSSSSS00SS	490
613146	136805	136824	AGTGGCCCGTGGGAAGGACAG	17	2496	2515	S0000SSSSSSSSSS00SS	491
613147	136838	136857	ACAACAGCACAGCGGCGCAG	61	2529	2548	S0000SSSSSSSSSS00SS	492
613148	136845	136864	ACGGCAGACAACAGCACAGC	59	2536	2555	S0000SSSSSSSSSS00SS	493
613149	136899	136918	GAATTCGGGACATTGTGACG	42	2590	2609	S0000SSSSSSSSSS00SS	494
613150	136933	136952	CAGGGTCATTACTGAGAAGG	39	2624	2643	S0000SSSSSSSSSS00SS	495
613151	136966	136985	CTCAGTATGGAGTAGGTACC	52	2657	2676	S0000SSSSSSSSSS00SS	496
613152	136999	137018	TGTGCCTGGACTTTGCCTTC	61	2690	2709	S0000SSSSSSSSSS00SS	497
613153	137032	137051	GGAAGTGAAGTGAAGAGGCT	62	2723	2742	S0000SSSSSSSSSS00SS	498
613154	137077	137096	GAATCAGATCATGAGATTCG	30	2768	2787	S0000SSSSSSSSSS00SS	499
613155	137110	137129	CACATCTGTGACGGGAGGAG	26	2801	2820	S0000SSSSSSSSSS00SS	500
613156	137143	137162	CACCTAGGGTCACAGCTGAG	33	2834	2853	S0000SSSSSSSSSS00SS	501
613157	137176	137195	GAAAGGGCTCTCTCCATGTC	54	2867	2886	S0000SSSSSSSSSS00SS	502
613158	137214	137233	GTGGGCTCAGCACAGGAAGG	23	2905	2924	S0000SSSSSSSSSS00SS	503
613159	137229	137248	ACCCAGCCTGCTGCTGTGGG	36	2920	2939	S0000SSSSSSSSSS00SS	504
613160	137247	137266	ACCACTGACAACCAAGACAC	22	2938	2957	S0000SSSSSSSSSS00SS	505
613161	137280	137299	GCCCTGGGTGCCTTGCCCTT	53	2971	2990	S0000SSSSSSSSSS00SS	506
613162	137322	137341	ACAAGCTAGGGTGCAAGTGG	47	3013	3032	S0000SSSSSSSSSS00SS	507
613163	137364	137383	GGAGCTGAGCAGCGGGCTGG	45	3055	3074	S0000SSSSSSSSSS00SS	508
613164	137401	137420	CCCTTTGTGCGGTGTGGAGG	8	3092	3111	S0000SSSSSSSSSS00SS	509
613165	137453	137472	TGGCTTCCAGCTGGGACTGG	65	3144	3163	S0000SSSSSSSSSS00SS	510
613166	137486	137505	ATATGTTTCAAGTGTCCAGC	58	3177	3196	S0000SSSSSSSSSS00SS	511
613167	137529	137548	ACTCAACAGGGTGCAAGTGG	54	3220	3239	S0000SSSSSSSSSS00SS	512
613168	137562	137581	GAATCCAAGCATAAACAGAC	55	3253	3272	S0000SSSSSSSSSS00SS	513
613169	137595	137614	TTTTTTCTTTTCACTATCA	34	3286	3305	S0000SSSSSSSSSS00SS	514
613170	137629	137648	AGCATTTCAAGATACATGCG	59	3320	3339	S0000SSSSSSSSSS00SS	515
613171	137692	137711	CACACGAGTCCCAGTGTGGG	11	3383	3402	S0000SSSSSSSSSS00SS	516
613172	137761	137780	TTGGGTCCCAGGTGCTGAGG	40	3452	3471	S0000SSSSSSSSSS00SS	517
613173	137794	137813	ACGGCCTCCTTAGCTGCTAG	73	3485	3504	S0000SSSSSSSSSS00SS	518
613174	137827	137846	TAATCCTGTGCTTCAGGCCT	32	3518	3537	S0000SSSSSSSSSS00SS	519
613175	137881	137900	TGACACAGGGAGCCCCAAGG	40	3572	3591	S0000SSSSSSSSSS00SS	520
613176	137914	137933	AGCCAGACCAGCCACAAGAC	16	3605	3624	S0000SSSSSSSSSS00SS	521
613177	137947	137966	GCTATGACCAGAGAGAACCA	29	3638	3657	S0000SSSSSSSSSS00SS	522
613178	137967	137986	GGACTGCCATGAGACTTCGG	26	3658	3677	S0000SSSSSSSSSS00SS	523
613179	137980	137999	TAAGCCTCCTTTGGGACTGC	64	3671	3690	S0000SSSSSSSSSS00SS	524
613180	138013	138032	AGTGGCTTCCTTTTCTTGT	69	3704	3723	S0000SSSSSSSSSS00SS	525

Table 14

Inhibition of Tau mRNA by 5-10-5 MOE gapmers with phosphorothioate and phosphodiester internucleoside linkages targeting SEQ ID NOs: 1 and 3

5

ISIS NO	SEQ ID NO: 1 Start	SEQ ID NO: 1 Stop	Sequence	% inhibition	SEQ ID NO: 3	SEQ ID NO: 3	Linkage chemistry	SEQ ID NO
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PCT/US2014/047486

	Site	Site			Start Site	Stop Site		
433475	n/a	n/a	TCTTCAGCTTTCAGGCCAGC	23	433	452	ssssssssssssssssss	96
613258	18371	18390	GGCAATGCCTGGAAGAACT	75	n/a	n/a	s0000ssssssssss00ss	526
613259	18411	18430	CGCTGGTGAGAGTGTGACTG	69	n/a	n/a	s0000ssssssssss00ss	527
613260	18449	18468	ATCCGAGGGTGAGATGATAA	75	n/a	n/a	s0000ssssssssss00ss	528
613261	19611	19630	AATAATTTCTCCAGGCTCAT	62	n/a	n/a	s0000ssssssssss00ss	529
613262	20955	20974	GCTGACTTCGATTGTATT	84	n/a	n/a	s0000ssssssssss00ss	530
613263	22139	22158	TATCATATGGCACAAATTCT	32	n/a	n/a	s0000ssssssssss00ss	531
613264	23662	23681	CTACCTGGGACCACACCTTA	61	n/a	n/a	s0000ssssssssss00ss	532
613265	25046	25065	GGGTGGAGAGCCTGATGGTC	47	n/a	n/a	s0000ssssssssss00ss	533
613266	25418	25437	CTGTGAGCATCATGAAAGCC	56	n/a	n/a	s0000ssssssssss00ss	534
613267	25606	25625	TTTTATTATGAGGGAGATCA	48	n/a	n/a	s0000ssssssssss00ss	535
613268	26186	26205	AATAGTAGAGAAATGGAAAT	39	n/a	n/a	s0000ssssssssss00ss	536
613269	26690	26709	TAACATGACAGGGTTAGGCC	67	n/a	n/a	s0000ssssssssss00ss	537
613270	26917	26936	GCCCACACACATGCTCATGC	57	n/a	n/a	s0000ssssssssss00ss	538
613271	27160	27179	TGTGTTTCAGTTACATGCCTT	82	n/a	n/a	s0000ssssssssss00ss	539
613272	27569	27588	GACCACCATGGTGGGCTGAC	39	n/a	n/a	s0000ssssssssss00ss	540
613273	28227	28246	GGCACCTCTCTGCAGACTTT	85	n/a	n/a	s0000ssssssssss00ss	541
613274	30102	30121	TGCTTCACACACCACAATGG	60	n/a	n/a	s0000ssssssssss00ss	542
613275	31769	31788	AACATTGCCGAGCACCAGCC	63	n/a	n/a	s0000ssssssssss00ss	543
613276	31832	31851	GACTCAGGAACATGTTAGCT	70	n/a	n/a	s0000ssssssssss00ss	544
613277	32045	32064	CACGGCTCAGCAGAGGAGAC	23	n/a	n/a	s0000ssssssssss00ss	545
613278	32324	32343	GCTGCTATCCTTCCTGGGCC	57	n/a	n/a	s0000ssssssssss00ss	546
613279	32760	32779	GGAAATGAAAGCTTCCCACG	61	n/a	n/a	s0000ssssssssss00ss	547
613280	33359	33378	AACAGTCAGAATACCCCAA	72	n/a	n/a	s0000ssssssssss00ss	548
613281	34056	34075	TATAGGTAGAATATAAACT	17	n/a	n/a	s0000ssssssssss00ss	549
613282	35266	35285	TATGAACAAAACATGCAGGAC	45	n/a	n/a	s0000ssssssssss00ss	550
613283	35839	35858	AGCCTCCAGAGTGACAGGTG	63	n/a	n/a	s0000ssssssssss00ss	551
613284	36223	36242	CCATAAGCCACTCCTGGTTG	0	n/a	n/a	s0000ssssssssss00ss	552
613285	36410	36429	CAGCTTGGAAGATACAGGAG	63	n/a	n/a	s0000ssssssssss00ss	553
613286	38647	38666	CAAACCTTAAGAAAAGTTGCA	67	n/a	n/a	s0000ssssssssss00ss	554
613287	39104	39123	TGCTGGCAAAGAAGACAGGA	69	n/a	n/a	s0000ssssssssss00ss	555
613288	40506	40525	CCACTGATGGCCGGGTGCAG	27	n/a	n/a	s0000ssssssssss00ss	556
613289	42727	42746	TGGGTGTCAAATGGCTGGCT	55	n/a	n/a	s0000ssssssssss00ss	557
613290	42955	42974	TAGAAAGCTATTTAATAAAT	0	n/a	n/a	s0000ssssssssss00ss	558
613291	43109	43128	AGCCGTACATCAATGGTACA	71	n/a	n/a	s0000ssssssssss00ss	559
613292	46627	46646	GGCCCTACCATGGTCGATTT	57	n/a	n/a	s0000ssssssssss00ss	560
613293	47399	47418	ATCAGTGCCAGAGACAGAGG	5	n/a	n/a	s0000ssssssssss00ss	561
613294	48115	48134	TATTATTAACGAACAAAAAA	0	n/a	n/a	s0000ssssssssss00ss	562
613295	48223	48242	AGAGCAATACTTTGTGCTTA	51	n/a	n/a	s0000ssssssssss00ss	563
613296	48608	48627	AGACTCCTCAAATGTGCGCC	53	n/a	n/a	s0000ssssssssss00ss	564

613297	49204	49223	GAATGACGGCCGCTCCTCT	39	n/a	n/a	S0000SSSSSSSSSO0SS	565
613298	49696	49715	TATGGAGGGCTTCTGGCCTC	18	n/a	n/a	S0000SSSSSSSSSO0SS	566
613299	51161	51180	GAGAAAGAGCGAGTAATTAG	44	n/a	n/a	S0000SSSSSSSSSO0SS	567
613300	52250	52269	TAGCTAGAACTGTGTCCCT	41	n/a	n/a	S0000SSSSSSSSSO0SS	568
613301	53908	53927	CTGTGAGATCATCCCCTGGT	51	n/a	n/a	S0000SSSSSSSSSO0SS	569
613302	54457	54476	CAGCGCAGTGCAGGGAGTCA	41	n/a	n/a	S0000SSSSSSSSSO0SS	570
613303	55975	55994	GGGTACACAGAGAGGCCACT	53	n/a	n/a	S0000SSSSSSSSSO0SS	571
613304	56155	56174	GAACGATGCACTGCCTTGGC	54	n/a	n/a	S0000SSSSSSSSSO0SS	572
613305	57402	57421	CACCATATTACACCAGTTGT	60	n/a	n/a	S0000SSSSSSSSSO0SS	573
613306	57696	57715	CTGAAATGAATCCCCTGAAC	0	n/a	n/a	S0000SSSSSSSSSO0SS	574
613307	57733	57752	GTGTCCACGAATGCCCTGG	40	n/a	n/a	S0000SSSSSSSSSO0SS	575
613308	58392	58411	ACGGATGGTTGCTGCTGATG	47	n/a	n/a	S0000SSSSSSSSSO0SS	576
613309	61917	61936	GTCCCTTTTGCTCCCAAAGA	18	n/a	n/a	S0000SSSSSSSSSO0SS	577
613310	62489	62508	CAGTCTTTTAATAAGTGAAA	50	n/a	n/a	S0000SSSSSSSSSO0SS	578
613311	63219	63238	TTAGCTAAATTGAGGCCCGG	31	n/a	n/a	S0000SSSSSSSSSO0SS	579
613312	63257	63276	GGAAAGGTATTGCCTCCTGA	42	n/a	n/a	S0000SSSSSSSSSO0SS	580
613313	63627	63646	GGTGACTACGCAGCCTGGAC	57	n/a	n/a	S0000SSSSSSSSSO0SS	581
613314	64559	64578	TTCAGGGCAATCCTTGAGGT	41	n/a	n/a	S0000SSSSSSSSSO0SS	582
613315	64872	64891	TGCTAATGCTTTGGGACCTA	44	n/a	n/a	S0000SSSSSSSSSO0SS	583
613316	66922	66941	TGGGTAGAGAGCAACTGTTC	32	n/a	n/a	S0000SSSSSSSSSO0SS	584
613317	67104	67123	ACACCCCTTCTCTGCACATC	25	n/a	n/a	S0000SSSSSSSSSO0SS	585
613318	68893	68912	CTGCTAGAGTTCGCCAACAG	59	n/a	n/a	S0000SSSSSSSSSO0SS	586
613319	69457	69476	TCTTATTCTCTAGGTGGGCT	70	n/a	n/a	S0000SSSSSSSSSO0SS	587
613320	70922	70941	CAGTGCAAGTGGGTATGAAG	30	n/a	n/a	S0000SSSSSSSSSO0SS	588
613321	70928	70947	CAGATGCAGTGCAAGTGGGT	44	n/a	n/a	S0000SSSSSSSSSO0SS	589
613322	71310	71329	GAAAACTTTGTCCATAATT	41	n/a	n/a	S0000SSSSSSSSSO0SS	590
613323	71665	71684	TAATGAATGTATAACAGAAA	0	n/a	n/a	S0000SSSSSSSSSO0SS	591
613324	71702	71721	AAAAGGCAGATACTTTGTGG	56	n/a	n/a	S0000SSSSSSSSSO0SS	592
613325	72456	72475	CAGAGGTGTGAAAGTAAAAG	0	n/a	n/a	S0000SSSSSSSSSO0SS	593
613326	72566	72585	CAGCTAAAGCTTTGTGAACA	31	n/a	n/a	S0000SSSSSSSSSO0SS	594
613327	72612	72631	TGCAGCCCAGGTGAGCCAGC	49	n/a	n/a	S0000SSSSSSSSSO0SS	595
613328	73748	73767	GCCTCTCCTCCAGTTCATG	12	n/a	n/a	S0000SSSSSSSSSO0SS	596
613329	75140	75159	GTTTTCTTATTTTAGCATT	87	n/a	n/a	S0000SSSSSSSSSO0SS	597
613330	76340	76359	GGAGGGACGAGAAACAGCAG	0	n/a	n/a	S0000SSSSSSSSSO0SS	598
613331	79041	79060	AGCTTCCAGCATGAACATAG	77	n/a	n/a	S0000SSSSSSSSSO0SS	599
613332	79971	79990	GAGCCCTGATATGATAGAGG	57	n/a	n/a	S0000SSSSSSSSSO0SS	600
613333	80360	80379	TGTACCATGCCTGGCAGATG	78	n/a	n/a	S0000SSSSSSSSSO0SS	601
613334	81325	81344	GTTAGATGTATGTATGATGG	0	n/a	n/a	S0000SSSSSSSSSO0SS	602
613412	73879	73898	GTGATCTTCCATCACTTCGA	80	345	364	S0000SSSSSSSSSO0SS	25

Table 15

Inhibition of Tau mRNA by 5-10-5 MOE gapmers with phosphorothioate and phosphodiester internucleoside linkages targeting SEQ ID NOs: 1 and 3

WO 2015/010135

PCT/US2014/047486

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	SEQ ID NO: 3 Start Site	SEQ ID NO: 3 Stop Site	Linkage chemistry	SEQ ID NO
433475	n/a	n/a	TCTTCAGCTTTCAGGCCAGC	31	443	462	ssssssssssssssssss	96
613335	82136	82155	GCCTCCTCCTAGAGCTCCTG	81	n/a	n/a	sooooooooooooooooo	603
613336	83231	83250	CGGCCTCGCAACAAACCCAC	55	n/a	n/a	sooooooooooooooooo	604
613337	83820	83839	TCCACTGACCTGCCCTTCC	66	n/a	n/a	sooooooooooooooooo	605
613338	84269	84288	TTTGCAACTTGTTCTGCTT	84	n/a	n/a	sooooooooooooooooo	606
613339	85073	85092	TCTTGGGTGCAGGCGGAGCA	53	n/a	n/a	sooooooooooooooooo	607
613340	86117	86136	ACCCAAGATTCAGGAGGCC	77	n/a	n/a	sooooooooooooooooo	608
613341	86191	86210	AGGCCCTAAATGCTCTGAGA	75	n/a	n/a	sooooooooooooooooo	609
613342	86251	86270	AGAAGTCTCTGGAAGTACG	70	n/a	n/a	sooooooooooooooooo	610
613343	86714	86733	TCACCAAACCAATGGCTGGC	67	n/a	n/a	sooooooooooooooooo	611
613344	86774	86793	GGTGAAATCCTGGCTAGGCC	89	n/a	n/a	sooooooooooooooooo	612
613345	88487	88506	TGCAGATTCGGCCTGAGTTT	72	n/a	n/a	sooooooooooooooooo	613
613346	89131	89150	CCAAACAAGAAAGACTGAGA	55	n/a	n/a	sooooooooooooooooo	614
613347	89994	90013	CCATGTCCCTCCCCCAACC	12	n/a	n/a	sooooooooooooooooo	615
613348	90126	90145	ATTAGAAAAAAACCACTAGG	37	n/a	n/a	sooooooooooooooooo	616
613349	92246	92265	AGCTTACTAGAGTGCTCTTG	81	n/a	n/a	sooooooooooooooooo	617
613350	92915	92934	ATTTTTTTCTGGTTCATTCA	71	n/a	n/a	sooooooooooooooooo	618
613351	94316	94335	CGCTTAAGAGAGGGAGCATC	72	n/a	n/a	sooooooooooooooooo	619
613352	94673	94692	GTGGAGATACGCAGTGGTGG	68	n/a	n/a	sooooooooooooooooo	620
613353	95790	95809	ACACCATGAGGGCACCCGTC	82	n/a	n/a	sooooooooooooooooo	35
613354	95918	95937	CCCAAACCTGGCTCTGTCAC	65	n/a	n/a	sooooooooooooooooo	621
613355	97224	97243	ATCAACCAGCACCATCCACG	65	n/a	n/a	sooooooooooooooooo	622
613356	97314	97333	GGGTCTGTAAGCCTAAAGTG	53	n/a	n/a	sooooooooooooooooo	623
613357	97315	97334	TGGGTCTGTAAGCCTAAAGT	56	n/a	n/a	sooooooooooooooooo	624
613358	97368	97387	TATACTATGTGGCAGAATCA	48	n/a	n/a	sooooooooooooooooo	625
613359	97478	97497	CACATTCCTCTACCCCATG	57	n/a	n/a	sooooooooooooooooo	626
613360	97507	97526	TCATAGATTTTCTTCTTIGG	75	n/a	n/a	sooooooooooooooooo	627
613361	98881	98900	ACACACCTTCATTTACTGTC	95	n/a	n/a	sooooooooooooooooo	313
	98918	98937			n/a	n/a	sooooooooooooooooo	
613362	98882	98901	AACACACCTTCATTTACTGT	83	n/a	n/a	sooooooooooooooooo	314
	98919	98938			n/a	n/a	sooooooooooooooooo	
613363	98883	98902	AAACACACCTTCATTTACTG	79	n/a	n/a	sooooooooooooooooo	315
	98920	98939			n/a	n/a	sooooooooooooooooo	
613364	98884	98903	CAAACACACCTTCATTTACT	63	n/a	n/a	sooooooooooooooooo	316
	98921	98940			n/a	n/a	sooooooooooooooooo	
613365	98885	98904	TCAAACACACCTTCATTTAC	59	n/a	n/a	sooooooooooooooooo	317
	98922	98941			n/a	n/a	sooooooooooooooooo	
613366	98886	98905	TTCAAACACACCTTCATTTA	67	n/a	n/a	sooooooooooooooooo	628

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	98923	98942			n/a	n/a	sooooooooooooo	
613367	98887	98906	TTTCAAACACACCTTCATTT	72	n/a	n/a	sooooooooooooo	318
	98924	98943			n/a	n/a	sooooooooooooo	
613368	98888	98907	TTTTCAAACACACCTTCATT	59	n/a	n/a	sooooooooooooo	319
	98925	98944			n/a	n/a	sooooooooooooo	
613369	98889	98908	GTTTTCAAACACACCTTCAT	90	n/a	n/a	sooooooooooooo	320
	98926	98945			n/a	n/a	sooooooooooooo	
613370	98890	98909	GGTTTTCAAACACACCTTCA	96	n/a	n/a	sooooooooooooo	321
	98927	98946			n/a	n/a	sooooooooooooo	
613371	98891	98910	TGGTTTTCAAACACACCTTC	95	n/a	n/a	sooooooooooooo	322
	98928	98947			n/a	n/a	sooooooooooooo	
613372	99560	99579	CCCCAGCTGGCCGAGGCCCA	81	n/a	n/a	sooooooooooooo	629
613373	99816	99835	GAGAAGGGTCCTGTCCCAGA	76	n/a	n/a	sooooooooooooo	630
613374	100743	100762	AGTAAGTTGATGGAGATCAT	83	n/a	n/a	sooooooooooooo	631
613375	102894	102913	CACCAGCCCCACTCCGCCAC	61	n/a	n/a	sooooooooooooo	632
613376	103875	103894	TGCTCTGTCTCCAGAGACAT	70	n/a	n/a	sooooooooooooo	633
613377	104615	104634	ATCCAAGATCCAGGCCAGGC	63	n/a	n/a	sooooooooooooo	634
613378	105870	105889	AGAGACCCAGGGTGACCAGT	76	n/a	n/a	sooooooooooooo	635
613379	106909	106928	CAAATTTCTCGATCCCCTTC	18	n/a	n/a	sooooooooooooo	636
613380	108411	108430	CCTGAGGAGGGCACTCACAG	61	n/a	n/a	sooooooooooooo	637
613381	108891	108910	GTGGCTACCCACGGCCACAG	1	n/a	n/a	sooooooooooooo	638
613382	108939	108958	CTACCAGGAGCACACACAGA	65	n/a	n/a	sooooooooooooo	639
613383	109303	109322	CCCTAAGCCATGGTGGGTTT	72	n/a	n/a	sooooooooooooo	640
613384	109995	110014	CCCTTGTCACCCACAGCCACA	72	n/a	n/a	sooooooooooooo	641
613385	110198	110217	GGGTCACCTGTGAGTTATTT	62	n/a	n/a	sooooooooooooo	642
613386	113567	113586	AGCTGCCTCCAGTTGTTTAT	85	n/a	n/a	sooooooooooooo	643
613387	114056	114075	ACTTTAGCTCCATCTTCTCA	49	n/a	n/a	sooooooooooooo	644
613388	114755	114774	CTATAATGGTCAGTGGTGTA	67	n/a	n/a	sooooooooooooo	645
613389	115899	115918	TGAAGGAGAGGCTGTGGTGA	41	n/a	n/a	sooooooooooooo	646
613390	117387	117406	TGTGACAACAAAGTTGTCCT	46	n/a	n/a	sooooooooooooo	647
613391	117654	117673	CCCTGCAATCAACACAGGAG	65	n/a	n/a	sooooooooooooo	648
613392	119050	119069	TCTAACATGCACATATTTAC	60	n/a	n/a	sooooooooooooo	649
613393	119190	119209	AGCACTGGGTGTTTACAACA	84	n/a	n/a	sooooooooooooo	650
613394	119594	119613	AGAAGTGATATCATATCCTA	85	n/a	n/a	sooooooooooooo	324
	119905	119924			n/a	n/a	sooooooooooooo	
613395	119595	119614	AAGAAGTGATATCATATCCT	68	n/a	n/a	sooooooooooooo	325
	119906	119925			n/a	n/a	sooooooooooooo	
613396	120782	120801	ACCCGGTGACCTTTCCTCTC	67	n/a	n/a	sooooooooooooo	651
613397	121728	121747	GAGTGACATGCGCCACCCTG	87	n/a	n/a	sooooooooooooo	203
613398	121794	121813	AAAAGGATGAGTGACACGCC	66	n/a	n/a	sooooooooooooo	205
613399	121940	121959	GCCACAGCACGGCGCATGGG	89	n/a	n/a	sooooooooooooo	652
613400	124954	124973	GCACCGCTCCCTCTGGGAAT	49	n/a	n/a	sooooooooooooo	653
613401	125298	125317	AAATCTTGCTGGAAAGGCAG	64	n/a	n/a	sooooooooooooo	654

613402	125428	125447	GACCCAGACATTTGCTCAGC	86	n/a	n/a	sooooooooooooooooo	655
613403	125982	126001	GGGCTCCCGCAAGTTTCACA	71	n/a	n/a	sooooooooooooooooo	656
613404	127460	127479	GAGAGGCCCTGTGGACAGCT	75	n/a	n/a	sooooooooooooooooo	657
613405	130381	130400	CCCACTGGATGCTGCTGAGG	34	n/a	n/a	sooooooooooooooooo	658
613406	131662	131681	GTGCCTAGTAACCCATTTAG	54	n/a	n/a	sooooooooooooooooo	659
613407	131796	131815	CACCCACAGCAAGACCTAGA	49	n/a	n/a	sooooooooooooooooo	660
613408	133056	133075	ACACAGAGAAGCTTCCAGAG	70	n/a	n/a	sooooooooooooooooo	661
613409	133304	133323	AGCTATCACATGGACGAGTT	67	n/a	n/a	sooooooooooooooooo	662
613410	133548	133567	CATTTAATACAGGCTTTGAT	38	n/a	n/a	sooooooooooooooooo	663
613411	134599	134618	AGCCACTGATGCCAGACAT	69	n/a	n/a	sooooooooooooooooo	664
613412	73879	73898	GTGATCTTCCATCACTTCGA	82	345	364	sooooooooooooooooo	25

Table 16

Inhibition of Tau mRNA by 5-10-5 MOE gapmers with phosphorothioate and phosphodiester internucleoside linkages targeting SEQ ID NOs: 5 and 6

5

ISIS NO	Target SEQ ID NO	Target Start Site	Sequence	% inhibition	Linkage chemistry	SEQ ID NO
613239	5	3	TGCCCTTCGCGGTCCCTTCG	11	sooooooooooooooooo	396
613241	5	424	CTGTCCCCCAAACCCGTACG	48	sooooooooooooooooo	397
613248	6	524	GCTTCCGCTGTTGGAGTGCT	59	sooooooooooooooooo	398

Example 8: Dose-dependent antisense inhibition of human tau in SH-SY5Y cells by 5-10-5 MOE gapmers with phosphorothioate and phosphodiester internucleoside linkages

Gapmers from studies described above exhibiting significant *in vitro* inhibition of tau mRNA were selected and tested at various doses in SH-SY-5Y cells. Cells were plated at a density of 20,000 cells per well and transfected using electroporation with 1.25 μ M, 2.500 μ M, 5.00 μ M, 10.00 μ M, and 20.00 μ M concentrations of antisense oligonucleotide, as specified in the Table below. After a treatment period of approximately 16 hours, RNA was isolated from the cells and Tau mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3104 was used to measure mRNA levels. Tau mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN[®]. Results are presented as percent inhibition of Tau, relative to untreated control cells. Tau mRNA levels were significantly reduced in a dose-dependent manner in antisense oligonucleotide treated cells.

Table 17

ISIS No	1.25 μ M	2.50 μ M	5.00 μ M	10.00 μ M	20.00 μ M
613118	46	47	73	92	93

613136	36	70	83	88	92
613115	32	49	82	86	94
613329	73	80	92	94	92
613273	46	24	48	60	85
613262	31	72	76	87	94
613271	44	66	84	89	94
613370	92	92	95	98	98
613361	88	86	89	94	96
613371	80	88	91	95	97
613369	58	85	89	95	96
613399	61	77	90	94	96
613344	80	79	93	95	95
613397	64	74	79	93	95
613412	45	66	70	81	96

Table 18

ISIS No	1.25 μM	2.50 μM	5.00 μM	10.00 μM	20.00 μM
613255	54	61	80	91	90
613065	22	61	62	83	89
613257	45	69	82	86	91
613098	70	57	83	92	98
613253	44	67	74	86	91
613039	21	77	85	90	95
613188	0	35	72	86	87
613042	33	45	73	90	94
613233	21	54	69	75	89
613073	59	67	83	92	97
613187	8	54	74	61	84
613402	10	58	62	81	87
613045	57	72	92	96	95
613412	20	52	67	84	90
613099	71	66	89	91	95

Example 9: Antisense inhibition of human Tau in SH-SY5Y cells by 5-10-5 MOE, 5-8-5 MOE, 4-8-6 MOE, or 6-8-4 MOE gapmers

Antisense oligonucleotides were designed targeting a tau nucleic acid and were tested for their effects on Tau mRNA in vitro. The antisense oligonucleotides were tested in a series of experiments that had similar culture conditions. ISIS 613412 was also included in the assays. The results for each experiment are presented in separate tables shown below. Cultured SH-SY5Y cells at a density of 20,000 cells per well were transfected using electroporation with 8,000 nM antisense oligonucleotide. After a treatment period of

approximately 24 hours, RNA was isolated from the cells and Tau mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3104 was used to measure mRNA levels. Tau mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of tau, relative to untreated control cells.

5 The newly designed chimeric antisense oligonucleotides in the Tables below were designed as 5-8-5 MOE, 4-8-6 MOE, or 6-8-4 MOE gapmers. The 5-8-5 MOE gapmers are 18 nucleosides in length, wherein the central gap segment comprises of eight 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising five nucleosides each. The 4-8-6 MOE gapmers are 18 nucleosides in length, wherein the central gap segment comprises of eight 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising four and six nucleosides respectively. The 6-8-4 MOE gapmers are 18 nucleosides in length, wherein the central gap segment comprises of eight 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising six and four nucleosides respectively. Each nucleoside in the 5' wing segment and each nucleoside in the 3' wing segment has a 2'-MOE modification. The internucleoside linkage motif throughout for each gapmer in the tables below, except for ISIS 613412, is 5'-sooooooooooooo-3', wherein each "s" represents a phosphorothioate internucleoside linkage and wherein each "o" represents a phosphodiester internucleoside linkage. The internucleoside linkage motif for ISIS 613412 is 5'-sooooooooooooo-3', wherein each "s" represents a phosphorothioate internucleoside linkage and wherein each "o" represents a phosphodiester internucleoside linkage. All cytosine residues throughout each gapmer are 5-methylcytosines. "Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. "Stop site" indicates the 3'-most nucleoside to which the gapmer is targeted human gene sequence. Each gapmer listed in the Tables below is targeted to either SEQ ID NO: 1 (GENBANK Accession No. NT_010783.15 truncated from nucleotides 9240000 to 9381000), SEQ ID NO: 4 (GENBANK Accession No. NT_010783.14 truncated from nucleotides 2624000 to 2761000), SEQ ID NO: 5 (GENBANK Accession No. DR002467.1), or SEQ ID NO: 6 (GENBANK Accession No. NM_001203251.1). 'n/a' indicates that the antisense oligonucleotide does not target that particular gene sequence with 100% complementarity.

Table 19

Inhibition of tau mRNA by 5-10-5 MOE and 5-8-5 MOE gapmers targeting SEQ ID NO: 1 and SEQ ID NO: 4

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	SEQ ID NO: 4 Start Site	SEQ ID NO: 4 Stop Site	Motif	SEQ ID NO
613412	73879	73898	GTGATCTTCCATCACTTCGA	83	69842	69861	5-10-5	25
620887	98891	98908	GTTTTCAAACACACCTTC	89	94855	94872	5-8-5	665
	98928	98945			94892	94909		
621197	n/a	n/a	TCGCCAACAGACATGTGA	39	64850	64867	5-8-5	666

621196	67898	67915	TGAAGGAGCCTGGGAAGT	15	63891	63908	5-8-5	667
621198	69079	69096	AGCAGAGATGTGGCTGGG	50	65044	65061	5-8-5	668
621199	69622	69639	GTGAGGTTGAAAAGTTTC	34	65587	65604	5-8-5	669
621200	69802	69819	TGGTTTCTGATGGTTTTT	43	65767	65784	5-8-5	670
621201	70023	70040	GTTGGAACCTCTGGGATC	27	65988	66005	5-8-5	671
621202	70259	70276	TCAGCATTTTTCTCCTCT	47	66224	66241	5-8-5	672
621203	70531	70548	CTGGAATGGTACGATCTC	52	66496	66513	5-8-5	673
621204	70750	70767	CCACTCTGGTGCAGGACG	29	66715	66732	5-8-5	674
621205	70930	70947	CAGATGCAGTGCAAGTGG	43	66895	66912	5-8-5	675
621206	71110	71127	GGGTTTCACCAGACCTCA	29	67075	67092	5-8-5	676
621207	71306	71323	CTTTGTCCATAATTTTTT	34	67271	67288	5-8-5	677
621208	71487	71504	TATAGCATGAGCATTTGT	42	67452	67469	5-8-5	678
621209	71667	71684	TAATGAATGTATAACAGA	2	67632	67649	5-8-5	679
621210	71850	71867	TCCTCCTGGCTGCCCTGT	33	67815	67832	5-8-5	680
621211	72030	72047	CATCCTGCCATACCAGAC	32	67995	68012	5-8-5	681
621212	72224	72241	TATCCGCCTCTCAAAGTG	0	68189	68206	5-8-5	682
621213	72410	72427	CACATTTGCATATTTTCA	65	68373	68390	5-8-5	683
621214	72590	72607	TCGGGTTGCCCCATTCAA	27	68553	68570	5-8-5	684
621215	72770	72787	AACCACCATTACTCACA	35	68733	68750	5-8-5	685
621216	72950	72967	ACCGGCACCCACCAGGTC	22	68913	68930	5-8-5	686
621217	73130	73147	AGGGACAGCATCAGCAGA	22	69093	69110	5-8-5	687
621218	73437	73454	AGGCATGTGGCAGGTGCC	12	69400	69417	5-8-5	688
621219	73617	73634	ACCAACACCGCAGCAGTT	35	69580	69597	5-8-5	689
621220	73797	73814	GTTCTGAGGAGTGTTGGG	0	69760	69777	5-8-5	690
621221	73978	73995	ACTAACCTTTCAGGCCAG	33	69941	69958	5-8-5	691
621222	74273	74290	TAAATTATTTAGAGACG	0	70236	70253	5-8-5	692
621223	74467	74484	CAAGGTAAATTTCTTTCT	69	70430	70447	5-8-5	693
621224	74647	74664	TCAGGCCTGATCTAAGTA	14	70610	70627	5-8-5	694
621225	74827	74844	TCCCCAACCATGTGGTCT	40	70790	70807	5-8-5	695
621226	75007	75024	TGCCAGCCACACCCATGG	52	70970	70987	5-8-5	696
621227	75187	75204	AACTCCACGGCTTCCATG	50	71150	71167	5-8-5	697
621228	75371	75388	AGATAGAAATCTGAAACG	34	71334	71351	5-8-5	698
621229	75551	75568	GCTGGGCCGAGCTGCATT	66	71514	71531	5-8-5	699
621230	75891	75908	GGATTCAAAGGAGAAAAC	35	71854	71871	5-8-5	700
621231	76192	76209	ATTATTATTTGACATGGG	75	72155	72172	5-8-5	701
621232	76373	76390	AGGGTAGGCAGTGTTGTG	4	72336	72353	5-8-5	702
621233	76553	76570	CTCTCTTTGTCAGGAAAA	58	72516	72533	5-8-5	703
621234	76942	76959	CCTTTTTTTTAGGACGG	0	72905	72922	5-8-5	704
621235	77222	77239	GAGTTGACTGGGCACGGT	33	73185	73202	5-8-5	705
621236	77414	77431	TCATCTGTGAAGCGGACG	81	73377	73394	5-8-5	706
621237	77594	77611	GGCACAATCCATATGAGG	56	73557	73574	5-8-5	707
621238	77781	77798	GTTATTTTGAACAGTTT	87	73744	73761	5-8-5	708
621239	78117	78134	CTGGACTTTATTTCAATT	77	74080	74097	5-8-5	709

621240	78319	78336	CAGTATATATAGTGCATA	76	74282	74299	5-8-5	710
621241	78499	78516	CAAAACAGCTCCTTGTA	14	74462	74479	5-8-5	711
621242	78679	78696	ACTTTCATCTACTTTTCA	32	74642	74659	5-8-5	712
621243	78859	78876	CCAATCTGTCCCCAGCTT	42	74822	74839	5-8-5	713
621244	79039	79056	TCCAGCATGAACATAGCT	65	75002	75019	5-8-5	714
621245	79219	79236	TAGAGTCAGTTTCAGGAT	75	75182	75199	5-8-5	715
621246	79399	79416	GGTGGTATCACCAACAGC	35	75362	75379	5-8-5	716
621247	79589	79606	TTAAGGAATGGCTCTGGG	42	75552	75569	5-8-5	717
621248	79769	79786	GAACATGAGACATCTTGA	8	75732	75749	5-8-5	718
621249	79949	79966	AGCTGTGCCCAGTTAAAA	53	75912	75929	5-8-5	719
621250	80129	80146	TCTGGTCATATGAGGAAA	55	76092	76109	5-8-5	720
621251	80309	80326	AGTCATTATCATGTCACC	89	76272	76289	5-8-5	721
621252	80489	80506	GCTGAGCGAATTACCTAA	75	76452	76469	5-8-5	722
621253	80669	80686	CCTCTGTATGACAGAAAT	48	76632	76649	5-8-5	723
621254	80849	80866	GGTAACATGTAAAGCTTC	79	76812	76829	5-8-5	724
621255	81033	81050	TGGATTATGTACAGATAT	28	76996	77013	5-8-5	725
	81136	81153			77099	77116		
621256	81110	81127	ATGGATGATAGGAAGGAT	20	77073	77090	5-8-5	726
	81213	81230			77176	77193		
621257	81393	81410	GATGGAGGAAGGAATGAT	5	77356	77373	5-8-5	727
621258	81629	81646	CTGGATGGTTACATGGAT	31	77592	77609	5-8-5	728
621259	81812	81829	ATAATTGATGTATAATTA	0	77775	77792	5-8-5	729
621260	81992	82009	GTTCTGCCCCACCTGGGC	56	77955	77972	5-8-5	730
621261	82198	82215	GCCTCTCAGGGCCTCCGT	76	78161	78178	5-8-5	731
621262	82378	82395	GAAGGATGGCCACACAGA	39	78341	78358	5-8-5	732
621263	82558	82575	ATGGGCTTATCAATGCAT	85	78521	78538	5-8-5	733
621264	82738	82755	GAGGCCCAAATGATCACA	56	78701	78718	5-8-5	734
621265	82918	82935	GCTCAGGGCAGACACGGT	66	78881	78898	5-8-5	735
621266	83098	83115	CTTAACCAGCTAGTGGTG	38	79061	79078	5-8-5	736
621267	83278	83295	GTCCTGTGGAGCTGAAAA	54	79241	79258	5-8-5	737
621268	83486	83503	GGCTGGAGGCATGGAGGG	7	79449	79466	5-8-5	738
621269	83666	83683	TGCCTCCAGAGCACACAC	55	79629	79646	5-8-5	739
621270	83846	83863	AGGATACTAAACCAAGAT	24	79809	79826	5-8-5	740
621271	84026	84043	CACAGATGGGAAGCAAGA	20	79989	80006	5-8-5	741
621272	84206	84223	CATGAGGCAACAATCCAA	70	80169	80186	5-8-5	742

Table 20

Inhibition of tau mRNA by 5-10-5 MOE and 5-8-5 MOE gapmers targeting SEQ ID NO: 1

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	Motif	SEQ ID NO
613412	73879	73898	GTGATCTTCCATCACTTCGA	80	5-10-5	25
620887	98891	98908	GTTTTCAAACACACCTTC	92	5-8-5	665

	98928	98945				
621273	84386	84403	GCCGTAAGACCCAGCTCT	58	5-8-5	743
621274	84566	84583	GAAGAAGTACTGAGAAAG	14	5-8-5	744
621275	84746	84763	TAAGAACCTCAGCGGCAA	56	5-8-5	745
621276	84926	84943	TGAGGGAGCACTGAGAGT	21	5-8-5	746
621277	85106	85123	AGTTCAATGAAGGACATT	69	5-8-5	747
621278	85287	85304	ACTGTTGGATGGGTCCAC	70	5-8-5	748
621279	85467	85484	TTGGTCCATTTTGATTGG	0	5-8-5	749
621280	85647	85664	CGGCAGCCCTGTGTAAAC	48	5-8-5	750
621281	85828	85845	CCTTTGCTTCTTGCGCAG	66	5-8-5	751
621282	86014	86031	AGGGCCTTGACTGCCTGG	15	5-8-5	752
621283	86194	86211	AAGGCCCTAAATGCTCTG	57	5-8-5	753
621284	86384	86401	CGCTCAGGTGATCTTGGG	76	5-8-5	754
621285	86564	86581	CTGATTGATTCCCCATCA	64	5-8-5	755
621286	86746	86763	TTCTTGTTGGGCAACTGG	59	5-8-5	756
621287	86928	86945	GAAATGCACTCAGAAGGG	52	5-8-5	757
621288	87108	87125	CCTCAGTGAAATAACTGT	55	5-8-5	758
621289	87288	87305	TGGCTGCAACTTTGAATG	0	5-8-5	759
621290	87470	87487	CTGGAGATGGCAGGCTGG	39	5-8-5	760
621291	87653	87670	CCCGTGGGCCCCATGTGG	1	5-8-5	761
621292	87834	87851	ATTGAGGACACCTGGTGT	6	5-8-5	762
621293	88014	88031	AAGGTCTGCATTGTCAGT	61	5-8-5	763
621294	88194	88211	CTGCTGGCCTCTCTGTAC	56	5-8-5	764
621295	88374	88391	TCGGACACGGTCACTGCC	60	5-8-5	765
621296	88554	88571	GTGCCTTGTCATGTGACA	79	5-8-5	766
621297	88734	88751	GGAAGCCATGTGGTAGCC	50	5-8-5	767
621298	88918	88935	CAGAGGCCACTGCCTCTG	0	5-8-5	768
621299	89098	89115	TTAATAGTACCAAAATCA	25	5-8-5	769
621300	89278	89295	TACATTTCTTCTCCTCCA	10	5-8-5	770
621301	89470	89487	CGGAGTCAGGCAGATGGG	43	5-8-5	771
621302	89650	89667	GCTATGACCTAGTAGGAA	84	5-8-5	772
621303	89830	89847	ATTGTTTACTAGAAACCA	39	5-8-5	773
621304	90010	90027	GGGCAGAGCCCACCCAT	40	5-8-5	774
621305	90190	90207	AGGCTGGACAAGGCTAGC	63	5-8-5	775
621306	90531	90548	CATATTTGAGTTTCTTTT	62	5-8-5	776
621307	90711	90728	AATGATTACACAAAGCTG	61	5-8-5	777
621308	90891	90908	GAACAGTGTCTTTCCAGC	73	5-8-5	778
621309	91071	91088	ATGTGCCTTTCTGTGCCA	89	5-8-5	779
621310	91251	91268	AATGATTCTAGAGGTCA	54	5-8-5	780
621311	91431	91448	CCATGATTCCAGGCTGCT	80	5-8-5	781
621312	91816	91833	CAGCCAGGCTAGTCTTGC	80	5-8-5	782
621313	92037	92054	AGGAGAATGTCTTTTTT	53	5-8-5	783
621314	92219	92236	TACTGTACTCTGATATA	41	5-8-5	784

621315	92399	92416	CCTTATGGGAGCCCTTTG	54	5-8-5	785
621316	92579	92596	CAGAGCGCAGCAGCACCT	64	5-8-5	786
621317	92759	92776	CTCACCAGCTCTGCTTTA	53	5-8-5	787
621318	92939	92956	CAGCTGATCAAGGGCACA	84	5-8-5	788
621319	93123	93140	AGACCTGCCATAAGACTC	39	5-8-5	789
621320	93380	93397	CTGACTAAAATGTTATTT	34	5-8-5	790
621321	93570	93587	ACAGGCATGAGTTTTTTT	61	5-8-5	791
621322	93840	93857	CCCCTTTTTTTTGGTTTG	2	5-8-5	792
621323	94020	94037	TCTGGAGCCGCCCTGGGC	36	5-8-5	793
621324	94200	94217	ATGACAGCTCTCCTGGTC	38	5-8-5	794
621325	94380	94397	ACTCTCAACTCCTCTGGT	49	5-8-5	795
621326	94576	94593	TCCTGTTGGAGGAGGCGC	7	5-8-5	796
621327	95433	95450	CCTTTGAGTTGAGGGACC	60	5-8-5	797
621328	95613	95630	GCCTGAGCACGGGAGGAG	41	5-8-5	798
621329	95793	95810	GACACCATGAGGGCACCC	69	5-8-5	799
621330	95986	96003	AGCACCTCCTGGGAGGCG	18	5-8-5	800
621331	96166	96183	GGTGGCATGTGGACCAGG	50	5-8-5	801
621332	96346	96363	TGTGGCTCTGAGGTCTCC	72	5-8-5	802
621333	96526	96543	GCCTCTGTCTTAACTTT	50	5-8-5	803
621334	96778	96795	TTAGGGTACAGTGGTGTG	18	5-8-5	804
621335	96958	96975	CCTCTAGTAGGCCAGTAT	62	5-8-5	805
621336	97141	97158	AATCAAGTAAGTTTGGGA	57	5-8-5	806
621337	97321	97338	CAACTGGGTCTGTAAGCC	47	5-8-5	807
621338	97506	97523	TAGATTTTCTTCTTTGGT	45	5-8-5	808
621339	97686	97703	GGGCACGAATTCTCACTG	53	5-8-5	809
621340	97866	97883	TCCAGAATAGGAGAGGCT	9	5-8-5	810
621341	98046	98063	ACACTGCAGCCAGGCTTG	63	5-8-5	811
621342	98226	98243	TGCAGTCTCCCTAACCCA	59	5-8-5	812
621343	98406	98423	CTCTTTTCCCTTGAATCT	33	5-8-5	813
621344	98607	98624	GTCAGCTTACCTTGGCTT	44	5-8-5	814
621345	98802	98819	CAACTGCTCTTCCCTGGG	68	5-8-5	815
621346	98982	98999	TCTGGGTGCAGTTTATGC	80	5-8-5	816
621347	99162	99179	AGAATTTATGCTGGAAAT	38	5-8-5	817
621348	99342	99359	GGCCAGCTCTCCAAATCC	56	5-8-5	818
621349	99522	99539	CCCTAGACTCTGGGCAAC	66	5-8-5	819

Table 21

Inhibition of Tau mRNA by 5-10-5 MOE and 5-8-5 MOE gapmers targeting SEQ ID NO: 1

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	Motif	SEQ ID NO
613412	73879	73898	GTGATCTTCCATCACTTCGA	91	5-10-5	25
620887	98891	98908	GTTTTCAAACACACCTTC	96	5-8-5	665

	98928	98945				
620965	20187	20204	TCTAAGTAATTCGATATG	27	5-8-5	820
620966	20375	20392	AAACAGAAACTAGGGTGG	63	5-8-5	821
620967	20571	20588	TCCCGCTGGGATCCATGG	40	5-8-5	822
620968	20751	20768	TGTTGCCATTGGGCAGCC	0	5-8-5	823
620969	20931	20948	GACCTTCTAATTAGTCCA	58	5-8-5	824
620970	21291	21308	GCGATTCTCTCCTGTCTC	53	5-8-5	825
620971	21567	21584	ACTCAGATTTATTATTTT	87	5-8-5	826
620972	21747	21764	AAAGTACTATCCACTTGT	77	5-8-5	827
620973	21927	21944	CAAATCCTGGGTTTCGAAT	39	5-8-5	828
620974	22107	22124	AGGTCTCTGCCCATGAAA	59	5-8-5	829
620975	22287	22304	AGATTTCTCCCTTCACCC	46	5-8-5	830
620976	22467	22484	TTAACATGATGGTGGTTT	86	5-8-5	831
620977	22652	22669	CATTGTGGAAATTAAACA	50	5-8-5	832
620978	22837	22854	TGTAGTCAATATTGAACT	86	5-8-5	833
620979	23269	23286	TTTTGAGAGCAGGTCTCG	61	5-8-5	834
620980	23449	23466	ATGGCAAACAGTACATGT	80	5-8-5	835
620981	23631	23648	AGGATTTAAGTGATTTTC	66	5-8-5	836
620982	23826	23843	TACAAAGACCCCTTTTCC	51	5-8-5	837
620983	24016	24033	AGCTGCCAGCAGTCCTTG	81	5-8-5	838
620984	24196	24213	CTGCTGTAGGAAATGACC	77	5-8-5	839
620985	24377	24394	AGCTCCAACCAGCTTTCT	58	5-8-5	840
620986	24557	24574	GTCCTGATTAACAGCTAA	69	5-8-5	841
620987	24744	24761	GTCTGTCTGCTGCCATCC	81	5-8-5	842
620988	24924	24941	GTAAGTATGATGGTAACA	85	5-8-5	843
620989	25286	25303	AGCCCTCTTTGTACAGGA	75	5-8-5	844
620990	25466	25483	CTGTTCCAGTTGATCCAG	53	5-8-5	845
620991	25668	25685	GCAGTCTTTTTAAATTA	80	5-8-5	846
620992	25848	25865	CCTCTGCTCACATAGAAA	64	5-8-5	847
620993	26028	26045	AGTACCTGCCTTGTTTCCT	52	5-8-5	848
620994	26208	26225	AAGCATGGTAATACAAAA	78	5-8-5	849
620995	26404	26421	TTGATTAAAAAAATAGC	4	5-8-5	850
620996	26584	26601	TTCATCCTTTCCAAGTGT	58	5-8-5	851
620997	26764	26781	CATGCTTACACACCACAC	23	5-8-5	852
	26948	26965				
620998	26762	26779	TGCTTACACACCACACAC	38	5-8-5	853
	26946	26963				
620999	27140	27157	ATATGCTGAACACACACA	75	5-8-5	854
621000	27320	27337	CCACCGAGGTCTCATTGG	52	5-8-5	855
621001	27500	27517	GGGAGACCTCCCTTTCAA	0	5-8-5	856
621002	27680	27697	TCTCTGGGTGTAGAGACG	54	5-8-5	857
621003	27861	27878	GCAGGCTCGGGCTCCACG	61	5-8-5	858
621004	28041	28058	CCTTGTCAGATGGTTGAT	55	5-8-5	859

621005	28221	28238	TCTGCAGACTTTTCTCAA	22	5-8-5	860
621006	28426	28443	CTGGAGGGAGGTGATGTG	7	5-8-5	861
621007	28616	28633	GAAAGCTGCTGCTGAGGG	63	5-8-5	862
621008	28981	28998	GGGCAAAGATAATTGAA	61	5-8-5	863
621009	29165	29182	CCTCACCTGGGCAAGAA	68	5-8-5	864
621010	29409	29426	TTGCTGCTCGGGAGGCCG	14	5-8-5	865
621011	29589	29606	AAATGAAAGATGCTGGCT	23	5-8-5	866
621012	29953	29970	CAGAGAGGTCCAGCTACT	58	5-8-5	867
621013	30133	30150	AGCTCACTACAGCAGGCA	93	5-8-5	868
621014	30607	30624	TATTTCTTGCAATTCTTT	78	5-8-5	869
621015	30787	30804	GGAGGACTGTCTCTAGAG	59	5-8-5	870
621016	30967	30984	TCCGGCCTGGCGAACTGA	40	5-8-5	871
621017	31278	31295	CCTGCAAAGCTAATTTTA	18	5-8-5	872
621018	31458	31475	GAGCCCCCTTTAAGCCTT	65	5-8-5	873
621019	31654	31671	GTACAAAGACTGTGTACG	47	5-8-5	874
621020	31834	31851	GACTCAGGAACATGTTAG	81	5-8-5	875
621021	32023	32040	TGAGGCAGCAATGCTGGG	34	5-8-5	876
621022	32203	32220	CACTGGGAGGTGTATAGA	0	5-8-5	877
621023	32383	32400	GCGAGGTGGGTGAAGGTT	25	5-8-5	878
621024	32563	32580	AAAAACTTTGGCAGTCAG	80	5-8-5	879
621025	32743	32760	GGTCTGCCCTGCACCAGG	59	5-8-5	880
621026	32923	32940	CTGAGCTCTCCGAGCTGC	61	5-8-5	881
621027	33103	33120	GTGAGGTGGTATCATTGG	51	5-8-5	882
621028	33283	33300	CTAGCTTGAATTCCTCCA	81	5-8-5	883
621029	33463	33480	AATCTGTGACTCAAGAAC	47	5-8-5	884
621030	33708	33725	GGGCCGTCTCTATTAATA	56	5-8-5	885
621031	33888	33905	GGTATAATTTGTTTGGAC	85	5-8-5	886
621032	34068	34085	CTTTATTGCATATAGGTA	86	5-8-5	887
621033	34248	34265	ATCCAGTCCCAACATTGG	30	5-8-5	888
621034	34428	34445	CGGTCTCTCTGACTTGCC	78	5-8-5	889
621035	34620	34637	GAGGGCATTCTCAAAGG	10	5-8-5	890
621036	34800	34817	AGTTCTCTGATTCTCAAA	63	5-8-5	891
621037	34980	34997	CCCCAGTGCCCACAAGT	48	5-8-5	892
621038	35160	35177	CTAAAAGCTAAAGTGGGT	49	5-8-5	893
621039	35340	35357	AGGACCTGGCAGAGCTGC	73	5-8-5	894
621040	35520	35537	AAATCGAACACTTACATA	20	5-8-5	895
621041	35721	35738	TTGCCATCTTGACAGGG	89	5-8-5	896

Table 22

Inhibition of Tau mRNA by 5-10-5 and 5-8-5 MOE gapmers targeting SEQ ID NO: 1

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	Motif	SEQ ID NO
613412	73879	73898	GTGATCTTCCATCACTTCGA	85	5-10-5	25
620887	98891	98908	GTTTTCAAACACACCTTC	93	5-8-5	665
	98928	98945				
620888	98881	98898	ACACCTTCATTTACTGTC	95	5-8-5	897
	98918	98935				
620889	98890	98907	TTTTCAAACACACCTTCA	74	5-8-5	898
	98927	98944				
620890	98892	98909	GGTTTTCAAACACACCTT	96	5-8-5	899
	98929	98946				
620891	98893	98910	TGGTTTTCAAACACACCT	96	5-8-5	900
	98930	98947				
620892	6191	6208	TACCTGATAGTCGACAGA	53	5-8-5	901
620893	6371	6388	GTCCCTTTCCAGGCCGCC	70	5-8-5	902
620894	6551	6568	CGCCCATGCGGCAAAAG	73	5-8-5	903
620895	6736	6753	CACTGCTCGGGAGGTGCA	62	5-8-5	904
620896	6938	6955	TGTTCTCAGGCACGGCGC	74	5-8-5	905
620897	7121	7138	GCCCTGCGCTCCGAGCGC	44	5-8-5	906
620898	7301	7318	AAAAAAGATGGCACCTCG	30	5-8-5	907
620899	7481	7498	ACAAAGCAAAGAGCCCCC	59	5-8-5	908
620900	7687	7704	TCACGCCCGTTCCATGCG	43	5-8-5	909
620901	7867	7884	CCGGATGGGTAGCCAGCG	47	5-8-5	910
620902	8047	8064	CCCTCTCCGGACACCTGT	69	5-8-5	911
620903	8227	8244	AAATACACCCAGGGCCGC	51	5-8-5	912
620904	8408	8425	GATAGAATTAACCAGAAA	33	5-8-5	913
620905	8588	8605	AGCCTCGCAGTACCCAGG	39	5-8-5	914
620906	8775	8792	TCGCGAGATGGCAATACG	55	5-8-5	915
620907	8956	8973	TTCCTCCATTAACAGCGC	49	5-8-5	916
620908	9157	9174	CCCGCCTGCTGGGAATGG	65	5-8-5	917
620909	9337	9354	AGAACTCAAATTGGTCCT	67	5-8-5	918
620910	9517	9534	TATAAGCAGCTTATACAG	34	5-8-5	919
620911	9697	9714	CCAAGCCAGGTTATTGCT	70	5-8-5	920
620912	9877	9894	TCTAACAATTTATGGGCA	81	5-8-5	921
620913	10057	10074	AACAAATGGACTGTAACA	59	5-8-5	922
620914	10240	10257	TTCAAGGAGGGAGTAAGG	12	5-8-5	923
620915	10420	10437	AGGAAAGTGGTGGTGGAG	22	5-8-5	924
620916	10600	10617	TGCAGCCCAGCTGGTGAG	35	5-8-5	925
620917	10781	10798	TCCTTG TAGGATGTTTAA	30	5-8-5	926

620918	10961	10978	ACCTGCTACATAGCGGAA	87	5-8-5	927
620919	11141	11158	TTATAGATCATATCTGGG	82	5-8-5	928
620920	11321	11338	AAACAGAGCACCAATGTA	36	5-8-5	929
620921	11501	11518	ACCTCAGAGACTTGACCT	54	5-8-5	930
620922	11681	11698	CCCAGGAAGTGAGAAAAG	20	5-8-5	931
620923	11864	11881	CAGTTGGGAGCCATCTGG	51	5-8-5	932
620924	12044	12061	ATTGGGCTCAGCATGGAG	30	5-8-5	933
620925	12224	12241	TCCTTAACCATTAGGCCA	70	5-8-5	934
620926	12404	12421	TGGCCCTAGTGAGTACCG	75	5-8-5	935
620927	12597	12614	GCCCAGTTTGGTGCAGGG	79	5-8-5	936
620928	12777	12794	GGCGGGAAGGCAGGTCAG	51	5-8-5	937
620929	12957	12974	CAGTTTACCAATGTCAGC	77	5-8-5	938
620930	13137	13154	ATATATTGTTACTTAGTC	83	5-8-5	939
620931	13317	13334	CATAGGCAAAACAGACAA	68	5-8-5	940
620932	13504	13521	TAGTTGAATGTTTTGGAA	73	5-8-5	941
620933	13702	13719	ACGGCGGAGGCTGAGGCG	10	5-8-5	942
620934	13882	13899	AGGTGCAAGCTGGCCGGG	44	5-8-5	943
620935	14062	14079	TGATACCCTGTAAGAATA	82	5-8-5	944
620936	14243	14260	AATATAGCAAAGGGAATT	54	5-8-5	945
620937	14423	14440	TAGAGATAATTATGTCCC	73	5-8-5	946
620938	14609	14626	GCAATTACAGAGCCAGGG	76	5-8-5	947
620939	14789	14806	GCAGAACTGGATCCGATC	69	5-8-5	948
620940	15035	15052	CAAAGCCAGGATGGTCTC	92	5-8-5	949
620941	15246	15263	CCAAAGAGATTCCTTTTT	79	5-8-5	950
620942	15924	15941	GGCCTCATTTATATATAT	20	5-8-5	951
620943	16156	16173	TATGGGACAATCATAGCT	56	5-8-5	952
620944	16336	16353	AATTCTGATACATTGTCA	81	5-8-5	953
620945	16516	16533	GATGACTCTTCCAAATGG	70	5-8-5	954
620946	16696	16713	TCACTTCATTATTCAAGC	84	5-8-5	955
620947	16876	16893	GTGCAGCCGCCACTGGCC	86	5-8-5	956
620948	17085	17102	CGATAAGATCTTTTTAAA	25	5-8-5	957
620949	17266	17283	GACAGTATAATCTCCATT	69	5-8-5	958
620950	17446	17463	AGGCTAAAGTCAGCCAC	29	5-8-5	959
620951	17639	17656	CTTGCACCCTGGTTTGGG	40	5-8-5	960
620952	17819	17836	TCCCTGTCTGGTTAGGAA	80	5-8-5	961
620953	17999	18016	ACGCGCCTGCCCCGTGCC	50	5-8-5	962
620954	18179	18196	CTCAAACCTGGCCACGCT	64	5-8-5	963
620955	18359	18376	GAAACTGGCGGGTCTGTT	64	5-8-5	964
620956	18539	18556	GGGAGGAATTTGGCAATG	37	5-8-5	965
620957	18719	18736	AAAGAGCACGGCATCTAT	76	5-8-5	966
620958	18905	18922	AAACTGTGAGGCACTGGG	87	5-8-5	967
620959	19088	19105	CATTTGACATTGGCCTGT	72	5-8-5	968
620960	19283	19300	ATTATTATCAGCATCTTC	77	5-8-5	969

620961	19467	19484	TTGCAGAGGCAGGAAGGC	67	5-8-5	970
620962	19647	19664	AGCAGCCTGGTTTAGAGG	31	5-8-5	971
620963	19827	19844	TCCACATCTTCCAGCCTC	74	5-8-5	972
620964	20007	20024	ATACAGACTCAGTCTCCT	79	5-8-5	973

Table 23

Inhibition of Tau mRNA by 5-10-5 and 5-8-5 MOE gapmers targeting SEQ ID NO: 1

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	Motif	SEQ ID NO
613412	73879	73898	GTGATCTTCCATCACTTCGA	78	5-10-5	25
620887	98891	98908	GTTTTCAAACACACCTTC	93	5-8-5	665
	98928	98945				
621042	35901	35918	AGTCGACCGCACTCCTGC	42	5-8-5	974
621043	36106	36123	GCCCTGAGGGTCCACAGG	20	5-8-5	975
621044	36286	36303	AGGGCAGTGTCTACCTC	50	5-8-5	976
621045	36466	36483	GTCCTCCCTTCCCCACAA	29	5-8-5	977
621046	36653	36670	CTGAATTCCTATCATGCG	51	5-8-5	978
621047	36833	36850	GAGAAAGAAGAGTGTGGT	23	5-8-5	979
621048	37024	37041	CTTAGGACAGATTCTAG	29	5-8-5	980
621049	37204	37221	GTCAGAAGTGTTTTCCCA	80	5-8-5	981
621050	37413	37430	TCCAATTTTAAACTTAAA	28	5-8-5	982
621051	37750	37767	CTACTGTTTAAAAAGGCT	66	5-8-5	983
621052	38013	38030	GTAAACACCATCTCTAAA	19	5-8-5	984
621053	38193	38210	CTCTGATACTATTATAAG	31	5-8-5	985
621054	38374	38391	CTGAGCTATTTGAGAATT	21	5-8-5	986
621055	38557	38574	TCTGCATATATAATTATA	57	5-8-5	987
621056	38737	38754	CACATTGTTTAGATTTTC	79	5-8-5	988
621057	38922	38939	TTAGCACACCTGAAACGC	51	5-8-5	989
621058	39102	39119	GGCAAAGAAGACAGGAGA	68	5-8-5	990
621059	39541	39558	TGCTGAGGATGCTTTTTT	72	5-8-5	991
621060	39721	39738	GCTGGAAGATGAGGTGGT	47	5-8-5	992
621061	39901	39918	TGGGTGTTGGAGAAAAC	24	5-8-5	993
621062	40100	40117	GCTTTAAAAGCTCCTCAG	65	5-8-5	994
621063	40347	40364	CGAGCACTTGTAGTTCCA	35	5-8-5	995
621064	40528	40545	GCAGTGCTTTAAAAATAT	22	5-8-5	996
621065	40709	40726	GAAATTTTCATGAAATATG	37	5-8-5	997
621066	40889	40906	TTACTTGCAATTGAAAGA	6	5-8-5	998
621067	41069	41086	GGAAAGACTACTCAGAGC	57	5-8-5	999
621068	41249	41266	GATGAAAGAGAATAACAA	20	5-8-5	1000
621069	41429	41446	ACCCATTATCTGCTCCCC	66	5-8-5	1001
621070	41611	41628	TTTTTCAGTAACAACATAA	51	5-8-5	1002
621071	41944	41961	CCTTTAGCTTTCCTTTTC	47	5-8-5	1003

621072	42124	42141	CAAATTCTGTTTCTGTAA	47	5-8-5	1004
621073	42304	42321	GCAAAAATAAGTGAAGT	38	5-8-5	1005
621074	42492	42509	TTGCAGTGACTTCTTGGG	71	5-8-5	1006
621075	42672	42689	AAACCCCTTCAACATCAG	45	5-8-5	1007
621076	42853	42870	ACAAGAGAAACATTTTAC	53	5-8-5	1008
621077	43033	43050	CACTTAGTAACCAAGCAA	53	5-8-5	1009
621078	43213	43230	CATAGATGATATATTTTG	78	5-8-5	1010
621079	43393	43410	AAATCTTGAAGTCTGAA	58	5-8-5	1011
621080	43620	43637	GGAGTTTTTGTGTTTCTT	77	5-8-5	1012
621081	43804	43821	AAATTCTTAATGGTTCAG	75	5-8-5	1013
621082	44051	44068	AGATAGATCTCGGCTCAC	81	5-8-5	1014
621083	44231	44248	AACCTTTAATAAACTTTT	43	5-8-5	1015
621084	44617	44634	GTCCAAGAGGTTTTTTTT	41	5-8-5	1016
621085	44809	44826	GCAGTCACTGCATTCCAG	27	5-8-5	1017
621086	45050	45067	CAAAAACAGGGCTAGGCA	21	5-8-5	1018
621087	45230	45247	TTCCCTGAACAAATGGCA	59	5-8-5	1019
621088	45412	45429	CTCAAATGTAACATTTTA	84	5-8-5	1020
621089	45592	45609	TACACCTGGCCCATGACC	41	5-8-5	1021
621090	45772	45789	AAGTTCTGGCTCAAGCAA	21	5-8-5	1022
621091	45955	45972	ACAACCTCTCTGGAAAAA	30	5-8-5	1023
621092	46135	46152	AGTCCACGCCTGCATCTG	63	5-8-5	1024
621093	46315	46332	CAAGGCAACAGAGAGGCA	42	5-8-5	1025
621094	46495	46512	AACATGCATATAATTACC	40	5-8-5	1026
621095	46675	46692	TTGGAGGGACAATTCTCA	46	5-8-5	1027
621096	46855	46872	CGAAGAGGCCAGGACTGC	34	5-8-5	1028
621097	47036	47053	TTGGCTCTGGTGATGGT	45	5-8-5	1029
621098	47216	47233	ACCAGGCAAAGGGACACC	68	5-8-5	1030
621099	47396	47413	TGCCAGAGACAGAGGTTG	68	5-8-5	1031
621100	47576	47593	CACACGCATGGCTTCATG	55	5-8-5	1032
621101	47756	47773	GAGGAAGGCATGAACTAA	60	5-8-5	1033
621102	47936	47953	TCCCATGCCCACGCATGT	26	5-8-5	1034
621103	48116	48133	ATTATTAACGAACAAAAA	2	5-8-5	1035
621104	48302	48319	ATGTCCAGATGTGGATCG	52	5-8-5	1036
621105	48482	48499	ATCAGACAGAAGAGCCAT	55	5-8-5	1037
621106	48678	48695	GCACAGTGCAACAGTGGG	78	5-8-5	1038
621107	49171	49188	GGCTTTCCCTTCCCTTCT	33	5-8-5	1039
621108	49361	49378	AGCTGGGAAAGTGGCAGG	23	5-8-5	1040
621109	49561	49578	ATGACAACTTGATTTGGG	65	5-8-5	1041
621110	49741	49758	GACCGCAACCTTGCCAAA	43	5-8-5	1042
621111	50111	50128	CTTTCAGAGACAGGCTCG	41	5-8-5	1043
621112	50298	50315	GGGCTCACCCCTGTAGTT	9	5-8-5	1044
621113	50766	50783	CTCTTAAGGCCGAGTGCA	39	5-8-5	1045
621114	50970	50987	TGCTAGGCAAAAAAACA	35	5-8-5	1046

621115	51150	51167	TAATTAGAAACCTCCTCG	10	5-8-5	1047
621116	51330	51347	CAGGTCATATATGAAATC	33	5-8-5	1048
621117	51521	51538	TGTGCTTCCGAAAGTAGT	63	5-8-5	1049
621118	51702	51719	GCATCAAATCCATGCATT	38	5-8-5	1050

Table 24

Inhibition of tau mRNA by 5-10-5 and 5-8-5 MOE gapmers targeting SEQ ID NO: 1

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	Motif	SEQ ID NO
613412	73879	73898	GTGATCTTCCATCACTTCGA	71	5-10-5	25
620887	98891	98908	GTTTTCAAACACACCTTC	84	5-8-5	665
	98928	98945				
621119	51894	51911	ACTCTGAAGCACAGACAG	21	5-8-5	1051
621120	52081	52098	CTTACCTGGGCTGGATGG	5	5-8-5	1052
621121	52261	52278	TTCTGTCTATAGCTAGAA	32	5-8-5	1053
621122	52441	52458	AGATGGCTTCCTATTGTT	32	5-8-5	1054
621123	52621	52638	TGGTTTGGTCAGGCCTCA	51	5-8-5	1055
621124	52803	52820	ATTGTAAC TCAAAGTGGG	50	5-8-5	1056
621125	53004	53021	AAACTCTACACCCCTGGG	17	5-8-5	1057
621126	53264	53281	CATACCAGGAAGGAAGGA	17	5-8-5	1058
621127	53444	53461	TGGACATATCAGAATTTG	64	5-8-5	1059
621128	53624	53641	CCCTTATTAGTGTCTACA	68	5-8-5	1060
621129	53805	53822	ACACTCTAGAGAGGTCCA	68	5-8-5	1061
621130	53985	54002	GACAGTACCCACGACACG	32	5-8-5	1062
621131	54165	54182	CCCCATTCTGGATCCTGG	40	5-8-5	1063
621132	54348	54365	ATTGTCTGTAAAATGTGG	57	5-8-5	1064
621133	54528	54545	ATTCTGTCTGACAGAGAC	40	5-8-5	1065
621134	54711	54728	CGATGGTGCACATCTATA	45	5-8-5	1066
621135	54891	54908	CAGTGTCGCTGAACACA	37	5-8-5	1067
621136	55073	55090	AGGAGGATTAGGAAGAAA	14	5-8-5	1068
621137	55261	55278	CAAGGAAGGCGATCTGGG	17	5-8-5	1069
621138	55623	55640	GGTGGCACTTGAACAAGC	61	5-8-5	1070
621139	55803	55820	GGTGGAAAGGGAACCCGG	43	5-8-5	1071
621140	55983	56000	CCCCACGGGTACACAGAG	20	5-8-5	1072
621141	56163	56180	CGCTGCGAACGATGCACT	63	5-8-5	1073
621142	56343	56360	GAATGGTCCTTCTTACAG	13	5-8-5	1074
621143	56526	56543	CTGGGAAAACCAAGGCAA	57	5-8-5	1075
621144	56706	56723	CCCAGGCTGAGGAAGGAC	40	5-8-5	1076
621145	56886	56903	GATTGGCTTTTACATCTT	48	5-8-5	1077
621146	57289	57306	CGGTTTGTAGTACAGTGGT	50	5-8-5	1078
621147	57470	57487	CTAACATCTTAGGGCACA	73	5-8-5	1079
621148	57650	57667	TTCCTCTGATGTCAGAAT	51	5-8-5	1080

621149	58090	58107	CCCCCTCGGTCGCCCAGG	37	5-8-5	1081
621150	58271	58288	TGTTTTAACTAAAAGCTT	24	5-8-5	1082
621151	58451	58468	GTATGAGGGCATAGATGA	26	5-8-5	1083
621152	58631	58648	ATCACACCACAGAATGTT	29	5-8-5	1084
621153	58812	58829	TACTCTTCTGTGGCAGCT	66	5-8-5	1085
621154	59198	59215	CAACAGCAAGGCCAGGCG	44	5-8-5	1086
621155	59380	59397	TAGATAATTTGAAATTTA	0	5-8-5	1087
621156	59786	59803	ACCTTAATCCCAGTATTT	12	5-8-5	1088
621157	59966	59983	TGCTTATGGTCCAGCTGT	40	5-8-5	1089
621158	60146	60163	GAGCCAGGCTTCAAAACC	26	5-8-5	1090
621159	60326	60343	TCCAGCACATTTAGGCGG	32	5-8-5	1091
621160	60522	60539	ATCTCAATAAAGCTATCG	70	5-8-5	1092
621161	60702	60719	CGCCCGCGGTGACTCAGC	32	5-8-5	1093
621162	60906	60923	GGAGTCAAGAGTCCAGGG	44	5-8-5	1094
621163	61109	61126	AGAAGGAATGATGAGGAA	24	5-8-5	1095
621164	61290	61307	GCAGTACAGTTTGGTAAT	32	5-8-5	1096
621165	61476	61493	TGGCTACTCTCTCAGGAG	9	5-8-5	1097
621166	61656	61673	GACCCTAGGTGGGTAAAG	21	5-8-5	1098
621167	61836	61853	GTCCCCTGAGGTGTTGTG	0	5-8-5	1099
621168	62016	62033	CCCAGACAACCTTCACCT	34	5-8-5	1100
621169	62208	62225	TGGGTAAAGACTCTGTCT	11	5-8-5	1101
621170	62467	62484	TGGAGCCGAGTGCGGTGG	12	5-8-5	1102
621171	62657	62674	TCTCTTCTGGATATTTTCG	49	5-8-5	1103
621172	62843	62860	CGATTTAAATGAATGAT	20	5-8-5	1104
621173	63023	63040	AGAACAAAGATAACAGTT	0	5-8-5	1105
621174	63218	63235	GCTAAATTGAGGCCCGGG	42	5-8-5	1106
621175	63398	63415	CTTCTCTCTTTCCTCAAT	26	5-8-5	1107
621176	63578	63595	TCTAAGCGAGACACACAG	26	5-8-5	1108
621177	63758	63775	TGATTCTCTGGAAGAAC	27	5-8-5	1109
621178	63938	63955	GCCTGTGTCTTCTAACTC	32	5-8-5	1110
621179	64184	64201	GGCTGAGAAGCTGGGACC	40	5-8-5	1111
621180	64365	64382	TTTTTACTTGAGATGTCA	38	5-8-5	1112
621181	64543	64560	GTAGGTGTCATCATCATC	83	5-8-5	1113
621182	64723	64740	CAACACTGACTGAGCACA	56	5-8-5	1114
621183	64903	64920	GCATTGGCTGGGCTAGGT	73	5-8-5	1115
621184	65092	65109	TATTTACTATGCAAAATA	18	5-8-5	1116
621185	65273	65290	AGCACCACAGAGCAGATG	19	5-8-5	1117
621186	65453	65470	CTCAGTGTGGAGTCTGC	44	5-8-5	1118
621187	65634	65651	CATTTTCAACCACTTAA	44	5-8-5	1119
621188	65815	65832	GTAAGGCTTTGTGGGCCA	32	5-8-5	1120
621189	66148	66165	TACTTTGCATTATTTATT	44	5-8-5	1121
621190	66535	66552	TTGGCTTTCATTATAATT	13	5-8-5	1122
621191	66736	66753	GGACGGTTGGGAAATAGG	18	5-8-5	1123

621192	66916	66933	GAGCAACTGTTCATAGGG	49	5-8-5	1124
621193	67096	67113	TCTGCACATCGACACATC	34	5-8-5	1125
621194	67538	67555	AGGCTAGGCCCCATGGCT	21	5-8-5	1126
621195	67718	67735	GCACCCCATCCTTCAGC	30	5-8-5	1127

Table 25

Inhibition of Tau mRNA by 5-10-5 and 5-8-5 MOE gapmers targeting SEQ ID NO: 1

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	% inhibition	Motif	SEQ ID NO:
613412	73879	73898	GTGATCTTCCATCACTTCGA	87	5-10-5	25
620887	98891	98908	GTTTTCAAACACACCTTC	96	5-8-5	665
	98928	98945				
621350	99702	99719	CCAGGAGATGAAGTAGCA	75	5-8-5	1128
621351	n/a	n/a	ACTCTTGGGAAACAAAGT	31	5-8-5	1129
621352	100065	100082	GGAAGCAGCCAGGGACGG	38	5-8-5	1130
621353	100288	100305	CTGCCTGGCCAATTAAAT	28	5-8-5	1131
621354	100468	100485	CAAATAATATTAACACT	0	5-8-5	1132
621355	100648	100665	TACTCAATTCAGGCAAG	71	5-8-5	1133
621356	100836	100853	AATGGAAGTTCTAGTACG	57	5-8-5	1134
621357	101188	101205	CAATCACAGTTCTTTTTC	45	5-8-5	1135
621358	101381	101398	GTCTTAAACATAAACATA	77	5-8-5	1136
621359	101759	101776	TGAGAGGGATGGCCCCCA	67	5-8-5	1137
621360	n/a	n/a	CGCATAACACCACGCCCCG	90	5-8-5	1138
621361	102169	102186	GCCAAAATCAGGAATGGG	94	5-8-5	1139
621362	102349	102366	GGCAGTCCCTGGGTTCG	77	5-8-5	1140
621363	102529	102546	GTTGAACCTGACCAAGGA	89	5-8-5	1141
621364	102709	102726	AGCATGAGTTGTGCCAAG	89	5-8-5	1142
621365	102889	102906	CCCACTCCGCCACCTTGA	67	5-8-5	1143
621366	103091	103108	TACCAGAGCTGGGTGGTG	13	5-8-5	1144
621367	103271	103288	ACATTTGCCTCAGAAATC	5	5-8-5	1145
621368	103593	103610	GATTCAGGCTGGGAGTGG	11	5-8-5	1146
621369	103773	103790	CTCCGAGAGCTGCCACTT	51	5-8-5	1147
621370	103966	103983	TGCAGCAGACTCCTAACG	33	5-8-5	1148
621371	104389	104406	AGGAATCTCACTTTTGTC	25	5-8-5	1149
621372	104569	104586	AGGCTGCCCCGTGCCACCA	30	5-8-5	1150
621373	104749	104766	TTAGTGAATGGCCATCCT	33	5-8-5	1151
621374	105023	105040	AAACTGCTTGAATTTGGG	31	5-8-5	1152
621375	105203	105220	TGTGAGTCCCCTGTAATC	18	5-8-5	1153
621376	105383	105400	TAAACAGGGCCTTAATGA	0	5-8-5	1154
621377	105563	105580	TCCTCCCGGCTCTAGAAA	10	5-8-5	1155
621378	105745	105762	GGAGACAGCCAGGCATGG	18	5-8-5	1156
621379	106173	106190	ATAATGTTTTTTATAGAG	0	5-8-5	1157
621380	106365	106382	GACTGGATTTTGTATTT	30	5-8-5	1158

621381	106545	106562	CGGAGTCTTATTCTGATG	39	5-8-5	1159
621382	106725	106742	CCGCAGCAATGCCCTGC	65	5-8-5	1160
621383	106905	106922	TCTCGATCCCCCTTCAAGA	23	5-8-5	1161
621384	107085	107102	CTGGGTGTCCTTTACCCT	5	5-8-5	1162
621385	107265	107282	CCTGCTCCACGCCTGCCT	82	5-8-5	1163
621386	107445	107462	TCAGGGCCTTTATCCTAA	51	5-8-5	1164
621387	107625	107642	TCGGCTCCACAGTCTTTG	60	5-8-5	1165
621388	107805	107822	CACCACTGGGTTAGGCAG	38	5-8-5	1166
621389	108170	108187	TCACCTTCCCGCCTCCCG	16	5-8-5	1167
621390	108359	108376	TTGAAGAGGGTCCAGAGG	3	5-8-5	1168
621391	108548	108565	TGCCCAGAAGGCAGGTGG	38	5-8-5	1169
621392	108728	108745	GGCCCCGAAGTCTGTGC	62	5-8-5	1170
621393	108908	108925	CGGTGCAGGACAGAGGTG	57	5-8-5	1171
621394	109135	109152	CGCGCACCACCACACGC	78	5-8-5	1172
621395	109315	109332	TCAGGCTGGGCCCTAAGC	50	5-8-5	1173
621396	109495	109512	TCACCTTCCCCAGCTCC	45	5-8-5	1174
621397	109675	109692	TCAGACCCAAGTGATAAG	64	5-8-5	1175
621398	109855	109872	GCAGGCTCTACACATGCG	76	5-8-5	1176
621399	110045	110062	CTGAGATGTTCTTCTCT	73	5-8-5	1177
621400	110225	110242	AGCTGCGGTACAGGACAG	68	5-8-5	1178
621401	110405	110422	CCAGTGAGGGCCCCTCTG	20	5-8-5	1179
621402	110585	110602	GCCCCCAGAGGTGCATGG	58	5-8-5	1180
621403	110769	110786	GGAGCAGCAGACACATGC	79	5-8-5	1181
621404	110949	110966	GGAAGCTACTTCCCATGC	43	5-8-5	1182
621406	111495	111512	GGAGGAGGCCTGACACCC	58	5-8-5	1183
621407	111675	111692	TTTCCCTTTGGTGTTAGC	91	5-8-5	1184
621408	111856	111873	CCCCAAAGCAATCTATGT	47	5-8-5	1185
621409	112036	112053	TCTGGAGGGAACACTGCC	60	5-8-5	1186
621410	112216	112233	GGTTGAGGTTGAGGGTAG	37	5-8-5	1187
621411	112396	112413	ACTCCCGCAGGCCAAACA	36	5-8-5	1188
621412	112603	112620	GAGTGCCAACAGGCCCAG	75	5-8-5	1189
621413	112784	112801	TTCTAAGTACAATTTGGG	67	5-8-5	1190
621414	112984	113001	TTACTGGTTGTGTTTCT	94	5-8-5	1191
621415	113164	113181	GAGTCTCAGTCTCACTGT	76	5-8-5	1192
621416	113347	113364	CATTCTCCTGCTGCTGT	83	5-8-5	1193
621417	113540	113557	GCTCTGAAGAGCTCCACG	83	5-8-5	1194
621418	113720	113737	CTCTCTTCAGGGCCACCG	82	5-8-5	1195
621419	113900	113917	CTCTCTCGCCCTGCATGG	48	5-8-5	1196
621420	114080	114097	CTGGACATCCTCCGAGAA	27	5-8-5	1197
621421	114260	114277	CACCCAGGCTGCGGCCCA	64	5-8-5	1198
621422	114440	114457	CTGTGGTGCAAGCCTGTG	42	5-8-5	1199
621423	114639	114656	AGACGAGAGTGCGCCAC	78	5-8-5	1200
621424	115155	115172	CCACATAAATGTTCTACA	94	5-8-5	1201

621425	115335	115352	GGTACAGGAAAAGATGCC	88	5-8-5	1202
621426	115515	115532	ATCAGCTTAGGAACTGAC	85	5-8-5	1203

Table 26

Inhibition of tau mRNA by 5-10-5 and 5-8-5 MOE gapmers targeting SEQ ID NO: 1

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	% inhibition	Motif	SEQ ID NO:
613412	73879	73898	GTGATCTTCCATCACTTCGA	86	5-10-5	25
620887	98891	98908	GTTTTCAAACACACCTTC	97	5-8-5	665
	98928	98945				
621427	115695	115712	GTGCCTCACAGTTGGCTC	39	5-8-5	1204
621428	115896	115913	GAGAGGCTGTGGTGAGGT	25	5-8-5	1205
621429	116077	116094	GAAATCAGAATCCTGAAA	66	5-8-5	1206
621430	116259	116276	ATGTGGCTTTTTCTTGTT	64	5-8-5	1207
621431	116595	116612	GTTTTTTTCTGGCCGGGC	90	5-8-5	1208
621432	116955	116972	TTTTCAGTGGATAAGGCT	78	5-8-5	1209
621433	117135	117152	ACATAAACTCCTTCTTTG	53	5-8-5	1210
621434	117315	117332	TGGTGAATGTTGAAATTC	78	5-8-5	1211
621435	117495	117512	AGGACAAGGAGGCCATGT	56	5-8-5	1212
621436	117787	117804	TCAAATGACAGATTCTCA	78	5-8-5	1213
621437	117967	117984	CATCCCTACTTTCTCCCT	24	5-8-5	1214
621438	118420	118437	TAGAATCTTGCCTTGTCG	34	5-8-5	1215
621439	118600	118617	GATACAGACATACATTGT	68	5-8-5	1216
621440	118831	118848	AATTCTTTGTGATGATGG	82	5-8-5	1217
621441	119044	119061	GCACATATTTACATTTTA	94	5-8-5	1218
621442	119224	119241	GGTGAGAGAGCCAGCCTC	59	5-8-5	1219
621443	119404	119421	CAAACAGCCTCCCATGAA	38	5-8-5	1220
621444	119584	119601	ATATCCTAAGCATTGTCT	71	5-8-5	1221
621445	119880	119897	TACAGTGGCTCCTGTAAT	18	5-8-5	1222
621446	120060	120077	GCTCATCAAAGCAAAAAC	84	5-8-5	1223
621447	120248	120265	CTGGGCTGTGCGATCTGG	69	5-8-5	1224
621448	120439	120456	AAGCCACCATGCCTGTAA	89	5-8-5	1225
621449	120660	120677	ACACCATCACGGCTCAGT	56	5-8-5	1226
621450	120840	120857	AGGGAGTTGGAAAACTG	46	5-8-5	1227
621451	121209	121226	CAGGTTTGAGAAGCCCTG	0	5-8-5	1228
621452	121389	121406	AGACCCACCGGCACATTC	56	5-8-5	1229
621453	121569	121586	ATTTCCAGCGGGCTTTAC	62	5-8-5	1230
621454	121761	121778	GCTTGCTCGCAAGGACGC	93	5-8-5	1231
621455	121941	121958	CCACAGCACGGCGCATGG	65	5-8-5	1232
621456	122121	122138	ACACCCCTCCTAGAATA	0	5-8-5	1233
621457	122301	122318	ACCACCTTCAGCCCACT	22	5-8-5	1234
621458	122481	122498	TAAGCTGGAGGCTTAGGA	40	5-8-5	1235
621459	122678	122695	GAACCTCCCGCCTTAGTC	19	5-8-5	1236

621460	122913	122930	TATATGATTGTTTTTTGA	0	5-8-5	1237
621461	123093	123110	AGGAGCCTCGGGTGCCCA	30	5-8-5	1238
621462	123273	123290	TCAGGCCAGGCATTTTCT	58	5-8-5	1239
621463	123453	123470	CACCTAGCAGACACTGGT	77	5-8-5	1240
621464	123633	123650	TCCTCTGGCCGAGCTCAC	58	5-8-5	1241
621465	123824	123841	ACAGCGCGGGACACACGG	77	5-8-5	1242
621466	124004	124021	GCATCTCTTCTCACCAGG	13	5-8-5	1243
621467	124184	124201	GGATACCTGGAGGGCAGG	13	5-8-5	1244
621468	124379	124396	TGAGGCCAGCACTGAGGG	29	5-8-5	1245
621469	124559	124576	ACTGGAACCATCCCGAAT	37	5-8-5	1246
621470	124752	124769	GCAGTGGCCTTGTGTGGG	19	5-8-5	1247
621471	124932	124949	ACCCTGAGCTGCCAGCTG	53	5-8-5	1248
621472	125112	125129	CTGCACACTCAGTGTCT	78	5-8-5	1249
621473	125292	125309	CTGGAAGGCAGGAGTGG	33	5-8-5	1250
621474	125472	125489	AAGAGCCTCTGGGAAAAA	50	5-8-5	1251
621475	125652	125669	GGTGTAACCAATGAGAA	41	5-8-5	1252
621476	125832	125849	GGCTACCTGGTTTATGAT	32	5-8-5	1253
621477	126012	126029	GGAGCGAGCTGGAGCCAC	75	5-8-5	1254
621478	126332	126349	GCTCACTCCGCTCACTGC	74	5-8-5	1255
621479	126527	126544	CTAGGTCTTATTCTATTT	38	5-8-5	1256
621480	127208	127225	AGGTTTTTGTGTGTGTT	54	5-8-5	1257
621481	127396	127413	CCTCTTCACTTAAAAAA	24	5-8-5	1258
621482	127591	127608	AAACAAAGTCACAGAGGG	67	5-8-5	1259
621483	127934	127951	AGGATCACTTTCTTTTCT	31	5-8-5	1260
621484	128271	128288	TTGCTGAGTCTCACTCTG	87	5-8-5	1261
621485	128451	128468	CAGAATCTATAGCTGTGT	51	5-8-5	1262
621486	128631	128648	ATACTTTCCACAGGGAGA	45	5-8-5	1263
621487	128811	128828	GAAGAAGGGTCCCTCTCT	38	5-8-5	1264
621488	128993	129010	ATGAGAGTACAACCTCCAT	44	5-8-5	1265
621489	129269	129286	ACCCTTTCAGGCCGGGCG	44	5-8-5	1266
621490	129678	129695	TAAGTAAAGTCTGTTTTT	47	5-8-5	1267
621491	129861	129878	TAGAATGGTGTTTGGATA	42	5-8-5	1268
621492	130040	130057	GCAGTCTACAGGGCAAAG	79	5-8-5	1269
621493	130234	130251	ACCTTTTTATTTCCTCCG	14	5-8-5	1270
621494	130414	130431	AGCTCCAGGTGATTGAGA	68	5-8-5	1271
621495	130691	130708	GTCGCCATGTAAGAAATG	46	5-8-5	1272
621496	130902	130919	AGGGAGACTGATATGGTT	31	5-8-5	1273
621497	131113	131130	ATATTGCTTGACCTCAGG	18	5-8-5	1274
621498	131543	131560	AGTGGTTCTCGCTTTTTT	75	5-8-5	1275
621499	131725	131742	CAAGACAGGCAGGCAGAG	19	5-8-5	1276
621500	131905	131922	GTGCTTGGCTGCGCTTCT	45	5-8-5	1277
621501	132085	132102	CAGACCTCTATCTTTTAG	24	5-8-5	1278
621502	132266	132283	AGGAGGGTCTTTCCCGTG	57	5-8-5	1279

621503	132446	132463	AACTGGGCCACCATGAGA	30	5-8-5	1280
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Table 27

Inhibition of Tau mRNA by 5-8-5 MOE gapmers targeting SEQ ID NO: 1

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	% inhibition	Motif	SEQ ID NO:
621519	5901	5918	CCTGCCGCTCGGCCGTCC	19	5-8-5	1281
621520	5904	5921	CGCCCTGCCGCTCGGCCG	0	5-8-5	1282
621521	5919	5936	GTGGGCGCGCGCGAGCGC	7	5-8-5	1283
621522	5922	5939	CTAGTGGGCGCGCGCGAG	6	5-8-5	1284
621523	5925	5942	CCACTAGTGGGCGCGCGC	0	5-8-5	1285
621524	5928	5945	CGGCCACTAGTGGGCGCG	18	5-8-5	1286
621525	5931	5948	CTCCGGCCACTAGTGGGC	39	5-8-5	1287
621526	5934	5951	CTCCTCCGGCCACTAGTG	37	5-8-5	1288
621527	5937	5954	CTTCTCCTCCGGCCACTA	15	5-8-5	1289
621528	5940	5957	AGCCTTCTCCTCCGGCCA	0	5-8-5	1290
621529	5943	5960	GGGAGCCTTCTCCTCCGG	0	5-8-5	1291
621530	5946	5963	CGCGGGAGCCTTCTCCTC	28	5-8-5	1292
621531	5949	5966	CTCCGCGGGAGCCTTCTC	0	5-8-5	1293
621532	5952	5969	GGCCTCCGCGGGAGCCTT	0	5-8-5	1294
621533	5955	5972	CGCGGCCTCCGCGGGAGC	0	5-8-5	1295
621534	5958	5975	CAGCGCGGCCTCCGCGGG	0	5-8-5	1296
621535	5961	5978	GGGCAGCGCGGCCTCCGC	31	5-8-5	1297
621536	5964	5981	GGCGGGCAGCGCGGCCTC	17	5-8-5	1298
621537	5987	6004	ACGCGAGCCTCCCCAGGG	10	5-8-5	1299
621538	5990	6007	GGAACGCGAGCCTCCCCA	33	5-8-5	1300
621539	5993	6010	GCGGGAACGCGAGCCTCC	0	5-8-5	1301
621540	5996	6013	GCAGCGGGAACGCGAGCC	0	5-8-5	1302
621541	5999	6016	CGAGCAGCGGGAACGCGA	0	5-8-5	1303
621542	6002	6019	GCGCGAGCAGCGGGAACG	9	5-8-5	1304
621543	6005	6022	CAGGCGCGAGCAGCGGGA	22	5-8-5	1305
621544	6008	6025	GCGCAGGCGCGAGCAGCG	1	5-8-5	1306
621545	6011	6028	GCGGCGCAGGCGCGAGCA	11	5-8-5	1307
621546	6014	6031	CGGGCGGCGCAGGCGCGA	47	5-8-5	1308
621547	6017	6034	CGGCGGGCGGCGCAGGCG	15	5-8-5	1309
621548	6020	6037	GGCCGCGGGCGGCGCAG	0	5-8-5	1310
621549	6023	6040	TGAGGCCGGCGGGCGGCG	5	5-8-5	1311
621550	6026	6043	TCCTGAGGCCGCGGGCG	20	5-8-5	1312
621551	6029	6046	CGTTCCTGAGGCCGCGCG	13	5-8-5	1313
621552	6045	6062	GCCGGCGAAGAGGGCGCG	0	5-8-5	1314
621553	6048	6065	CGCGCCGGCGAAGAGGGC	0	5-8-5	1315
621554	6051	6068	GCGCGCGCCGGCGAAGAG	0	5-8-5	1316
621555	6054	6071	AGGGCGCGCGCCGGCGAA	32	5-8-5	1317

621556	6057	6074	GCGAGGGCGCGCGCCGGC	15	5-8-5	1318
621557	6060	6077	ACTGCGAGGGCGCGGCC	30	5-8-5	1319
621558	6063	6080	GTGACTGCGAGGGCGCGC	38	5-8-5	1320
621559	6066	6083	GCGGTGACTGCGAGGGCG	30	5-8-5	1321
621560	6069	6086	GTGGCGGTGACTGCGAGG	37	5-8-5	1322
621561	6072	6089	TGGGTGGCGGTGACTGCG	48	5-8-5	1323
621562	6075	6092	TGGTGGGTGGCGGTGACT	34	5-8-5	1324
621563	6078	6095	AGCTGGTGGGTGGCGGTG	54	5-8-5	1325
621564	6081	6098	CGGAGCTGGTGGGTGGCG	36	5-8-5	1326
621565	6084	6101	TGCCGAGCTGGTGGGTG	52	5-8-5	1327
621566	6087	6104	TGGTGCCGAGCTGGTGG	64	5-8-5	1328
621567	6090	6107	TGTTGGTGCCGAGCTGG	74	5-8-5	1329
621568	6093	6110	TGCTGTTGGTGCCGAGC	50	5-8-5	1330
621569	6096	6113	CGCTGCTGTTGGTGCCGG	47	5-8-5	1331
621570	6111	6128	GGGCGGTGGCAGCGGCGC	86	5-8-5	1332
621571	6114	6131	GGTGGGCGGTGGCAGCGG	61	5-8-5	1333
621572	6117	6134	GAAGGTGGGCGGTGGCAG	19	5-8-5	1334
621573	6120	6137	GCAGAAGGTGGGCGGTGG	22	5-8-5	1335
621574	6123	6140	GCGGCAGAAGGTGGGCGG	18	5-8-5	1336
621575	6126	6143	GCGGCGGCAGAAGGTGGG	62	5-8-5	1337
621576	6129	6146	GTGGCGGCGGCAGAAGGT	79	5-8-5	1338
621577	6132	6149	GTGGTGGCGGCGGCAGAA	70	5-8-5	1339
621578	6135	6152	GCTGTGGTGGCGGCGGCA	78	5-8-5	1340
621579	6138	6155	GTGGCTGTGGTGGCGGCG	78	5-8-5	1341
621580	6141	6158	AAGGTGGCTGTGGTGGCG	72	5-8-5	1342
613412	73879	73898	GTGATCTTCCATCACTTCGA	78	5-8-5	25
620887	98891	98908	GTTTTCAAACACACCTTC	94	5-8-5	665
	98928	98945				
621504	132626	132643	AAACCCTTCTCACAAAAC	17	5-8-5	1343
621505	132812	132829	CCTCCTGGTCCCTCCTCG	12	5-8-5	1344
621506	132992	133009	CCTATCCAGACCCACTCA	10	5-8-5	1345
621507	133179	133196	CACAACCACCCGGGACG	8	5-8-5	1346
621508	133359	133376	GGACCAGGATGGTGTTTT	44	5-8-5	1347
621509	133539	133556	GGCTTTGATAAAAATATT	8	5-8-5	1348
621510	133788	133805	CGCCTCCGGGATCAAGCA	47	5-8-5	1349
621511	133968	133985	GGTTCGCATTTAAGCTAG	28	5-8-5	1350
621512	134148	134165	ACGGTCATTCTCAGCCCT	59	5-8-5	1351
621513	134333	134350	TAACCTCCAGAGCAACTG	26	5-8-5	1352
621514	134513	134530	GGCAGGTGGGCCACAAAA	17	5-8-5	1353
621515	134696	134713	TCAAAAGGCATGCACATT	44	5-8-5	1354
621516	134876	134893	TAGTATTCCGTCGCCACG	40	5-8-5	1355
621517	135057	135074	GAGCTGTTGTTTTTATTG	7	5-8-5	1356
621518	135369	135386	GCCAGGGACTGTTTTTTG	62	5-8-5	1357

Table 28
Inhibition of tau mRNA by 5-8-5 MOE gapmers targeting SEQ ID NOs: 1 and 2

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	% inhibition	SEQ ID NO: 2 start site	SEQ ID NO: 2 stop site	Motif	SEQ ID NO:
621596	n/a	n/a	TCACCTGATAGTCGACAG	70	292	309	5-8-5	1358
621597	n/a	n/a	AGTTCACCTGATAGTCGA	61	295	312	5-8-5	1359
621598	n/a	n/a	CAAAGTTCACCTGATAGT	44	298	315	5-8-5	1360
621599	n/a	n/a	GTTCAAAGTTCACCTGAT	72	301	318	5-8-5	1361
621629	n/a	n/a	GATTCTTTCAGGCCAGCG	42	442	459	5-8-5	1362
621630	n/a	n/a	GGAGATTCTTTCAGGCCA	0	445	462	5-8-5	1363
621649	n/a	n/a	ATCTTCCGCTGTTGGAGT	43	527	544	5-8-5	1364
621650	n/a	n/a	CACATCTTCCGCTGTTGG	3	530	547	5-8-5	1365
621651	n/a	n/a	TGTCACATCTTCCGCTGT	0	533	550	5-8-5	1366
621652	n/a	n/a	TGCTGTCACATCTTCCGC	30	536	553	5-8-5	1367
621653	n/a	n/a	AGGGTGCTGTCACATCTT	61	540	557	5-8-5	1368
621581	6144	6161	GAGAAGGTGGCTGTGGTG	14	244	261	5-8-5	1369
621582	6147	6164	GAGGAGAAGGTGGCTGTG	53	247	264	5-8-5	1370
621583	6153	6170	GCGGAGGAGGAGAAGGTG	25	253	270	5-8-5	1371
621584	6156	6173	ACAGCGGAGGAGGAGAAG	2	256	273	5-8-5	1372
621585	6159	6176	AGGACAGCGGAGGAGGAG	38	259	276	5-8-5	1373
621586	6162	6179	GAGAGGACAGCGGAGGAG	53	262	279	5-8-5	1374
621587	6165	6182	CGGGAGAGGACAGCGGAG	43	265	282	5-8-5	1375
621588	6168	6185	GGACGGGAGAGGACAGCG	69	268	285	5-8-5	1376
621589	6171	6188	CGAGGACGGGAGAGGACA	0	271	288	5-8-5	1377
621590	6174	6191	AGGCGAGGACGGGAGAGG	13	274	291	5-8-5	1378
621591	6177	6194	CAGAGGCGAGGACGGGAG	10	277	294	5-8-5	1379
621592	6180	6197	CGACAGAGGCGAGGACGG	57	280	297	5-8-5	1380
621593	6183	6200	AGTCGACAGAGGCGAGGA	61	283	300	5-8-5	1381
621594	6186	6203	GATAGTCGACAGAGGCGA	65	286	303	5-8-5	1382
621595	6189	6206	CCTGATAGTCGACAGAGG	51	289	306	5-8-5	1383
621600	73838	73855	CTGGTTCAAAGTTCACCT	52	304	321	5-8-5	1384
621601	73841	73858	ATCCTGGTTCAAAGTTCA	62	307	324	5-8-5	1385
621602	73844	73861	GCCATCCTGGTTCAAAGT	42	310	327	5-8-5	1386
621603	73847	73864	TCAGCCATCCTGGTTCAA	38	313	330	5-8-5	1387
621604	73850	73867	GGCTCAGCCATCCTGGTT	65	316	333	5-8-5	1388
621605	73867	73884	CTTCGAACTCCTGGCGGG	20	333	350	5-8-5	1389
621606	73870	73887	TCACTTCGAACTCCTGGC	51	336	353	5-8-5	1390
621607	73873	73890	CCATCACTTCGAACTCCT	68	339	356	5-8-5	1391
621608	73876	73893	CTTCCATCACTTCGAACT	28	342	359	5-8-5	1392
613412	73879	73898	GTGATCTTCCATCACTTCGA	75	345	364	5-8-5	25
621609	73879	73896	GATCTTCCATCACTTCGA	68	345	362	5-8-5	1393

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621610	73882	73899	CGTGATCTTCCATCACTT	13	348	365	5-8-5	1394
621611	73906	73923	TGTCCCCCAACCCGTACG	46	372	389	5-8-5	1395
621612	73909	73926	TCCTGTCCCCCAACCCGT	54	375	392	5-8-5	1396
621613	73912	73929	CTTTCCTGTCCCCAACC	43	378	395	5-8-5	1397
621614	73915	73932	GATCTTTCTGTCCCCCA	71	381	398	5-8-5	1398
621615	73918	73935	CCTGATCTTTCTGTCCC	71	384	401	5-8-5	1399
621616	73921	73938	CCCCCTGATCTTTCTGT	54	387	404	5-8-5	1400
621617	73924	73941	AGCCCCCTGATCTTTCC	40	390	407	5-8-5	1401
621618	73927	73944	TGTAGCCCCCTGATCTT	35	393	410	5-8-5	1402
621619	73930	73947	TGGTGTAGCCCCCTGAT	31	396	413	5-8-5	1403
621620	73933	73950	GCATGGTGTAGCCCCCT	71	399	416	5-8-5	1404
621621	73936	73953	GGTGCATGGTGTAGCCCC	62	402	419	5-8-5	1405
621622	73939	73956	CTTGGTGCATGGTGTAGC	54	405	422	5-8-5	1406
621623	73942	73959	GGTCTTGGTGCATGGTGT	65	408	425	5-8-5	1407
621624	73945	73962	CTTGGTCTTGGTGCATGG	63	411	428	5-8-5	1408
621625	73948	73965	CCTCTTGGTCTTGGTGCA	49	414	431	5-8-5	1409
621626	73951	73968	CACCCTCTTGGTCTTGGT	65	417	434	5-8-5	1410
621627	73956	73973	CGTGTCACCCCTCTTGGTC	49	422	439	5-8-5	1411
621628	73959	73976	GTCCGTGTCACCCCTCTTG	70	425	442	5-8-5	1412
621631	83395	83412	AGATCCGTCCTCAGTGGG	48	473	490	5-8-5	1413
621632	83398	83415	CTCAGATCCGTCCTCAGT	38	476	493	5-8-5	1414
621633	83401	83418	TTCCTCAGATCCGTCCTC	11	479	496	5-8-5	1415
621634	83404	83421	CGGTTCTCAGATCCGTC	57	482	499	5-8-5	1416
621635	83407	83424	GCCCGGTTCTCAGATCC	38	485	502	5-8-5	1417
621636	83410	83427	AGAGCCCGGTTCTCAGA	63	488	505	5-8-5	1418
621637	83413	83430	TTCAGAGCCCGGTTCTC	50	491	508	5-8-5	1419
621638	83416	83433	GGTTTCAGAGCCCGGTTTC	48	494	511	5-8-5	1420
621639	83419	83436	AGAGGTTTCAGAGCCCGG	41	497	514	5-8-5	1421
621640	83422	83439	ATCAGAGGTTTCAGAGCC	40	500	517	5-8-5	1422
621641	83425	83442	AGCATCAGAGGTTTCAGA	23	503	520	5-8-5	1423
621642	83428	83445	CTTAGCATCAGAGGTTTC	50	506	523	5-8-5	1424
621643	83431	83448	GCTCTTAGCATCAGAGGT	69	509	526	5-8-5	1425
621644	83434	83451	AGTGCTCTTAGCATCAGA	80	512	529	5-8-5	1426
621645	83437	83454	TGGAGTGCTCTTAGCATC	50	515	532	5-8-5	1427
621646	83440	83457	TGTTGGAGTGCTCTTAGC	59	518	535	5-8-5	1428
621647	83443	83460	CGCTGTTGGAGTGCTCTT	70	521	538	5-8-5	1429
621648	83446	83463	TTCCGCTGTTGGAGTGCT	52	524	541	5-8-5	1430
621654	85904	85921	CTAAGGGTGCTGTACAT	64	543	560	5-8-5	1431
621655	85907	85924	CCACTAAGGGTGCTGTCA	44	546	563	5-8-5	1432
621656	85910	85927	CATCCACTAAGGGTGCTG	55	549	566	5-8-5	1433
621657	85913	85930	CCTCATCCACTAAGGGTG	41	552	569	5-8-5	1434
620887	98891	98908	GTTTTCAAACACACCTTC	81	n/a	n/a	5-8-5	665
	98928	98945			n/a	n/a		

Table 29
Inhibition of Tau mRNA by 5-8-5 MOE gapmers targeting SEQ ID NOs: 1 and 2

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	% inhibition	SEQ ID NO: 2 start site	SEQ ID NO: 2 stop site	Motif	SEQ ID NO
621672	n/a	n/a	GCTGTGGTTCCTTCTGGG	51	613	630	5-8-5	1435
621676	n/a	n/a	TCAGGCTCTTGGGTCACG	0	685	702	5-8-5	1436
621677	n/a	n/a	CTTTCAGGCTCTTGGGTC	0	688	705	5-8-5	1437
621678	n/a	n/a	CCACTTTCAGGCTCTTGG	51	691	708	5-8-5	1438
613412	73879	73898	GTGATCTTCCATCACTTCGA	79	345	364	5-10-5	25
621658	85916	85933	CTCCCTCATCCACTAAGG	27	555	572	5-8-5	1439
621659	85919	85936	GAGCTCCCTCATCCACTA	35	558	575	5-8-5	1440
621660	85922	85939	CGGGAGCTCCCTCATCCA	25	561	578	5-8-5	1441
621661	85925	85942	TGCCGGGAGCTCCCTCAT	40	564	581	5-8-5	1442
621662	85928	85945	GCTTGCCGGGAGCTCCCT	47	567	584	5-8-5	1443
621663	85931	85948	CCTGCTTGCCGGGAGCTC	46	570	587	5-8-5	1444
621664	85934	85951	CAGCCTGCTTGCCGGGAG	45	573	590	5-8-5	1445
621665	85937	85954	CGGCAGCCTGCTTGCCGG	1	576	593	5-8-5	1446
621666	85940	85957	GCGCGGCAGCCTGCTTGC	31	579	596	5-8-5	1447
621667	85943	85960	GCTGCGCGGCAGCCTGCT	50	582	599	5-8-5	1448
621668	85962	85979	TCTGGGATCTCCGTGTGG	39	601	618	5-8-5	1449
621669	85965	85982	CCTTCTGGGATCTCCGTG	56	604	621	5-8-5	1450
621670	85968	85985	GTTCTTCTGGGATCTCC	79	607	624	5-8-5	1451
621671	85971	85988	GTGGTTCCTTCTGGGATC	49	610	627	5-8-5	1452
621673	89894	89911	CAATGCCTGCTTCTTCAG	31	630	647	5-8-5	1453
621674	89899	89916	GTCTCCAATGCCTGCTTC	43	635	652	5-8-5	1454
621675	89902	89919	GGTGTCTCCAATGCCTGC	74	638	655	5-8-5	1455
621679	94695	94712	TTACCACTTTCAGGCTCT	63	694	711	5-8-5	1456
621680	94700	94717	CCACCTTACCACTTTCAG	28	699	716	5-8-5	1457
621681	94703	94720	GGACCACCTTACCACTTT	62	702	719	5-8-5	1458
621682	94706	94723	CCTGGACCACCTTACCAC	33	705	722	5-8-5	1459
621683	94709	94726	CTTCCTGGACCACCTTAC	18	708	725	5-8-5	1460
621684	94712	94729	AGCCTTCCTGGACCACCT	61	711	728	5-8-5	1461
621685	94715	94732	GGAAGCCTTCCTGGACCA	54	714	731	5-8-5	1462
621686	94718	94735	GGAGGAAGCCTTCCTGGA	24	717	734	5-8-5	1463
621687	94721	94738	CTCGGAGGAAGCCTTCCT	48	720	737	5-8-5	1464
621688	94724	94741	GCTCTCGGAGGAAGCCTT	27	723	740	5-8-5	1465
621689	94727	94744	CTGGCTCTCGGAGGAAGC	19	726	743	5-8-5	1466
621690	94730	94747	GGCCTGGCTCTCGGAGGA	46	729	746	5-8-5	1467
621691	94749	94766	TGGTGGCTCAGACCTGGG	49	748	765	5-8-5	1468
621692	94752	94769	AGCTGGTGGCTCAGACCT	50	751	768	5-8-5	1469
621693	94755	94772	ATGAGCTGGTGGCTCAGA	17	754	771	5-8-5	1470
621694	94758	94775	GACATGAGCTGGTGGCTC	54	757	774	5-8-5	1471
621695	94761	94778	CCGGACATGAGCTGGTGG	26	760	777	5-8-5	1472

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621696	94764	94781	ATGCCGGACATGAGCTGG	12	763	780	5-8-5	1473
621697	94767	94784	GGCATGCCGGACATGAGC	11	766	783	5-8-5	1474
621698	94770	94787	CCAGGCATGCCGGACATG	41	769	786	5-8-5	1475
621699	94773	94790	GCCCCAGGCATGCCGGAC	57	772	789	5-8-5	1476
621700	94776	94793	GGAGCCCCAGGCATGCCG	47	775	792	5-8-5	1477
621701	94793	94810	GGCCCTCAGGCAGGAGGG	0	792	809	5-8-5	1478
621702	94825	94842	TGTCCCCGAAGGTTGGCG	50	824	841	5-8-5	1479
621703	94828	94845	TCCTGTCCCCGAAGGTTG	38	827	844	5-8-5	1480
621704	94831	94848	AGGTCCTGTCCCCGAAGG	41	830	847	5-8-5	1481
621705	94834	94851	CTCAGGTCCTGTCCCCGA	60	833	850	5-8-5	1482
621706	94837	94854	GTCCTCAGGTCCTGTCCC	0	836	853	5-8-5	1483
621707	94840	94857	TGTGTCCTCAGGTCCTGT	23	839	856	5-8-5	1484
621708	94843	94860	CTCTGTGTCTCAGGTCC	55	842	859	5-8-5	1485
621709	94846	94863	GCCCTCTGTGTCTCAGG	35	845	862	5-8-5	1486
621710	94849	94866	GCCGCCCTCTGTGTCTC	45	848	865	5-8-5	1487
621711	94852	94869	GCGGCCGCCCTCTGTGTC	0	851	868	5-8-5	1488
621712	94855	94872	GTGGCGGCCGCCCTCTGT	0	854	871	5-8-5	1489
621713	94875	94892	TGCTTGAGCAGCTCAGGG	67	874	891	5-8-5	1490
621714	94878	94895	TGGTGCTTGAGCAGCTCA	51	877	894	5-8-5	1491
621715	94882	94899	AAGCTGGTGCTTGAGCAG	27	881	898	5-8-5	1492
621716	94885	94902	TAGAAGCTGGTGCTTGAG	14	884	901	5-8-5	1493
621717	94888	94905	TCCTAGAAGCTGGTGCTT	0	887	904	5-8-5	1494
621718	94891	94908	GTCTCCTAGAAGCTGGTG	45	890	907	5-8-5	1495
621719	94894	94911	CAGGTCTCCTAGAAGCTG	47	893	910	5-8-5	1496
621720	94897	94914	GTGCAGGTCTCCTAGAAG	41	896	913	5-8-5	1497
621721	94900	94917	CTGGTGAGGTCTCCTAG	36	899	916	5-8-5	1498
621722	94903	94920	CTCCTGGTGAGGTCTCC	41	902	919	5-8-5	1499
621723	94906	94923	CCCCTCCTGGTGAGGTCT	39	905	922	5-8-5	1500
621724	94909	94926	CGGCCCTCCTGGTGAG	19	908	925	5-8-5	1501
621725	94912	94929	CGGCGGCCCTCCTGGTG	22	911	928	5-8-5	1502
621726	94915	94932	CAGCGGCGGCCCTCCTG	35	914	931	5-8-5	1503
621727	94918	94935	CTTCAGCGGCGGCCCTC	46	917	934	5-8-5	1504
621728	94921	94938	CCCCTTCAGCGGCGGCC	36	920	937	5-8-5	1505
621729	94924	94941	TGCCCCCTTCAGCGGCGG	17	923	940	5-8-5	1506
621730	94927	94944	CCCTGCCCCCTTCAGCGG	15	926	943	5-8-5	1507
621731	94930	94947	GCCCCCTGCCCCCTTCAG	27	929	946	5-8-5	1508
621732	94933	94950	TTTGCCCCCTGCCCCCTT	49	932	949	5-8-5	1509
621733	94936	94953	CTCTTTGCCCCCTGCCCC	22	935	952	5-8-5	1510
621734	94939	94956	CCTCTCTTTGCCCCCTGC	28	938	955	5-8-5	1511
620887	98891	98908	GTTTTCAAACACACCTTC	90	n/a	n/a	5-8-5	665
	98928	98945			n/a	n/a		

Table 30

Inhibition of tau mRNA by 5-10-5 MOE and 5-8-5 MOE gapmers targeting SEQ ID NO: 1

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	% inhibition	Motif	SEQ ID NO:
613412	73879	73898	GTGATCTTCCATCACTTCGA	82	5-10-5	25
620887	98891	98908	GTTTTCAAACACACCTTC	92	5-8-5	665
	98928	98945				
621735	94942	94959	CGGCCTCTCTTTGCCCCC	34	5-8-5	1512
621736	94945	94962	CCCCGGCCTCTCTTTGCC	27	5-8-5	1513
621737	94948	94965	GCTCCCCGGCCTCTCTTT	44	5-8-5	1514
621738	94951	94968	CTTGCTCCCCGGCCTCTC	38	5-8-5	1515
621739	94954	94971	CTCCTTGCTCCCCGGCCT	37	5-8-5	1516
621740	94957	94974	CTCCTCCTTGCTCCCCGG	33	5-8-5	1517
621741	94960	94977	CACCTCCTCCTTGCTCCC	37	5-8-5	1518
621742	94963	94980	ATCCACCTCCTCCTTGCT	32	5-8-5	1519
621743	94967	94984	CTTCATCCACCTCCTCCT	51	5-8-5	1520
621744	94970	94987	GGTCTTCATCCACCTCCT	61	5-8-5	1521
621745	94973	94990	CGCGGTCTTCATCCACCT	71	5-8-5	1522
621746	94976	94993	CGTCGCGGTCTTCATCCA	48	5-8-5	1523
621747	95038	95055	CCGCCCATCTTGGGCTGG	12	5-8-5	1524
621748	95041	95058	AGGCCGCCCATCTTGGGC	18	5-8-5	1525
621749	95044	95061	GGGAGGCCGCCCATCTTG	21	5-8-5	1526
621750	95060	95077	CTCTGGCGGCTGTCTGGG	47	5-8-5	1527
621751	95063	95080	CTTCTCTGGCGGCTGTCT	41	5-8-5	1528
621752	95066	95083	TGGCTTCTCTGGCGGCTG	53	5-8-5	1529
621753	95069	95086	TGGTGGCTTCTCTGGCGG	26	5-8-5	1530
621754	95072	95089	TGCTGGTGGCTTCTCTGG	57	5-8-5	1531
621755	95075	95092	GGATGCTGGTGGCTTCTC	65	5-8-5	1532
621756	95078	95095	CTGGGATGCTGGTGGCTT	66	5-8-5	1533
621757	95081	95098	AGCCTGGGATGCTGGTGG	51	5-8-5	1534
621758	95084	95101	GGAAGCCTGGGATGCTGG	57	5-8-5	1535
621759	95092	95109	CTCCGCTGGGAAGCCTGG	48	5-8-5	1536
621760	95095	95112	ACCCTCCGCTGGGAAGCC	38	5-8-5	1537
621761	95098	95115	GGCACCTCCGCTGGGAA	54	5-8-5	1538
621762	95101	95118	GATGGCACCTCCGCTGG	27	5-8-5	1539
621763	95121	95138	AGGAAATCCACAGGGAGG	15	5-8-5	1540
621764	95124	95141	GAGAGGAAATCCACAGGG	29	5-8-5	1541
621765	95127	95144	TTGGAGAGGAAATCCACA	45	5-8-5	1542
621766	95130	95147	ACTTTGGAGAGGAAATCC	38	5-8-5	1543
621767	95134	95151	GGAACTTTGGAGAGGAA	56	5-8-5	1544
621768	95137	95154	TGTGGAACTTTGGAGAG	26	5-8-5	1545
621769	95140	95157	CTCTGTGGAACTTTGGA	69	5-8-5	1546
621770	95143	95160	GATCTCTGTGGAACTTT	62	5-8-5	1547

621771	95146	95163	TGGGATCTCTGTGGAAAC	61	5-8-5	1548
621772	95149	95166	GGCTGGGATCTCTGTGGA	47	5-8-5	1549
621773	95152	95169	TGAGGCTGGGATCTCTGT	32	5-8-5	1550
621774	95155	95172	CTCTGAGGCTGGGATCTC	64	5-8-5	1551
621775	95161	95178	GTCGGGCTCTGAGGCTGG	42	5-8-5	1552
621776	95164	95181	CCCGTCGGGCTCTGAGGC	34	5-8-5	1553
621777	95174	95191	CTACACTGGGCCCGTCGG	31	5-8-5	1554
621778	95177	95194	GCCCTACACTGGGCCCGT	48	5-8-5	1555
621779	95180	95197	CCCGCCCTACACTGGGCC	35	5-8-5	1556
621780	95183	95200	TGGCCCGCCCTACACTGG	51	5-8-5	1557
621781	95186	95203	CTTTGGCCCGCCCTACAC	4	5-8-5	1558
621782	95189	95206	GCCCTTTGGCCCGCCCTA	52	5-8-5	1559
621783	95192	95209	CCTGCCCTTTGGCCCGCC	42	5-8-5	1560
621784	95195	95212	CATCCTGCCCTTTGGCCC	49	5-8-5	1561
621785	95198	95215	GGGCATCCTGCCCTTTGG	15	5-8-5	1562
621786	95235	95252	TTGGGTGTGATTTCCACG	52	5-8-5	1563
621787	95253	95270	GCCTGCTCCTTCTGCACG	44	5-8-5	1564
621788	95256	95273	TGCGCCTGCTCCTTCTGC	64	5-8-5	1565
621789	95259	95276	GAGTGCGCCTGCTCCTTC	70	5-8-5	1566
621790	95262	95279	TCCGAGTGCGCCTGCTCC	53	5-8-5	1567
621791	95265	95282	TCCTCCGAGTGCGCCTGC	54	5-8-5	1568
621792	95268	95285	TGCTCCTCCGAGTGCGCC	52	5-8-5	1569
621793	95271	95288	AAATGCTCCTCCGAGTGC	72	5-8-5	1570
621794	95274	95291	CCCAAATGCTCCTCCGAG	75	5-8-5	1571
621795	95277	95294	CTTCCCAAATGCTCCTCC	47	5-8-5	1572
621796	95280	95297	GCCCTTCCCAAATGCTCC	58	5-8-5	1573
621797	95283	95300	GCAGCCCTTCCCAAATGC	39	5-8-5	1574
621798	95286	95303	AATGCAGCCCTTCCCAA	61	5-8-5	1575
621799	95291	95308	CTGGAAATGCAGCCCTTC	64	5-8-5	1576
621800	95294	95311	CCCCTGGAAATGCAGCCC	49	5-8-5	1577
621801	95297	95314	GGGCCCTGGAAATGCAG	29	5-8-5	1578
621802	95313	95330	TCTGGCCCTCTCCAGGG	41	5-8-5	1579
621803	95316	95333	GCCTCTGGCCCTCTCCA	42	5-8-5	1580
621804	95319	95336	CGGGCCTCTGGCCCTCT	11	5-8-5	1581
621805	95322	95339	CCCCGGGCCTCTGGCCCC	13	5-8-5	1582
621806	95341	95358	GTCCTCTCCCAAAGAGGG	25	5-8-5	1583
621807	95344	95361	TGTGTCTCTCCCAAAGA	20	5-8-5	1584
621808	95347	95364	TTTTGTGTCCTCTCCCAA	66	5-8-5	1585
621809	95365	95382	CTCTGGAAGGTCAGCCTC	53	5-8-5	1586
621810	95368	95385	GGGCTCTGGAAGGTCAGC	72	5-8-5	1587
621811	95371	95388	AGAGGGCTCTGGAAGGTC	57	5-8-5	1588

Table 31
Inhibition of tau mRNA by 5-10-5 and 5-8-5 MOE gapmers targeting SEQ ID NO: 1

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	% inhibition	Motif	SEQ ID NO:
613412	73879	73898	GTGATCTTCCATCACTTCGA	88	5-10-5	25
620887	98891	98908	GTTTTCAAACACACCTTC	96	5-8-5	665
	98928	98945				
623737	111219	111236	CCTCCACCCAGCATGGTG	56	5-8-5	1589
623738	111267	111284	TCAAGTCACCCTTTCTCC	78	5-8-5	1590
623739	111368	111385	TTCAGACAATTTTCTAG	66	5-8-5	1591
623740	111629	111646	TCAGACTCCGCCAGCTTT	79	5-8-5	1592
623741	111678	111695	TCTTTTCCCTTTGGTGTT	34	5-8-5	1593
623742	111753	111770	TTTCCCCCAATGATTTGC	77	5-8-5	1594
623743	112016	112033	CCACGACTCCCACAAGAT	32	5-8-5	1595
623744	112213	112230	TGAGGTTGAGGGTAGGTG	50	5-8-5	1596
623745	112219	112236	AGTGTTGAGGTTGAGGG	31	5-8-5	1597
623746	112304	112321	CAGGCACTTGGAAGTGC	90	5-8-5	1598
623747	112877	112894	TTGTACTCTTTTCCCT	65	5-8-5	1599
623748	112949	112966	TTAGGAGTGCAAGGTTGT	49	5-8-5	1600
623749	113352	113369	TCCTACATTCTCCTGCT	67	5-8-5	1601
623750	113523	113540	GTTGCAGTGTTCCACTAT	90	5-8-5	1602
623751	113783	113800	CCAGCAGATGCCGACAGC	74	5-8-5	1603
623752	113809	113826	GGGCCCTCACCCCTGCTT	14	5-8-5	1604
623753	113830	113847	CCAAGAAGGGCTGCTGAG	8	5-8-5	1605
623754	114267	114284	AAGCAGCCACCCAGGCTG	17	5-8-5	1606
623755	114739	114756	TATGAGGAGGGAGGAAAG	13	5-8-5	1607
623756	115242	115259	CTGACATCTCAGCCCAAG	93	5-8-5	1608
621425	115335	115352	GGTACAGGAAAAGATGCC	77	5-8-5	1202
623757	115522	115539	CAAGGTGATCAGCTTAGG	82	5-8-5	1609
623758	115526	115543	AGTCCAAGGTGATCAGCT	89	5-8-5	1610
623759	115547	115564	CCCACACAAGCCTCCTCT	66	5-8-5	1611
623760	115791	115808	TTTGTTTGGGTTTCAGTTC	59	5-8-5	1612
623761	115803	115820	CCTTGATCTGGTTTGT	77	5-8-5	1613
623762	115993	116010	ATCAAGGGAGAGAACGAT	52	5-8-5	1614
623763	116229	116246	AAAAGGCAACAAGCCTTT	0	5-8-5	1615
623764	116769	116786	CGAGGCAAAAAGGGAAAT	45	5-8-5	1616
623765	116791	116808	TAACCTTTGAGCTTCCTGG	65	5-8-5	1617
623766	116944	116961	TAAGGCTTAGAAGATTG	45	5-8-5	1618
623767	116978	116995	GACGATCATTTTTATTC	72	5-8-5	1619
623768	116983	117000	GGCTTGACGATCATTTTT	77	5-8-5	1620
623769	117421	117438	AGATCTCAGAGTTTGTAG	68	5-8-5	1621
623770	117472	117489	TCGCTGAGGTTCCGCAAC	37	5-8-5	1622
623771	117489	117506	AGGAGGCCATGTGAGGCT	61	5-8-5	1623

623772	117547	117564	TGGATAAATCTCTAGTGC	54	5-8-5	1624
623773	117564	117581	CACTCCTCCTTTAGAGAT	38	5-8-5	1625
623774	117599	117616	TTGTAATTCCTTCTCTGG	65	5-8-5	1626
623775	117971	117988	TAACCATCCCTACTTTCT	42	5-8-5	1627
623776	119098	119115	ACTGAAATCGCTCCTTTA	58	5-8-5	1628
623777	119107	119124	CCAATTATGACTGAAATC	32	5-8-5	1629
623778	119313	119330	GGTCAAAGTTATAAATAT	57	5-8-5	1630
623779	119431	119448	GGATTTGATGCAAAGAAA	70	5-8-5	1631
623780	119740	119757	GCGCAACCCAGCTACTCG	7	5-8-5	1632
621445	119880	119897	TACAGTGGCTCCTGTAAT	28	5-8-5	1222
623781	119964	119981	CTGTATACCTATACTTGG	34	5-8-5	1633
623782	120043	120060	CCGTTTTCTTACCACCCT	92	5-8-5	1634
623783	120177	120194	TTACTTGTCTGAATCTTC	83	5-8-5	1635
623784	120204	120221	TTCATCCCGTTTTTTTTC	54	5-8-5	1636
623785	120309	120326	GACCTCAGTGGCTCTTTT	68	5-8-5	1637
623786	120513	120530	TGTCCAGGATAGTTTGAA	44	5-8-5	1638
623787	121033	121050	GCTGAGCAAATGCTCCCG	54	5-8-5	1639
623788	121194	121211	CTGACCCCGTAGGCAGGA	29	5-8-5	1640
623789	121478	121495	ACCAGCCTGAGGTCAAGT	73	5-8-5	1641
623790	121538	121555	CAGGTCCTCACTTCACAA	42	5-8-5	1642
623791	121767	121784	CCGCCTGCTTGCTCGCAA	92	5-8-5	1643
623792	121787	121804	AGTGACACGCCACCCTGG	80	5-8-5	1644
623793	121797	121814	AAAAAGGATGAGTGACAC	28	5-8-5	1645
623794	121807	121824	GGTAGCCAGAAAAAAGGA	49	5-8-5	1646
623795	121812	121829	CCTTTGGTAGCCAGAAAA	63	5-8-5	1647
623796	121817	121834	CTGCACCTTTGGTAGCCA	87	5-8-5	1648
623797	121822	121839	ATTATCTGCACCTTTGGT	67	5-8-5	1649
623798	121824	121841	TAATTATCTGCACCTTTG	49	5-8-5	1650
623799	121905	121922	CACTGCCGCCTCCCGGGA	65	5-8-5	1651
623800	121909	121926	CTCACACTGCCGCCTCCC	75	5-8-5	1652
623801	121911	121928	TACTCACACTGCCGCCTC	54	5-8-5	1653
623679	121913	121930	GGTACTCACACTGCCGCC	81	5-8-5	1654
623802	121915	121932	AAGGTA CTCACTGCCG	69	5-8-5	1655
623803	121920	121937	GTGTGAAGGTA CTCACT	18	5-8-5	1656
623804	121942	121959	GCCACAGCACGGCGCATG	80	5-8-5	1657
623805	121952	121969	AATAATTCAAGCCACAGC	88	5-8-5	1658
623806	121962	121979	ACCACTTCCTAATAATTC	39	5-8-5	1659
623807	121972	121989	ACGCACTCACACCACTTC	83	5-8-5	1660
623808	121982	121999	TCGCAAGTGTACGCACTC	94	5-8-5	1661
623809	121992	122009	ATGCAGTGTCTCGCAAGT	93	5-8-5	1662
623810	122227	122244	TGATGGGTATTCTCAGCT	77	5-8-5	1663

Table 32

Inhibition of tau mRNA by 5-10-5 MOE and 5-8-5 MOE gapmers targeting SEQ ID NO: 1

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	% inhibition	Motif	SEQ ID NO:
613412	73879	73898	GTGATCTTCCATCACTTCG A	87	5-10-5	25
620887	98891	98908	GTTTTCAAACACACCTTC	83	5-8-5	665
	98928	98945				
622186	5897	5914	CCGCTCGGCCGTCGGCG	6	5-8-5	1664
622187	5900	5917	CTGCCGCTCGGCCGTCCG	6	5-8-5	1665
622174	103089	103106	CCAGAGCTGGGTGGTGTC	12	5-8-5	1666
622182	125760	125777	TGTAGACTATTTGCACCT	74	5-8-5	1667
622120	135855	135872	ATCACTGATTTTGAAGTC	36	5-8-5	1668
622121	135858	135875	CCCATCACTGATTTTGAA	59	5-8-5	1669
622122	135861	135878	ACTCCCATCACTGATTTT	70	5-8-5	1670
622123	135864	135881	CTTACTCCCATCACTGAT	41	5-8-5	1671
622124	135867	135884	GCTCTTACTCCCATCACT	82	5-8-5	1672
622125	135870	135887	TTTGCTCTTACTCCCATC	87	5-8-5	1673
622126	135873	135890	AAATTTGCTCTTACTCCC	62	5-8-5	1674
622127	135876	135893	ATGAAATTTGCTCTTACT	70	5-8-5	1675
622128	135879	135896	AAGATGAAATTTGCTCTT	55	5-8-5	1676
622129	135882	135899	GGAAAGATGAAATTTGCT	84	5-8-5	1677
622130	135885	135902	TTTGGAAGATGAAATTT	12	5-8-5	1678
622131	135891	135908	CATCAATTTGGAAAGATG	43	5-8-5	1679
622132	135894	135911	ACCCATCAATTTGGAAAG	18	5-8-5	1680
622133	135897	135914	CCCACCCATCAATTTGGA	34	5-8-5	1681
622134	135900	135917	TAGCCACCCATCAATTT	17	5-8-5	1682
622135	135903	135920	TACTAGCCCACCCATCAA	14	5-8-5	1683
622136	135906	135923	TATTACTAGCCCACCCAT	24	5-8-5	1684
622137	135909	135926	TTTTATTACTAGCCCACC	24	5-8-5	1685
622138	135912	135929	ATATTTTATTACTAGCCC	33	5-8-5	1686
622139	135915	135932	TAAATATTTTATTACTAG	0	5-8-5	1687
622140	135918	135935	TTTTAAATATTTTATTAC	0	5-8-5	1688
622141	135926	135943	ATGTTTTTTTTTAAATAT	0	5-8-5	1689
622142	135939	135956	GCCATGTTTTTGAATGTT	60	5-8-5	1690
622143	135942	135959	GTGGCCATGTTTTTGAAT	28	5-8-5	1691
622144	135945	135962	GATGTGGCCATGTTTTTG	63	5-8-5	1692
622145	135948	135965	TTGGATGTGGCCATGTTT	78	5-8-5	1693
622146	135951	135968	ATGTTGGATGTGGCCATG	71	5-8-5	1694
622147	135954	135971	GAAATGTTGGATGTGGCC	72	5-8-5	1695
622148	135957	135974	GAGGAAATGTTGGATGTG	55	5-8-5	1696
622149	135960	135977	CCTGAGGAAATGTTGGAT	77	5-8-5	1697
622150	135963	135980	TTGCCTGAGGAAATGTTG	55	5-8-5	1698

622151	139811	139828	CCAAATTCACCTTTTACAG	54	5-8-5	1699
622152	139813	139830	TTCCAAATTCACCTTTTAC	67	5-8-5	1700
622153	139815	139832	ATTTCCAAATTCACCTTTT	52	5-8-5	1701
622154	139817	139834	TTATTTCCAAATTCACCTT	52	5-8-5	1702
622155	139819	139836	CTTTATTTCCAAATTCAC	61	5-8-5	1703
622156	139821	139838	AACTTTATTTCCAAATTC	26	5-8-5	1704
622157	139823	139840	ATAACTTTATTTCCAAAT	23	5-8-5	1705
622158	139826	139843	GTAATAACTTTATTTCCA	65	5-8-5	1706
622159	139828	139845	GAGTAATAACTTTATTTTC	25	5-8-5	1707
622160	139830	139847	CAGAGTAATAACTTTATT	9	5-8-5	1708
622161	139832	139849	ATCAGAGTAATAACTTTA	23	5-8-5	1709
622162	139834	139851	TAATCAGAGTAATAACTT	14	5-8-5	1710
622163	139836	139853	TTAATCAGAGTAATAAC	4	5-8-5	1711

Table 33

Inhibition of Tau mRNA by 5-8-5 MOE gapmers targeting SEQ ID NO: 5 and 6

ISIS NO	SEQ ID NO: 5 Start Site	SEQ ID NO: 5 Stop Site	Sequence	% inhibition	SEQ ID NO: 6 Start Site	SEQ ID NO: 6 Stop Site	Motif	SEQ ID NO
622164	n/a	n/a	GCTTCCGCTGTTGGAGTG	22	526	543	5-8-5	1712
622165	n/a	n/a	TCAGCTTCCGCTGTTGGA	15	529	546	5-8-5	1713
622166	n/a	n/a	TCTTCAGCTTCCGCTGTT	0	532	549	5-8-5	1714
622167	n/a	n/a	GCTTCTTCAGCTTCCGCT	43	535	552	5-8-5	1715
622171	n/a	n/a	GCCCCCTTGGCTTTTTTG	16	652	669	5-8-5	1716
622172	n/a	n/a	TCAGCCCCCTTGGCTTTT	15	655	672	5-8-5	1717
622173	n/a	n/a	ACCATCAGCCCCCTTGGC	49	659	676	5-8-5	1718
622175	n/a	n/a	TCACCAGAGCTGGGTGGT	15	778	795	5-8-5	1719
622176	n/a	n/a	GGTTCACCAGAGCTGGGT	80	781	798	5-8-5	1720
622177	n/a	n/a	GGAGGTTCAACCAGAGCTG	79	784	801	5-8-5	1721
622178	n/a	n/a	TTTGAGGTTCAACCAGAG	45	787	804	5-8-5	1722
622179	n/a	n/a	GATTTTGGAGGTTACCA	68	790	807	5-8-5	1723
622180	n/a	n/a	TTGCACCTTCCCGCCTCC	19	1046	1063	5-8-5	1724
622181	n/a	n/a	AGACTATTTGCACCTTCC	70	1053	1070	5-8-5	1725
622183	3	20	CCCTTCGCGGTCCCTTCG	0	n/a	n/a	5-8-5	1726
622184	6	23	CTGCCCTTCGCGGTCCCT	12	n/a	n/a	5-8-5	1727
622185	9	26	GCGCTGCCCTTCGCGGTC	0	n/a	n/a	5-8-5	1728
622188	424	441	GTCCCCCAAACCCGTACG	15	n/a	n/a	5-8-5	1729
622189	427	444	CCTGTCCCCCAAACCCGT	45	n/a	n/a	5-8-5	1730
622190	430	447	TTCTGTCCCCCAAACC	57	n/a	n/a	5-8-5	1731
622191	436	453	TTGATCTTTCCTGTCCCC	74	n/a	n/a	5-8-5	1732
622192	439	456	CCCTTGATCTTTCCTGTC	69	n/a	n/a	5-8-5	1733

622193	442	459	GCCCCCTTGATCTTTCCT	7	n/a	n/a	5-8-5	1734
622194	445	462	GTAGCCCCCTTGATCTTT	3	n/a	n/a	5-8-5	1735
622195	448	465	GGTGTAGCCCCCTTGATC	8	n/a	n/a	5-8-5	1736
622196	451	468	CATGGTGTAGCCCCCTTG	83	n/a	n/a	5-8-5	1737
622168	564	581	ATGCGAGCTTGGGTCACG	65	598	615	5-8-5	1738
622169	567	584	ACCATGCGAGCTTGGGTC	62	601	618	5-8-5	1739
622170	570	587	CTGACCATGCGAGCTTGG	91	604	621	5-8-5	1740

Table 34

Inhibition of tau mRNA by 5-10-5 MOE and 5-8-5 MOE gapmers targeting SEQ ID NO: 1 and 2

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	% inhibition	SEQ ID NO: 2 start site	SEQ ID NO: 2 stop site	Motif	SEQ ID NO:
613412	73879	73898	GTGATCTTCCATCACTTCGA	91	345	364	5-10-5	25
620887	98891	98908	GTTTTCAAACACACCTTC	97	n/a	n/a	5-8-5	665
	98928	98945			n/a	n/a		
621832	n/a	n/a	GAGCTTTGAGTTGAGGGA	14	1434	1451	5-8-5	1741
621833	n/a	n/a	TGCGAGCTTTGAGTTGAG	0	1437	1454	5-8-5	1742
621834	n/a	n/a	CCATGCGAGCTTTGAGTT	10	1440	1457	5-8-5	1743
621835	n/a	n/a	TGACCATGCGAGCTTTGA	83	1443	1460	5-8-5	1744
621836	n/a	n/a	TACTGACCATGCGAGCTT	91	1446	1463	5-8-5	1745
621848	n/a	n/a	GATGTCTTGGCTTTTTTG	3	1492	1509	5-8-5	1746
621849	n/a	n/a	GTGTGGATGTCTTGGCTT	15	1497	1514	5-8-5	1747
621812	95374	95391	TTCAGAGGGCTCTGGAAG	0	1373	1390	5-8-5	1748
621813	95377	95394	CTTTTCAGAGGGCTCTGG	44	1376	1393	5-8-5	1749
621814	95380	95397	CTGCTTTTCAGAGGGCTC	56	1379	1396	5-8-5	1750
621815	95383	95400	AGGCTGCTTTTCAGAGGG	38	1382	1399	5-8-5	1751
621816	95386	95403	AGCAGGCTGCTTTTCAGA	40	1385	1402	5-8-5	1752
621817	95389	95406	AGCAGCAGGCTGCTTTTC	26	1388	1405	5-8-5	1753
621818	95392	95409	AGCAGCAGCAGGCTGCTT	12	1391	1408	5-8-5	1754
621819	95395	95412	CGGAGCAGCAGCAGGCTG	23	1394	1411	5-8-5	1755
621820	95398	95415	CCGCGGAGCAGCAGCAGG	34	1397	1414	5-8-5	1756
621821	95401	95418	CCCCCGCGGAGCAGCAGC	50	1400	1417	5-8-5	1757
621822	95404	95421	CTTCCCCCGCGGAGCAGC	48	1403	1420	5-8-5	1758
621823	95407	95424	GGGCTTCCCCCGCGGAGC	0	1406	1423	5-8-5	1759
621824	95410	95427	GACGGGCTTCCCCCGCGG	7	1409	1426	5-8-5	1760
621825	95413	95430	GCTGACGGGCTTCCCCCG	36	1412	1429	5-8-5	1761
621826	95416	95433	CCGGCTGACGGGCTTCCC	54	1415	1432	5-8-5	1762
621827	95419	95436	GACCCGGCTGACGGGCTT	7	1418	1435	5-8-5	1763
621828	95423	95440	GAGGGACCCGGCTGACGG	6	1422	1439	5-8-5	1764
621829	95426	95443	GTTGAGGGACCCGGCTGA	27	1425	1442	5-8-5	1765
621830	95429	95446	TGAGTTGAGGGACCCGGC	50	1428	1445	5-8-5	1766
621831	95432	95449	CTTTGAGTTGAGGGACCC	50	1431	1448	5-8-5	1767
621837	98559	98576	TTTACTGACCATGCGAG	77	1449	1466	5-8-5	1768

621838	98562	98579	TGCTTTTACTGACCATGC	95	1452	1469	5-8-5	1769
621839	98565	98582	CTTTGCTTTTACTGACCA	85	1455	1472	5-8-5	1770
621840	98568	98585	CGTCTTTGCTTTTACTGA	66	1458	1475	5-8-5	1771
621841	98571	98588	TCCCGTCTTTGCTTTTAC	79	1461	1478	5-8-5	1772
621842	98575	98592	CCAGTCCCGTCTTTGCTT	87	1465	1482	5-8-5	1773
621843	98578	98595	CTTCCAGTCCCGTCTTTG	64	1468	1485	5-8-5	1774
621844	98581	98598	TCGCTTCCAGTCCCGTCT	88	1471	1488	5-8-5	1775
621845	98584	98601	TCATCGCTTCCAGTCCCG	90	1474	1491	5-8-5	1776
621846	98587	98604	TTGTCATCGCTTCCAGTC	88	1477	1494	5-8-5	1777
621847	98590	98607	TTTTTGTCATCGCTTCCA	80	1480	1497	5-8-5	1778
621850	101406	101423	GGTTTTAGCAGAGGAACG	75	1514	1531	5-8-5	1779
621851	101409	101426	CAAGGTTTTAGCAGAGGA	83	1517	1534	5-8-5	1780
621852	101412	101429	TTCAAGGTTTTAGCAGA	35	1520	1537	5-8-5	1781
621853	101415	101432	ATTTTCAAGGTTTATAGC	79	1523	1540	5-8-5	1782
621854	101418	101435	CCTATTTTCAAGGTTTT	71	1526	1543	5-8-5	1783
621855	101425	101442	GGCAAGGCCTATTTTCA	83	1533	1550	5-8-5	1784
621856	101428	101445	TAAGGCAAGGCCTATTTT	23	1536	1553	5-8-5	1785
621857	101431	101448	GGCTAAGGCAAGGCCTAT	69	1539	1556	5-8-5	1786
621858	101457	101474	TGAGCTACCAGGAGTGGG	75	1565	1582	5-8-5	1787
621859	101460	101477	GTCTGAGCTACCAGGAGT	78	1568	1585	5-8-5	1788
621860	101463	101480	AGGGTCTGAGCTACCAGG	82	1571	1588	5-8-5	1789
621861	101466	101483	CAGAGGGTCTGAGCTACC	88	1574	1591	5-8-5	1790
621862	101469	101486	GATCAGAGGGTCTGAGCT	72	1577	1594	5-8-5	1791
621863	101472	101489	TTGGATCAGAGGGTCTGA	83	1580	1597	5-8-5	1792
621864	101478	101495	GGAGGGTTGGATCAGAGG	0	1586	1603	5-8-5	1793
621865	101481	101498	GCTGGAGGGTTGGATCAG	16	1589	1606	5-8-5	1794
621866	101491	101508	ACACAGCAGGGCTGGAGG	34	1599	1616	5-8-5	1795
621867	101494	101511	GGCACACAGCAGGGCTGG	67	1602	1619	5-8-5	1796
621868	101499	101516	CTCTGGGCACACAGCAGG	75	1607	1624	5-8-5	1797
621869	101502	101519	TGGCTCTGGGCACACAGC	90	1610	1627	5-8-5	1798
621870	101505	101522	AGGTGGCTCTGGGCACAC	92	1613	1630	5-8-5	1799
621871	101508	101525	GGAAGGTGGCTCTGGGCA	67	1616	1633	5-8-5	1800
621872	101511	101528	AGAGGAAGGTGGCTCTGG	43	1619	1636	5-8-5	1801
621873	101514	101531	AGGAGAGGAAGGTGGCTC	65	1622	1639	5-8-5	1802
621874	101517	101534	TTAGGAGAGGAAGGTGG	26	1625	1642	5-8-5	1803
621875	101520	101537	GTATTTAGGAGAGGAAGG	0	1628	1645	5-8-5	1804
621876	101537	101554	GAAGTGACAGAAGAGACG	37	1645	1662	5-8-5	1805
621877	101540	101557	CGGGAAGTGACAGAAGAG	59	1648	1665	5-8-5	1806
621878	101543	101560	GTTCGGGAAGTGACAGAA	65	1651	1668	5-8-5	1807
621879	101546	101563	CCAGTTCGGGAAGTGACA	35	1654	1671	5-8-5	1808
621880	101549	101566	CTGCCAGTTCGGGAAGTG	69	1657	1674	5-8-5	1809
621881	101552	101569	GAACTGCCAGTTCGGGAA	48	1660	1677	5-8-5	1810
621882	101555	101572	CCAGAACTGCCAGTTCGG	66	1663	1680	5-8-5	1811

621883	101558	101575	GCTCCAGAACTGCCAGTT	69	1666	1683	5-8-5	1812
621884	101561	101578	TTTGCTCCAGAACTGCCA	74	1669	1686	5-8-5	1813
621885	101564	101581	TCCTTTGCTCCAGAACTG	61	1672	1689	5-8-5	1814
621886	101567	101584	ATCTCCTTTGCTCCAGAA	64	1675	1692	5-8-5	1815
621887	101570	101587	TTCATCTCCTTTGCTCCA	36	1678	1695	5-8-5	1816
621888	101573	101590	AGTTTCATCTCCTTTGCT	32	1681	1698	5-8-5	1817

Table 35

Inhibition of tau mRNA by 5-10-5 MOE and 5-8-5 MOE gapmers targeting SEQ ID NO: 1 and 2

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	% inhibition	SEQ ID NO: 2 start site	SEQ ID NO: 2 stop site	Motif	SEQ ID NO:
613412	73879	73898	GTGATCTTCCATCACTTCGA	87	345	364	5-10-5	25
620887	98891	98908	GTTTTCAAACACACCTTC	95	n/a	n/a	5-8-5	665
	98928	98945			n/a	n/a		
621890	n/a	n/a	CCCTTGAGTTTCATCTCC	30	1687	1704	5-8-5	1818
621891	n/a	n/a	GCCCCCTTGAGTTTCATC	8	1690	1707	5-8-5	1819
621892	n/a	n/a	TCAGCCCCCTTGAGTTTC	0	1693	1710	5-8-5	1820
621893	n/a	n/a	CCATCAGCCCCCTTGAGT	4	1696	1713	5-8-5	1821
621894	n/a	n/a	TTACCATCAGCCCCCTTG	75	1699	1716	5-8-5	1822
621912	n/a	n/a	CGCAGAGCTGGGTGGTGT	0	1814	1831	5-8-5	1823
621913	n/a	n/a	AGTCGCAGAGCTGGGTGG	0	1817	1834	5-8-5	1824
621914	n/a	n/a	CTTAGTCGCAGAGCTGGG	21	1820	1837	5-8-5	1825
621915	n/a	n/a	TTGCTTAGTCGCAGAGCT	12	1823	1840	5-8-5	1826
621916	n/a	n/a	GACTTGCTTAGTCGCAGA	29	1826	1843	5-8-5	1827
621925	n/a	n/a	TTACCTCTCTCAGATCT	4	1871	1888	5-8-5	1828
621926	n/a	n/a	AGGTTACCTCTCTCAGA	9	1874	1891	5-8-5	1829
621927	n/a	n/a	TGGAGTTACCTCTCTC	7	1877	1894	5-8-5	1830
621928	n/a	n/a	TTTTGGAGGTTACCTCT	11	1880	1897	5-8-5	1831
621889	101576	101593	TTGAGTTTCATCTCCTTT	23	1684	1701	5-8-5	1832
621895	102978	102995	GTTTTACCATCAGCCCC	88	1702	1719	5-8-5	1833
621896	102995	103012	GCGGTGTGGCGATCTTCG	42	1719	1736	5-8-5	1834
621897	102998	103015	CCCGCGGTGTGGCGATCT	33	1722	1739	5-8-5	1835
621898	103001	103018	CTCCCCGCGGTGTGGCGA	37	1725	1742	5-8-5	1836
621899	103004	103021	CTGCTCCCCGCGGTGTGG	50	1728	1745	5-8-5	1837
621900	103007	103024	GGGCTGCTCCCCGCGGTG	43	1731	1748	5-8-5	1838
621901	103025	103042	GGCCCTTCTGGCCTGGAG	29	1749	1766	5-8-5	1839
621902	103029	103046	GCCTGGCCCTTCTGGCCT	34	1753	1770	5-8-5	1840
621903	103032	103049	TTGGCCTGGCCCTTCTGG	49	1756	1773	5-8-5	1841
621904	103050	103067	GCTGGAATCCTGGTGGCG	58	1774	1791	5-8-5	1842
621905	103053	103070	TTTGCTGGAATCCTGGTG	50	1777	1794	5-8-5	1843
621906	103056	103073	GTTTTTGCTGGAATCCTG	62	1780	1797	5-8-5	1844
621907	103075	103092	TGTCTTTGGAGCGGGCGG	21	1799	1816	5-8-5	1845
621908	103078	103095	TGGTGTCTTTGGAGCGGG	57	1802	1819	5-8-5	1846

621909	103081	103098	GGGTGGTGTCTTTGGAGC	17	1805	1822	5-8-5	1847
621910	103084	103101	GCTGGGTGGTGTCTTTGG	44	1808	1825	5-8-5	1848
621911	103087	103104	AGAGCTGGGTGGTGTCTT	47	1811	1828	5-8-5	1849
621917	105442	105459	CTGGACTTGCTTAGTCGC	27	1829	1846	5-8-5	1850
621918	105445	105462	TCTCTGGACTTGCTTAGT	0	1832	1849	5-8-5	1851
621919	105448	105465	TCTTCTCTGGACTTGCTT	48	1835	1852	5-8-5	1852
621920	105451	105468	TGGTCTTCTCTGGACTTG	49	1838	1855	5-8-5	1853
621921	105454	105471	GGGTGGTCTTCTCTGGAC	33	1841	1858	5-8-5	1854
621922	105473	105490	CAGATCTGGGCCCTGCAG	36	1860	1877	5-8-5	1855
621923	105476	105493	TCTCAGATCTGGGCCCTG	70	1863	1880	5-8-5	1856
621924	105479	105496	CTCTCTCAGATCTGGGCC	32	1866	1883	5-8-5	1857
621929	107917	107934	TGATTTTGGAGGTTTACC	44	1883	1900	5-8-5	1858
621930	107920	107937	CCCTGATTTTGGAGGTTT	74	1886	1903	5-8-5	1859
621931	107923	107940	ATCCCCTGATTTTGGAGG	26	1889	1906	5-8-5	1860
621932	107926	107943	GCGATCCCCTGATTTTGG	45	1892	1909	5-8-5	1861
621933	107929	107946	GCTGCGATCCCCTGATTT	38	1895	1912	5-8-5	1862
621934	107932	107949	GCCGCTGCGATCCCCTGA	42	1898	1915	5-8-5	1863
621935	107935	107952	GTAGCCGCTGCGATCCCC	31	1901	1918	5-8-5	1864
621936	107938	107955	GCTGTAGCCGCTGCGATC	67	1904	1921	5-8-5	1865
621937	107941	107958	GCTGCTGTAGCCGCTGCG	23	1907	1924	5-8-5	1866
621938	107971	107988	GCGGCTGCCGGGAGTGCC	40	1937	1954	5-8-5	1867
621939	107974	107991	GGAGCGGCTGCCGGGAGT	1	1940	1957	5-8-5	1868
621940	107978	107995	TGCGGGAGCGGCTGCCGG	48	1944	1961	5-8-5	1869
621941	108021	108038	ACCTTCTTGGGCTCCCGG	24	1987	2004	5-8-5	1870
621942	108024	108041	GCCACCTTCTTGGGCTCC	28	1990	2007	5-8-5	1871
621943	108027	108044	ACTGCCACCTTCTTGGGC	19	1993	2010	5-8-5	1872
621944	108030	108047	ACCACTGCCACCTTCTTG	28	1996	2013	5-8-5	1873
621945	108033	108050	CGGACCACTGCCACCTTC	72	1999	2016	5-8-5	1874
621946	108036	108053	GTACGGACCACTGCCACC	57	2002	2019	5-8-5	1875
621947	108039	108056	GGAGTACGGACCACTGCC	25	2005	2022	5-8-5	1876
621948	108042	108059	GGTGGAGTACGGACCACT	30	2008	2025	5-8-5	1877
621949	108045	108062	TTGGGTGGAGTACGGACC	24	2011	2028	5-8-5	1878
621950	108052	108069	CGGCGACTTGGGTGGAGT	1	2018	2035	5-8-5	1879
621951	108055	108072	AGACGGCGACTTGGGTGG	4	2021	2038	5-8-5	1880
621952	108058	108075	GGAAGACGGCGACTTGGG	50	2024	2041	5-8-5	1881
621953	108061	108078	GGCGGAAGACGGCGACTT	66	2027	2044	5-8-5	1882
621954	108064	108081	CTTGCGGAAGACGGCGA	38	2030	2047	5-8-5	1883
621955	108067	108084	GCTCTTGCGGAAGACGG	24	2033	2050	5-8-5	1884
621956	108070	108087	GCGGCTCTTGCGGAAGA	20	2036	2053	5-8-5	1885
621957	108073	108090	CAGGCGGCTCTTGCGGA	46	2039	2056	5-8-5	1886
621958	108076	108093	CTGCAGGCGGCTCTTGGC	72	2042	2059	5-8-5	1887
621959	108079	108096	TGTCTGCAGGCGGCTCTT	52	2045	2062	5-8-5	1888
621960	108082	108099	GGCTGTCTGCAGGCGGCT	47	2048	2065	5-8-5	1889

621961	108101	108118	GGTCTGGCATGGGCACGG	73	2067	2084	5-8-5	1890
621962	108137	108154	TCTCAGTGGAGCCGATCT	39	2103	2120	5-8-5	1891
621963	108140	108157	GGTTCTCAGTGGAGCCGA	66	2106	2123	5-8-5	1892
621964	108143	108160	TCAGGTTCTCAGTGGAGC	65	2109	2126	5-8-5	1893
621965	108146	108163	GCTTCAGGTTCTCAGTGG	44	2112	2129	5-8-5	1894

Table 36

Inhibition of tau mRNA by 5-10-5 MOE and 5-8-5 MOE gapmers targeting SEQ ID NO: 1 and 2

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	% inhibition	SEQ ID NO: 2 start site	SEQ ID NO: 2 stop site	Motif	SEQ ID NO:
613412	73879	73898	GTGATCTTCCATCACTTCGA	88	345	364	5-10-5	25
620887	98891	98908	GTTTTCAAACACACCTTC	94	n/a	n/a	5-8-5	665
	98928	98945			n/a	n/a		
621973	n/a	n/a	TGCACCTTCCCGCCTCCC	66	2137	2154	5-8-5	1895
621974	n/a	n/a	TATCTGCACCTTCCCGCC	17	2141	2158	5-8-5	1896
621975	n/a	n/a	AATTATCTGCACCTTCCC	27	2144	2161	5-8-5	1897
621994	n/a	n/a	TGCACACTGCCGCCTCCC	74	2230	2247	5-8-5	1898
621995	n/a	n/a	ACTATTTGCACACTGCCG	28	2236	2253	5-8-5	1899
621996	n/a	n/a	TAGACTATTTGCACACTG	29	2239	2256	5-8-5	1900
621997	n/a	n/a	TTGTAGACTATTTGCACA	62	2242	2259	5-8-5	1901
622012	n/a	n/a	CTCCTGGTTTATGATGGA	24	2310	2327	5-8-5	1902
622013	n/a	n/a	GGCCACCTCCTGGTTTAT	21	2316	2333	5-8-5	1903
622014	n/a	n/a	CACCTGGCCACCTCCTGG	44	2321	2338	5-8-5	1904
622041	n/a	n/a	ATCTTTTTATTTCTCCG	32	2422	2439	5-8-5	1905
622042	n/a	n/a	TTTCAATCTTTTATTTTC	16	2427	2444	5-8-5	1906
621966	108149	108166	GGTGCTTCAGGTTCTCAG	48	2115	2132	5-8-5	1907
621967	108153	108170	GGCTGGTGCTTCAGGTTTC	46	2119	2136	5-8-5	1908
621968	108156	108173	CCCGGCTGGTGCTTCAGG	50	2122	2139	5-8-5	1909
621969	108159	108176	CCTCCCGGCTGGTGCTTC	22	2125	2142	5-8-5	1910
621970	108162	108179	CCGCCTCCCGGCTGGTGC	27	2128	2145	5-8-5	1911
621971	108165	108182	TTCCCGCCTCCCGGCTGG	5	2131	2148	5-8-5	1912
621972	108168	108185	ACCTTCCCGCCTCCCGGC	39	2134	2151	5-8-5	1913
621976	121826	121843	ATTAATTATCTGCACCTT	76	2147	2164	5-8-5	1914
621977	121829	121846	CTTATTAATTATCTGCAC	73	2150	2167	5-8-5	1915
621978	121833	121850	GCTTCTTATTAATTATCT	68	2154	2171	5-8-5	1916
621979	121836	121853	CCAGCTTCTTATTAATTA	44	2157	2174	5-8-5	1917
621980	121839	121856	GATCCAGCTTCTTATTAA	31	2160	2177	5-8-5	1918
621981	121842	121859	TAAGATCCAGCTTCTTAT	44	2163	2180	5-8-5	1919
621982	121845	121862	TGCTAAGATCCAGCTTCT	69	2166	2183	5-8-5	1920
621983	121848	121865	CGTTGCTAAGATCCAGCT	82	2169	2186	5-8-5	1921
621984	121864	121881	CCACACTTGGACTGGACG	73	2185	2202	5-8-5	1922
621985	121867	121884	GAGCCACACTTGGACTGG	80	2188	2205	5-8-5	1923
621986	121870	121887	TTTGAGCCACACTTGGAC	59	2191	2208	5-8-5	1924

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621987	121873	121890	TCCTTTGAGCCACACTTG	66	2194	2211	5-8-5	1925
621988	121876	121893	TTATCCTTTGAGCCACAC	77	2197	2214	5-8-5	1926
621989	121879	121896	ATATTATCCTTTGAGCCA	54	2200	2217	5-8-5	1927
621990	121882	121899	TTGATATTATCCTTTGAG	69	2203	2220	5-8-5	1928
621991	121885	121902	TGTTTGATATTATCCTTT	92	2206	2223	5-8-5	1929
621992	121903	121920	CTGCCGCCTCCCGGGACG	51	2224	2241	5-8-5	1930
621993	121906	121923	ACACTGCCGCCTCCCGGG	70	2227	2244	5-8-5	1931
621998	125764	125781	GGTTTGTAGACTATTGTC	76	2245	2262	5-8-5	1932
621999	125767	125784	ACTGGTTTGTAGACTATT	62	2248	2265	5-8-5	1933
622000	125770	125787	TCAACTGGTTTGTAGACT	39	2251	2268	5-8-5	1934
622001	125777	125794	GCTCAGGTCAACTGGTTT	87	2258	2275	5-8-5	1935
622002	125780	125797	CTTGCTCAGGTCAACTGG	53	2261	2278	5-8-5	1936
622003	125783	125800	CACCTTGCTCAGGTCAAC	68	2264	2281	5-8-5	1937
622004	125805	125822	CTAATGAGCCACACTTGG	51	2286	2303	5-8-5	1938
622005	125808	125825	TGCCTAATGAGCCACACT	65	2289	2306	5-8-5	1939
622006	125811	125828	TGTTGCCTAATGAGCCAC	69	2292	2309	5-8-5	1940
622007	125814	125831	GGATGTTGCCTAATGAGC	70	2295	2312	5-8-5	1941
622008	125817	125834	GATGGATGTTGCCTAATG	61	2298	2315	5-8-5	1942
622009	125820	125837	TATGATGGATGTTGCCTA	44	2301	2318	5-8-5	1943
622010	125823	125840	GTTTATGATGGATGTTGC	57	2304	2321	5-8-5	1944
622011	125826	125843	CTGGTTTATGATGGATGT	26	2307	2324	5-8-5	1945
622015	130141	130158	TTTACTTCCACCTGGCCA	36	2329	2346	5-8-5	1946
622016	130144	130161	GATTTTACTTCCACCTGG	49	2332	2349	5-8-5	1947
622017	130147	130164	TCAGATTTTACTTCCACC	76	2335	2352	5-8-5	1948
622018	130150	130167	TTCTCAGATTTTACTTCC	24	2338	2355	5-8-5	1949
622019	130153	130170	AGCTTCTCAGATTTTACT	30	2341	2358	5-8-5	1950
622020	130156	130173	TCAAGCTTCTCAGATTTT	39	2344	2361	5-8-5	1951
622021	130159	130176	AAGTCAAGCTTCTCAGAT	2	2347	2364	5-8-5	1952
622022	130162	130179	TTGAAGTCAAGCTTCTCA	53	2350	2367	5-8-5	1953
622023	130165	130182	TCCTTGAAGTCAAGCTTC	39	2353	2370	5-8-5	1954
622024	130168	130185	CTGTCCTTGAAGTCAAGC	19	2356	2373	5-8-5	1955
622025	130171	130188	ACTCTGTCCTTGAAGTCA	39	2359	2376	5-8-5	1956
622026	130174	130191	TGGACTCTGTCCTTGAAG	36	2362	2379	5-8-5	1957
622027	130177	130194	GACTGGACTCTGTCCTTG	75	2365	2382	5-8-5	1958
622028	130180	130197	TTCGACTGGACTCTGTCC	29	2368	2385	5-8-5	1959
622029	130183	130200	ATCTTCGACTGGACTCTG	33	2371	2388	5-8-5	1960
622030	130186	130203	CCAATCTTCGACTGGACT	49	2374	2391	5-8-5	1961
622031	130189	130206	GACCCAATCTTCGACTGG	74	2377	2394	5-8-5	1962
622032	130192	130209	AGGGACCCAATCTTCGAC	79	2380	2397	5-8-5	1963
622033	130195	130212	TCCAGGGACCCAATCTTC	77	2383	2400	5-8-5	1964
622034	130198	130215	TTGTCCAGGGACCCAATC	68	2386	2403	5-8-5	1965
622035	130201	130218	ATATTGTCCAGGGACCCA	6	2389	2406	5-8-5	1966
622036	130204	130221	GTGATATTGTCCAGGGAC	86	2392	2409	5-8-5	1967

622037	130207	130224	TGGGTGATATTGTCCAGG	68	2395	2412	5-8-5	1968
622038	130225	130242	TTTCCTCCGCCAGGGACG	77	2413	2430	5-8-5	1969
622039	130228	130245	TTATTTCTCCGCCAGGG	52	2416	2433	5-8-5	1970
622040	130231	130248	TTTTTATTTCTCCGCCA	61	2419	2436	5-8-5	1971

Table 37

Inhibition of tau mRNA by 5-10-5 MOE and 5-8-5 MOE gapmers targeting SEQ ID NO: 1 and 2

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	% inhibition	SEQ ID NO: 2 start site	SEQ ID NO: 2 stop site	Motif	SEQ ID NO:
613412	73879	73898	GTGATCTTCCATCACTTCGA	89	345	364	5-10-5	25
620887	98891	98908	GTTTTCAAACACACCTTC	98	n/a	n/a	5-8-5	665
	98928	98945			n/a	n/a		
622043	n/a	n/a	GGGTTTCAATCTTTTTAT	65	2430	2447	5-8-5	1972
622044	135477	135494	GTCAGCTTGTGGGTTTCA	86	2440	2457	5-8-5	1973
622045	135480	135497	AAGGTCAGCTTGTGGGTT	49	2443	2460	5-8-5	1974
622046	135484	135501	GCGGAAGGTCAGCTTGTG	26	2447	2464	5-8-5	1975
622047	135488	135505	TCTCGCGGAAGGTCAGCT	54	2451	2468	5-8-5	1976
622048	135491	135508	CGTTCTCGCGGAAGGTCA	63	2454	2471	5-8-5	1977
622049	135507	135524	TCTGTCTTGGCTTTGGCG	30	2470	2487	5-8-5	1978
622050	135510	135527	TGGTCTGTCTTGGCTTTG	72	2473	2490	5-8-5	1979
622051	135513	135530	CCGTGGTCTGTCTTGGCT	75	2476	2493	5-8-5	1980
622052	135516	135533	GCCCCGTGGTCTGTCTTG	39	2479	2496	5-8-5	1981
622053	135527	135544	ACACGATCTCCGCCCCGT	80	2490	2507	5-8-5	1982
622054	135530	135547	TGTACACGATCTCCGCCC	72	2493	2510	5-8-5	1983
622055	135533	135550	ACTTGTACACGATCTCCG	30	2496	2513	5-8-5	1984
622056	135536	135553	GCGACTTGTACACGATCT	72	2499	2516	5-8-5	1985
622057	135539	135556	CTGGCGACTTGTACACGA	65	2502	2519	5-8-5	1986
622058	135542	135559	CCACTGGCGACTTGTACA	35	2505	2522	5-8-5	1987
622059	135545	135562	ACACCACTGGCGACTTGT	46	2508	2525	5-8-5	1988
622060	135548	135565	CAGACACCACTGGCGACT	61	2511	2528	5-8-5	1989
622061	135551	135568	CCCCAGACACCACTGGCG	74	2514	2531	5-8-5	1990
622062	135554	135571	TGTCCCCAGACACCACTG	38	2517	2534	5-8-5	1991
622063	135572	135589	TGAGATGCCGTGGAGACG	36	2535	2552	5-8-5	1992
622064	135575	135592	TGCTGAGATGCCGTGGAG	34	2538	2555	5-8-5	1993
622065	135599	135616	CGATGCTGCCGTTGGAGG	43	2562	2579	5-8-5	1994
622066	135602	135619	TGTCGATGCTGCCGTTGG	51	2565	2582	5-8-5	1995
622067	135605	135622	CCATGTCGATGCTGCCGG	66	2568	2585	5-8-5	1996
622068	135608	135625	CTACCATGTCGATGCTGC	68	2571	2588	5-8-5	1997
622069	135611	135628	AGTCTACCATGTCGATGC	56	2574	2591	5-8-5	1998
622070	135614	135631	GCGAGTCTACCATGTCGA	68	2577	2594	5-8-5	1999
622071	135654	135671	AGGGAGGCAGACACCTCG	24	2617	2634	5-8-5	2000
622072	135657	135674	GCCAGGGAGGCAGACACC	73	2620	2637	5-8-5	2001
622073	135661	135678	CTTGGCCAGGGAGGCAGA	50	2624	2641	5-8-5	2002

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622074	135664	135681	CTGCTTGGCCAGGGAGGC	44	2627	2644	5-8-5	2003
622075	135667	135684	ACCCTGCTTGGCCAGGGA	18	2630	2647	5-8-5	2004
622076	135678	135695	CCTGATCACAAACCCTGC	65	2641	2658	5-8-5	2005
622077	135681	135698	GGGCCTGATCACAAACCC	82	2644	2661	5-8-5	2006
622078	135697	135714	TTATTGACCGCCCCAGGG	42	2660	2677	5-8-5	2007
622079	135700	135717	CAATTATTGACCGCCCCA	54	2663	2680	5-8-5	2008
622080	135703	135720	CCACAATTATTGACCGCC	95	2666	2683	5-8-5	2009
622081	135706	135723	TCTCCACAATTATTGACC	63	2669	2686	5-8-5	2010
622082	135709	135726	TCCTCTCCACAATTATTG	41	2672	2689	5-8-5	2011
622083	135712	135729	CTCTCCTCTCCACAATTA	76	2675	2692	5-8-5	2012
622084	135715	135732	ATTCTCTCCTCTCCACAA	57	2678	2695	5-8-5	2013
622085	135718	135735	CTCATTCTCTCCTCTCCA	72	2681	2698	5-8-5	2014
622086	135721	135738	TCTCTCATTCTCTCCTCT	69	2684	2701	5-8-5	2015
622087	135724	135741	CACTCTCTCATTCTCTCC	75	2687	2704	5-8-5	2016
622088	135727	135744	CCACACTCTCTCATTCTC	90	2690	2707	5-8-5	2017
622089	135730	135747	TTTCCACACTCTCTCATT	70	2693	2710	5-8-5	2018
622090	135733	135750	TTTTTCCACACTCTCTC	76	2696	2713	5-8-5	2019
622091	135737	135754	CTTTTTTTTCCACACTC	84	2700	2717	5-8-5	2020
622092	135740	135757	ATTCTTTTTTTTCCACA	67	2703	2720	5-8-5	2021
622093	135746	135763	GTCATTATTCTTTTTTTT	54	2709	2726	5-8-5	2022
622094	135749	135766	CGGGTCATTATTCTTTTT	82	2712	2729	5-8-5	2023
622095	135752	135769	GGCCGGGTCATTATTCTT	72	2715	2732	5-8-5	2024
622096	135783	135800	CTGCGAGGAGCAGCTGGG	52	2746	2763	5-8-5	2025
622097	135786	135803	GAAGTGCAGGAGCAGCT	59	2749	2766	5-8-5	2026
622098	135789	135806	ACCGAACTGCGAGGAGCA	77	2752	2769	5-8-5	2027
622099	135792	135809	TTAACCGAACTGCGAGGA	62	2755	2772	5-8-5	2028
622100	135795	135812	CAATTAACCGAACTGCGA	55	2758	2775	5-8-5	2029
622101	135798	135815	AACCAATTAACCGAACTG	59	2761	2778	5-8-5	2030
622102	135801	135818	ATTAACCAATTAACCGAA	71	2764	2781	5-8-5	2031
622103	135804	135821	GTGATTAACCAATTAACC	70	2767	2784	5-8-5	2032
622104	135807	135824	TAAGTGATTAACCAATTA	42	2770	2787	5-8-5	2033
622105	135810	135827	GGTTAAGTGATTAACCAA	42	2773	2790	5-8-5	2034
622106	135813	135830	GCAGGTTAAGTGATTAAC	78	2776	2793	5-8-5	2035
622107	135816	135833	AAAGCAGGTTAAGTGATT	38	2779	2796	5-8-5	2036
622108	135819	135836	ACAAAAGCAGGTTAAGTG	55	2782	2799	5-8-5	2037
622109	135822	135839	GTGACAAAAGCAGGTTAA	82	2785	2802	5-8-5	2038
622110	135825	135842	CGAGTGACAAAAGCAGGT	86	2788	2805	5-8-5	2039
622111	135828	135845	AGCCGAGTGACAAAAGCA	93	2791	2808	5-8-5	2040
622112	135831	135848	CAAAGCCGAGTGACAAA	73	2794	2811	5-8-5	2041
622113	135834	135851	AGCCAAAGCCGAGTGACA	82	2797	2814	5-8-5	2042
622114	135837	135854	CCGAGCCAAAGCCGAGTG	82	2800	2817	5-8-5	2043
622115	135840	135857	GTCCCGAGCCAAAGCCGA	63	2803	2820	5-8-5	2044
622116	135843	135860	GAAGTCCCGAGCCAAAGC	59	2806	2823	5-8-5	2045

622117	135846	135863	TTTGAAGTCCCGAGCCAA	76	2809	2826	5-8-5	2046
622118	135849	135866	GATTTTGAAGTCCCGAGC	72	2812	2829	5-8-5	2047
622119	135852	135869	ACTGATTTTGAAGTCCCG	73	2815	2832	5-8-5	2048

Table 38
Inhibition of tau mRNA by 5-8-5 MOE gapmers targeting SEQ ID NO: 1

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	% inhibition	Motif	SEQ ID NO:
620887	98891	98908	GTTTTCAAACACACCTTC	96	5-8-5	665
	98928	98945				
623853	12069	12086	TGTTTGGATTTCTATCGG	82	5-8-5	2049
623854	12077	12094	TGACATGGTGTGTTGGATT	47	5-8-5	2050
623855	12079	12096	GCTGACATGGTGTGTTGGA	77	5-8-5	2051
623856	12080	12097	CGCTGACATGGTGTGTTGG	78	5-8-5	2052
623857	12081	12098	TCGCTGACATGGTGTGTTG	83	5-8-5	2053
623858	12082	12099	CTCGCTGACATGGTGTGTT	84	5-8-5	2054
623859	12083	12100	ACTCGCTGACATGGTGTGTT	74	5-8-5	2055
623860	12084	12101	GACTCGCTGACATGGTGTGTT	89	5-8-5	2056
623861	12085	12102	GGACTCGCTGACATGGTGTGTT	77	5-8-5	2057
623862	16753	16770	TTATCCAGGAAAAATATT	21	5-8-5	2058
623863	16756	16773	GGATTATCCAGGAAAAAT	86	5-8-5	2059
623864	16758	16775	TAGGATTATCCAGGAAAA	76	5-8-5	2060
623865	16759	16776	ATAGGATTATCCAGGAAA	84	5-8-5	2061
623866	16760	16777	TATAGGATTATCCAGGAA	62	5-8-5	2062
623867	16761	16778	CTATAGGATTATCCAGGA	87	5-8-5	2063
623868	16763	16780	CCCTATAGGATTATCCAG	76	5-8-5	2064
623869	16764	16781	TCCCTATAGGATTATCCA	34	5-8-5	2065
623870	16766	16783	TATCCCTATAGGATTATC	56	5-8-5	2066
623871	16769	16786	AGTTATCCCTATAGGATT	16	5-8-5	2067
623872	16774	16791	AGGCAAGTTATCCCTATA	86	5-8-5	2068
623873	17416	17433	ATCAGCACCTGACTGCGG	78	5-8-5	2069
623874	17421	17438	TTCAGATCAGCACCTGAC	91	5-8-5	2070
623875	17424	17441	GACTTCAGATCAGCACCT	92	5-8-5	2071
623876	17426	17443	AAGACTTCAGATCAGCAC	92	5-8-5	2072
623877	17427	17444	AAAGACTTCAGATCAGCA	95	5-8-5	2073
623878	17428	17445	CAAAGACTTCAGATCAGC	96	5-8-5	2074
623879	17429	17446	CCAAAGACTTCAGATCAG	86	5-8-5	2075
623880	17430	17447	ACCAAAGACTTCAGATCA	65	5-8-5	2076
623881	17431	17448	CACCAAAGACTTCAGATC	51	5-8-5	2077
623882	17432	17449	CCACCAAAGACTTCAGAT	55	5-8-5	2078
623883	17434	17451	GCCCCACCAAAGACTTCAG	77	5-8-5	2079
623884	17437	17454	TCAGCCCACCAAAGACTT	56	5-8-5	2080
623885	17442	17459	TAAAGTCAGCCCACCAA	2	5-8-5	2081

623886	20943	20960	GTTATTGGGACTGACCTT	69	5-8-5	2082
623887	20948	20965	GATTTGTTATTGGGACTG	78	5-8-5	2083
613412	73879	73898	GTGATCTTCCATCACTTCGA	89	5-8-5	25
623811	122370	122387	CAGTGGAGCCACTCAACG	41	5-8-5	2084
623812	122380	122397	CACCTGTCCACAGTGGAG	58	5-8-5	2085
623813	122391	122408	AACAAACGGGTCACCTGT	63	5-8-5	2086
623814	122445	122462	CGTGTAGGAGCAGCAGCT	81	5-8-5	2087
623815	122538	122555	CTTTGGTTTGGCTCTTTG	64	5-8-5	2088
623816	123104	123121	GCTGGTGGGAGAGGAGCC	9	5-8-5	2089
623817	123288	123305	ATGCGGGTGGCTGCCTCA	65	5-8-5	2090
623818	123293	123310	GCTGGATGCGGGTGGCTG	24	5-8-5	2091
623819	123341	123358	GTGCTCAGGGCAGGAAGC	45	5-8-5	2092
623820	123590	123607	CAAAGCTCAAACAGCTGA	56	5-8-5	2093
623821	123601	123618	AGAACCAGGATCAAAGCT	41	5-8-5	2094
623822	123704	123721	GCTCCGCCTCAGCAGCAC	71	5-8-5	2095
623823	123722	123739	GTGTGCACTCTCTCCCA	45	5-8-5	2096
623824	123877	123894	GGCTAGCCCGCAGACGAG	31	5-8-5	2097
623825	123976	123993	CCTGTGAAGGTGCTCAGA	58	5-8-5	2098
623826	124033	124050	GATCCAGTGCCCCCAGAT	54	5-8-5	2099
623827	124057	124074	GGAGAGGCTAGGGCTCAG	68	5-8-5	2100
623828	124223	124240	AGAGGAGTGGATGGCAGT	37	5-8-5	2101
623829	124293	124310	TGGCCTGGGTGAGGTAAC	23	5-8-5	2102
623830	124296	124313	CTCTGGCCTGGGTGAGGT	28	5-8-5	2103
623831	124596	124613	AGGGCAGGTGGTGGTTTC	8	5-8-5	2104
623832	124780	124797	GACATTCTGGAGTCCCC	83	5-8-5	2105
623833	124859	124876	TGGCAGACAGACAGGTCC	87	5-8-5	2106
623834	124909	124926	AGTCAAAGAACCAGCTCC	68	5-8-5	2107
623835	124949	124966	TCCCTCTGGGAATGATGA	41	5-8-5	2108
623836	124965	124982	GCCTCCAGGGCACCCTC	76	5-8-5	2109
623837	124972	124989	GCCTGTGGCCTCCAGGGC	43	5-8-5	2110
623838	124977	124994	AGGAGGCCTGTGGCCTCC	11	5-8-5	2111
623839	125075	125092	AATAGGAACAAAGCAACA	25	5-8-5	2112
623840	125086	125103	CTGTCTTTAGCAATAGGA	84	5-8-5	2113
623841	125100	125117	TGTCCTGGACATTCTGT	66	5-8-5	2114
623842	125291	125308	TGGAAAGGCAGGAGTGGG	0	5-8-5	2115
623843	125306	125323	TCTGAAAAATCTTGCTGG	51	5-8-5	2116
623844	125310	125327	AGCATCTGAAAAATCTTG	82	5-8-5	2117
623845	125322	125339	ATGAGTATGCACAGCATC	68	5-8-5	2118
623846	125337	125354	AAAGTGATCAATATGATG	33	5-8-5	2119
623847	125390	125407	GTCACCTCCCTTCCTGAC	68	5-8-5	2120
623848	125408	125425	ACGCTTAAGTGTA AAAAAT	38	5-8-5	2121
623849	125557	125574	AAATGTGTTGTCGAAATT	19	5-8-5	2122
623850	125567	125584	CAGGGTGGAAAAATGTGT	33	5-8-5	2123

623851	125598	125615	TTCCCAGCTGCCATGAGG	33	5-8-5	2124
623852	125743	125760	TGGAGATGAGAGAGGAGG	0	5-8-5	2125

Table 39
Inhibition of Tau mRNA by 5-8-5 MOE gapmers targeting SEQ ID NO: 1

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	% inhibition	Motif	SEQ ID NO:
623661	6196	6213	GCGCTTACCTGATAGTCG	36	5-8-5	2126
613412	73879	73898	GTGATCTTCCATCACTTCGA	87	5-8-5	25
623662	73981	73998	TCCACTAACCTTTCAGGC	30	5-8-5	2127
623663	83368	83385	GGGAGATTCTGGAACACA	72	5-8-5	2128
623664	83455	83472	GGGCCACCTTCCGCTGT	22	5-8-5	2129
623665	85895	85912	CTGTACATCTAGAAACC	21	5-8-5	2130
623666	85982	85999	TACCCTCACCTGTGGTTC	0	5-8-5	2131
623667	89885	89902	CTTCTTCAGCTGGTGTAT	22	5-8-5	2132
623668	89951	89968	TTCCTGACCTTGGGTCA	0	5-8-5	2133
623669	94688	94705	TTTCAGGCTCTGTGTGGA	61	5-8-5	2134
623670	95441	95458	GACACAGACCTTTGAGTT	53	5-8-5	2135
623671	98550	98567	CCATGCGAGCTGATAAAA	39	5-8-5	2136
621344	98607	98624	GTCAGCTTACCTTGGCTT	34	5-8-5	814
620887	98891	98908	GTTTTCAAACACACCTTC	94	5-8-5	665
	98928	98945				
623672	101387	101404	GTGGATGTCTTAAACATA	89	5-8-5	2137
623673	101586	101603	TTTCCTTACCTTGAGTTT	0	5-8-5	2138
623674	102970	102987	ATCAGCCCCCTGTAAATG	7	5-8-5	2139
623675	103097	103114	TCTTCTTACCAGAGCTGG	0	5-8-5	2140
623676	107909	107926	GAGGTTACCTGGGAAGG	0	5-8-5	2141
623677	108175	108192	CACTCTCACCTTCCCGCC	6	5-8-5	2142
623712	108255	108272	CCTCCAGGCGCAGCCCTA	92	5-8-5	2143
623713	108413	108430	CCTGAGGAGGGCACTCAC	28	5-8-5	2144
623714	108530	108547	GGAACCGCTGTGGGTGCC	60	5-8-5	2145
623715	108565	108582	TGGGTGGCAGTGTATTCT	63	5-8-5	2146
623716	108690	108707	GGAGAGCTCGCGAGCACC	69	5-8-5	2147
623717	108896	108913	GAGGTGGCTACCCACGGC	59	5-8-5	2148
623718	109561	109578	CCAGAAGGCCCAGCACAT	51	5-8-5	2149
623719	109574	109591	CGAGGCCCAGTGCCAGAG	59	5-8-5	2150
623720	109607	109624	AGGCCCAGGGTTCCAGAA	55	5-8-5	2151
623721	109623	109640	AGGCAAGCTGACACGCAG	73	5-8-5	2152
623722	110101	110118	CAGGAAAAGGCCGGACCT	37	5-8-5	2153
623723	110103	110120	AGCAGGAAAAGGCCGGAC	78	5-8-5	2154
623724	110182	110199	TTCCCCAAGGTCTCTAAC	14	5-8-5	2155
623725	110413	110430	AGGAAAGGCCAGTGAGGG	8	5-8-5	2156
623726	110500	110517	TTGTTATGTGACTTGAGG	74	5-8-5	2157

623727	110630	110647	ATTCCCCACCATGGGACA	17	5-8-5	2158
623728	110635	110652	AGGACATTCCCCACCATG	9	5-8-5	2159
623729	110648	110665	AGATAAGGAGAGAAGGAC	15	5-8-5	2160
623730	110755	110772	ATGCTCAGTGTGGTCAGA	73	5-8-5	2161
623731	110852	110869	AGGGCCGGCCACCTGCAC	56	5-8-5	2162
623732	110919	110936	TCTGTCTCTGGCAACCTG	85	5-8-5	2163
623733	110954	110971	AACAGGGAAGCTACTTCC	6	5-8-5	2164
623734	111077	111094	GGGCCTTCAATGGAAAGT	21	5-8-5	2165
623735	111153	111170	GGTCGCTGACTCTCACC	66	5-8-5	2166
623736	111174	111191	CCCTTTCTACACTTGGCA	81	5-8-5	2167
623678	121820	121837	TATCTGCACCTTTGGTAG	30	5-8-5	2168
623685	121830	121847	TCTTATTAATTATCTGCA	81	5-8-5	2169
623686	121831	121848	TTCTTATTAATTATCTGC	74	5-8-5	2170
623687	121834	121851	AGCTTCTTATTAATTATC	46	5-8-5	2171
623688	121835	121852	CAGCTTCTTATTAATTAT	6	5-8-5	2172
623689	121837	121854	TCCAGCTTCTTATTAATT	4	5-8-5	2173
623690	121838	121855	ATCCAGCTTCTTATTAAT	2	5-8-5	2174
623691	121840	121857	AGATCCAGCTTCTTATTA	2	5-8-5	2175
623692	121841	121858	AAGATCCAGCTTCTTATT	17	5-8-5	2176
623693	121843	121860	CTAAGATCCAGCTTCTTA	41	5-8-5	2177
623694	121844	121861	GCTAAGATCCAGCTTCTT	75	5-8-5	2178
623695	121846	121863	TTGCTAAGATCCAGCTTC	50	5-8-5	2179
623696	121847	121864	GTTGCTAAGATCCAGCTT	52	5-8-5	2180
623697	121865	121882	GCCACACTTGGACTGGAC	88	5-8-5	2181
623698	121866	121883	AGCCACACTTGGACTGGA	89	5-8-5	2182
623699	121868	121885	TGAGCCACACTTGGACTG	59	5-8-5	2183
623700	121869	121886	TTGAGCCACACTTGGACT	62	5-8-5	2184
623701	121872	121889	CCTTTGAGCCACACTTGG	69	5-8-5	2185
623702	121874	121891	ATCCTTTGAGCCACACTT	64	5-8-5	2186
623703	121875	121892	TATCCTTTGAGCCACACT	69	5-8-5	2187
623704	121877	121894	ATTATCCTTTGAGCCACA	76	5-8-5	2188
623705	121878	121895	TATTATCCTTTGAGCCAC	76	5-8-5	2189
623706	121880	121897	GATATTATCCTTTGAGCC	54	5-8-5	2190
623707	121881	121898	TGATATTATCCTTTGAGC	65	5-8-5	2191
623708	121884	121901	GTTTGATATTATCCTTTG	94	5-8-5	2192
623709	121886	121903	GTGTTTGATATTATCCTT	85	5-8-5	2193
623710	121887	121904	CGTGTGTTGATATTATCCT	78	5-8-5	2194
623711	121904	121921	ACTGCCGCCCTCCCGGGAC	50	5-8-5	2195
623679	121913	121930	GGTACTCACACTGCCGCC	72	5-8-5	1654
623680	125753	125770	TATTTGCACCTGGAGATG	0	5-8-5	2196
623681	125835	125852	CAGGGCTACCTGGTTTAT	26	5-8-5	2197
623682	130128	130145	GGCCACCTCCTAGAACAC	8	5-8-5	2198
623683	130241	130258	CCCCTTACCTTTTTTATT	0	5-8-5	2199

623684	135466	135483	GGTTTCAATCTGCAAGAA	39	5-8-5	2200
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Example 11: Dose-dependent antisense inhibition of human Tau in SH-SY5Y cells

Gapmers from studies described above exhibiting significant *in vitro* inhibition of tau mRNA were selected and tested at various doses in SH-SY5Y cells. 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. Cells were plated at a density of 20,000 cells per well and transfected using electroporation with 0.938 μ M, 0.1.875 μ M, 3.750 μ M, 7.500 μ M, and 15.00 μ M concentrations of antisense oligonucleotide, as specified in the Tables below. After a treatment period of approximately 16 hours, RNA was isolated from the cells and tau mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3104 was used to measure mRNA levels. Tau mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN[®]. Results are presented as percent inhibition of tau, relative to untreated control cells. Tau mRNA levels were significantly reduced in a dose-dependent manner in antisense oligonucleotide treated cells.

Table 40

ISIS No	0.938 μ M	1.875 μ M	3.750 μ M	7.500 μ M	15.00 μ M
613369	57	67	81	91	96
613370	83	91	96	98	97
613371	68	78	95	95	97
613412	41	55	73	86	96
620887	53	76	90	93	95
621238	58	80	76	93	96
621251	68	77	87	89	90
621263	57	69	81	92	95
621302	46	66	80	78	87
621309	56	64	84	86	90
621311	38	54	69	77	86
621312	42	36	57	83	90
621318	40	54	71	87	87
621346	42	46	60	64	78
621870	42	62	76	85	92

Table 41

ISIS No	0.938 μ M	1.875 μ M	3.750 μ M	7.500 μ M	15.00 μ M
613412	14	45	68	84	92
620887	57	74	87	93	95
620888	63	78	76	94	96
620890	76	86	92	96	97
620891	67	79	91	96	96
620918	38	55	65	81	88
620940	38	52	73	89	96
620947	26	47	58	78	87
620958	32	38	61	79	93
621013	49	75	86	92	94
621049	38	45	68	78	80
621056	40	45	70	81	90
621078	23	28	48	67	84
621082	22	32	53	62	90
621088	26	43	59	80	92

Table 42

ISIS No	0.938 μ M	1.875 μ M	3.750 μ M	7.500 μ M	15.00 μ M
613412	17	45	62	84	89
620887	52	71	91	96	95
621147	28	37	59	69	84
621181	39	61	78	85	83
621183	31	43	64	72	87
621836	24	39	64	81	93
621838	33	59	70	91	97
621844	20	38	64	80	91
621845	30	37	62	72	90
621861	19	35	59	80	92
621869	30	56	64	83	91
622125	14	28	52	73	85
622129	26	36	60	71	84
622170	18	42	72	77	91
622196	11	39	59	74	89

Table 43

ISIS No	0.938 μ M	1.875 μ M	3.750 μ M	7.500 μ M	15.00 μ M
613412	21	42	64	82	95

620887	60	79	92	95	95
623746	19	43	54	81	91
623750	50	63	75	83	90
623758	37	54	72	80	82
623805	25	33	48	74	86
623807	15	29	44	75	88
623833	16	60	65	86	89
623860	51	71	80	85	85
623867	9	51	48	74	86
623874	24	28	72	84	94
623875	38	62	80	93	95
623876	40	63	83	93	95
623877	59	76	92	97	96
623878	50	73	90	94	95

Table 44

ISIS No	0.938 μ M	1.875 μ M	3.750 μ M	7.500 μ M	15.00 μ M
613412	8	25	58	77	87
620887	49	77	87	95	86
621360	27	46	68	83	90
621361	52	73	89	92	94
621363	28	45	71	76	77
621364	39	58	77	90	95
621407	38	60	75	82	78
621414	41	66	80	90	83
621424	54	72	87	94	90
621425	8	22	52	74	84
621426	33	46	63	84	91
621740	0	1	6	33	65
621793	4	15	30	41	52
621794	29	38	57	78	85
621810	15	39	45	73	79

Table 45

ISIS No	0.938 μ M	1.875 μ M	3.750 μ M	7.500 μ M	15.00 μ M
613412	40	72	78	92	94
620887	58	79	92	96	97
621431	62	63	79	85	87
621441	71	80	84	95	95
621446	53	70	82	89	94

621448	46	60	85	89	93
621454	63	70	81	89	94
621484	60	65	75	88	93
621570	26	55	81	79	90
621576	23	34	71	75	80
621578	30	45	67	81	90
621579	14	28	49	69	88
621598	38	55	73	88	94
621670	37	57	79	82	92
621675	31	35	51	79	87

Table 46

ISIS No	0.938 μ M	1.875 μ M	3.750 μ M	7.500 μ M	15.00 μ M
613412	21	38	70	84	92
620887	50	63	83	91	96
621894	35	16	32	54	70
621895	23	48	61	82	89
621961	8	14	47	57	75
621983	33	52	63	72	83
621991	36	56	68	86	92
622001	8	33	60	77	90
622080	29	53	69	67	93
622088	20	45	66	84	91
622091	14	33	47	70	82
622110	25	24	64	80	90
622111	17	41	74	86	92
623747	12	47	53	82	87

Table 47

ISIS No	0.938 μ M	1.875 μ M	3.750 μ M	7.500 μ M	15.00 μ M
613412	22	34	49	77	77
620887	51	68	83	94	95
623672	33	43	64	82	88
623697	37	53	59	80	90
623698	32	57	63	84	92
623708	47	68	82	88	95
623709	14	37	62	76	89
623712	22	45	70	86	92
623732	18	37	54	76	87
623756	23	38	68	86	94

623782	50	72	83	90	93
623791	58	71	87	93	95
623796	44	57	74	79	85
623808	30	55	73	84	91
623809	31	42	66	82	93

Example 12: Antisense inhibition of human Tau in HepG2 cells by 5-10-5 MOE, 5-8-5 MOE, 4-8-6 MOE, or 6-8-4 MOE gapmers

Antisense oligonucleotides were designed targeting a tau nucleic acid and were tested for their effects on tau mRNA in vitro. The antisense oligonucleotides were tested in a series of experiments that had similar culture conditions. ISIS 613412 was also included in the assays. The results for each experiment are presented in separate tables shown below. Cultured HepG2 cells at a density of 20,000 cells per well were transfected using electroporation with 8,000 nM antisense oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and tau mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3104 was used to measure mRNA levels. Tau mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of tau, relative to untreated control cells.

The newly designed chimeric antisense oligonucleotides in the Tables below were designed as 5-8-5 MOE, 4-8-6 MOE, or 6-8-4 MOE gapmers. The 5-8-5 MOE gapmers are 18 nucleosides in length, wherein the central gap segment comprises of eight 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising five nucleosides each. The 4-8-6 MOE gapmers are 18 nucleosides in length, wherein the central gap segment comprises of eight 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising four and six nucleosides respectively. The 6-8-4 MOE gapmers are 18 nucleosides in length, wherein the central gap segment comprises of eight 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising six and four nucleosides respectively. Each nucleoside in the 5' wing segment and each nucleoside in the 3' wing segment has a 2'-MOE modification. The internucleoside linkage motif throughout for each gapmer in the tables below, except for ISIS 613412, is 5'-sooooooooooooo-3', wherein each "s" represents a phosphorothioate internucleoside linkage and wherein each "o" represents a phosphodiester internucleoside linkage. The internucleoside linkage motif for ISIS 613412 is 5'-sooooooooooooo-3', wherein each "s" represents a phosphorothioate internucleoside linkage and wherein each "o" represents a phosphodiester internucleoside linkage. All cytosine residues throughout each gapmer are 5-methylcytosines. "Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. "Stop site" indicates the 3'-most nucleoside to which the gapmer is targeted human gene sequence. Each gapmer listed

in the Tables below is targeted to human tau genomic sequence, designated herein as SEQ ID NO: 1 (GENBANK Accession No. NT_010783.15 truncated from nucleotides 9240000 to 9381000).

Table 48
Inhibition of tau mRNA by 5-10-5 MOE gapmers targeting SEQ ID NO: 1

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Motif	% inhibition	SEQ ID NO
613412	73879	73898	GTGATCTTCCATCACTTCGA	5-10-5	90	25
620887	98891	98908	GTTTTCAAACACACCTTC	5-10-5	93	665
	98928	98945				
623888	20951	20968	TTCGATTTGTTATTGGGA	5-10-5	79	2201
623889	20953	20970	ACTTCGATTTGTTATTGG	5-10-5	61	2202
623890	20954	20971	GACTTCGATTTGTTATTG	5-10-5	30	2203
623891	20955	20972	TGACTTCGATTTGTTATT	5-10-5	62	2204
623892	20956	20973	CTGACTTCGATTTGTTAT	5-10-5	60	2205
623893	20957	20974	GCTGACTTCGATTTGTTA	5-10-5	43	2206
623894	20958	20975	AGCTGACTTCGATTTGTT	5-10-5	83	2207
623895	20959	20976	CAGCTGACTTCGATTTGT	5-10-5	68	2208
623896	20961	20978	CCCAGCTGACTTCGATTT	5-10-5	11	2209
623897	20964	20981	ACGCCCAGCTGACTTCGA	5-10-5	65	2210
623898	27148	27165	TGCCTTATATATGCTGAA	5-10-5	82	2211
623899	27153	27170	TTACATGCCTTATATATG	5-10-5	31	2212
623900	27156	27173	CAGTTACATGCCTTATAT	5-10-5	33	2213
623901	27158	27175	TTCAGTTACATGCCTTAT	5-10-5	72	2214
623902	27159	27176	G TTCAGTTACATGCCTTA	5-10-5	92	2215
623903	27169	27186	AAAGTGCTGTGTTTCAGTT	5-10-5	71	2216
623904	27174	27191	CCTCTAAAGTGCTGTGTT	5-10-5	35	2217
623905	28215	28232	GACTTTTCTCAATGTAAC	5-10-5	43	2218
623906	28220	28237	CTGCAGACTTTTCTCAAT	5-10-5	61	2219
623907	28226	28243	ACCTCTCTGCAGACTTTT	5-10-5	79	2220
623908	28227	28244	CACCTCTCTGCAGACTTT	5-10-5	81	2221
623909	28228	28245	GCACCTCTCTGCAGACTT	5-10-5	82	2222
623910	28229	28246	GGCACCTCTCTGCAGACT	5-10-5	81	2223
623911	28230	28247	TGGCACCTCTCTGCAGAC	5-10-5	36	2224
623912	28231	28248	CTGGCACCTCTCTGCAGA	5-10-5	11	2225
623913	28233	28250	TGCTGGCACCTCTCTGCA	5-10-5	51	2226
623914	28236	28253	TGATGCTGGCACCTCTCT	5-10-5	63	2227
623915	28241	28258	CCTTGTGATGCTGGCACC	5-10-5	79	2228
623916	75133	75150	TTTTTAGCATTA AAAAGAG	5-10-5	0	2229
623917	75144	75161	GTGTTTTCTTATTTTAG	5-10-5	80	2230
623918	75149	75166	GCAAGGTGTTTTCTTATT	5-10-5	55	2231
623919	86762	86779	TAGGCCTCTTCTGCATTT	5-10-5	27	2232

623920	86767	86784	CTGGCTAGGCCTCTTCTG	5-10-5	54	2233
623921	86770	86787	ATCCTGGCTAGGCCTCTT	5-10-5	69	2234
623922	86772	86789	AAATCCTGGCTAGGCCTC	5-10-5	67	2235
623923	86773	86790	GAAATCCTGGCTAGGCCT	5-10-5	55	2236
623924	86774	86791	TGAAATCCTGGCTAGGCC	5-10-5	64	2237
623925	86775	86792	GTGAAATCCTGGCTAGGC	5-10-5	77	2238
623926	86776	86793	GGTGAAATCCTGGCTAGG	5-10-5	57	2239
623927	86777	86794	TGGTGAAATCCTGGCTAG	5-10-5	8	2240
623928	86778	86795	CTGGTGAAATCCTGGCTA	5-10-5	45	2241
623929	86780	86797	TGCTGGTGAAATCCTGGC	5-10-5	63	2242
623930	86783	86800	CACTGCTGGTGAAATCCT	5-10-5	70	2243
623931	121716	121733	ACCCTGGACCCGCGCTACT	5-10-5	49	2244
623932	121721	121738	GCGCCACCCTGGACCCGC	5-10-5	84	2245
623933	121724	121741	CATGCGCCACCCTGGACC	5-10-5	52	2246
623934	121726	121743	GACATGCGCCACCCTGGA	5-10-5	80	2247
623935	121727	121744	TGACATGCGCCACCCTGG	5-10-5	74	2248
623936	121728	121745	GTGACATGCGCCACCCTG	5-10-5	90	2249
623937	121729	121746	AGTGACATGCGCCACCCT	5-10-5	84	2250
623938	121730	121747	GAGTGACATGCGCCACCC	5-10-5	92	2251
623939	121731	121748	TGAGTGACATGCGCCACC	5-10-5	86	2252
623940	121732	121749	ATGAGTGACATGCGCCAC	5-10-5	64	2253
623941	121734	121751	CGATGAGTGACATGCGCC	5-10-5	76	2254
623942	121737	121754	TTTCGATGAGTGACATGC	5-10-5	60	2255
623943	121742	121759	TCCACTTTCGATGAGTGA	5-10-5	34	2256
623944	121938	121955	CAGCACGGCGCATGGGAC	5-10-5	26	2257
623945	121939	121956	ACAGCACGGCGCATGGGA	5-10-5	62	2258
623946	121940	121957	CACAGCACGGCGCATGGG	5-10-5	57	2259
621455	121941	121958	CCACAGCACGGCGCATGG	5-10-5	44	1232
623804	121942	121959	GCCACAGCACGGCGCATG	5-10-5	85	1657
623947	121943	121960	AGCCACAGCACGGCGCAT	5-10-5	83	2260
623948	121944	121961	AAGCCACAGCACGGCGCA	5-10-5	56	2261
623949	121946	121963	TCAAGCCACAGCACGGCG	5-10-5	58	2262
623950	121949	121966	AATTCAAGCCACAGCACG	5-10-5	52	2263
623951	121954	121971	CTAATAATTCAAGCCACA	5-10-5	56	2264
623952	125424	125441	GACATTTGCTCAGCAAAC	5-10-5	74	2265
623953	125426	125443	CAGACATTTGCTCAGCAA	5-10-5	62	2266
623954	125427	125444	CCAGACATTTGCTCAGCA	5-10-5	75	2267
623955	125428	125445	CCCAGACATTTGCTCAGC	5-10-5	65	2268
623956	125429	125446	ACCCAGACATTTGCTCAG	5-10-5	30	2269
623957	125430	125447	GACCCAGACATTTGCTCA	5-10-5	30	2270
623958	125431	125448	AGACCCAGACATTTGCTC	5-10-5	41	2271
623959	125432	125449	AAGACCCAGACATTTGCT	5-10-5	69	2272
623960	125434	125451	GCAAGACCCAGACATTTG	5-10-5	73	2273

623961	125437	125454	TGTGCAAGACCCAGACAT	5-10-5	62	2274
623962	125442	125459	GTCATTGTGCAAGACCCA	5-10-5	87	2275

Table 49

Inhibition of tau mRNA by 5-10-5 MOE, 5-8-5 MOE, 4-8-6 MOE, and 6-8-4 gapmers targeting SEQ ID NO: 1

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Motif	% inhibition	SEQ ID NO
613412	73879	73898	GTGATCTTCCATCACTTCGA	5-10-5	87	25
620887	98891	98908	GTTTTCAAACACACCTTC	5-8-5	96	665
	98928	98945				
620888	98881	98898	ACACCTTCATTTACTGTC	5-8-5	96	897
	98918	98935				
620889	98890	98907	TTTTCAAACACACCTTCA	5-8-5	85	898
	98927	98944				
620890	98892	98909	GGTTTTCAAACACACCTT	5-8-5	95	899
	98929	98946				
620891	98893	98910	TGGTTTTCAAACACACCT	5-8-5	96	900
	98930	98947				
623963	73877	73894	TCTTCCATCACTTCGAAC	5-8-5	58	2276
623964	73878	73895	ATCTTCCATCACTTCGAA	5-8-5	44	2277
623965	73880	73897	TGATCTTCCATCACTTCG	5-8-5	51	2278
623966	73881	73898	GTGATCTTCCATCACTTC	5-8-5	45	2279
623967	73931	73948	ATGGTGTAGCCCCCCTGA	5-8-5	66	2280
623968	73932	73949	CATGGTGTAGCCCCCCTG	5-8-5	87	2281
623969	73934	73951	TGCATGGTGTAGCCCCC	5-8-5	94	2282
623970	73935	73952	GTGCATGGTGTAGCCCC	5-8-5	90	2283
623971	73957	73974	CCGTGTCACCCTCTTGGT	5-8-5	83	2284
623972	73958	73975	TCCGTGTCACCCTCTTGG	5-8-5	79	2285
623973	73960	73977	CGTCCGTGTCACCCTCTT	5-8-5	92	2286
623974	83429	83446	TCTTAGCATCAGAGGTTT	5-8-5	70	2287
623975	83430	83447	CTCTTAGCATCAGAGGTT	5-8-5	76	2288
623976	83432	83449	TGCTCTTAGCATCAGAGG	5-8-5	72	2289
623977	83433	83450	GTGCTCTTAGCATCAGAG	5-8-5	86	2290
623978	95266	95283	CTCCTCCGAGTGCGCCTG	5-8-5	24	2291
623979	95267	95284	GCTCCTCCGAGTGCGCCT	5-8-5	77	2292
623980	95269	95286	ATGCTCCTCCGAGTGCGC	5-8-5	58	2293
623981	95270	95287	AATGCTCCTCCGAGTGCG	5-8-5	79	2294
623982	95272	95289	CAAATGCTCCTCCGAGTG	5-8-5	34	2295

623983	98557	98574	TTACTGACCATGCGAGCT	5-8-5	79	2296
623984	98558	98575	TTTACTGACCATGCGAGC	5-8-5	73	2297
623985	98560	98577	CTTTTACTGACCATGCGA	5-8-5	85	2298
623986	98561	98578	GCTTTTACTGACCATGCG	5-8-5	91	2299
623987	98563	98580	TTGCTTTTACTGACCATG	5-8-5	96	2300
623988	135784	135801	ACTGCGAGGAGCAGCTGG	5-8-5	43	2301
623989	135785	135802	AACTGCGAGGAGCAGCTG	5-8-5	31	2302
623990	135787	135804	CGAACTGCGAGGAGCAGC	5-8-5	62	2303
623991	135788	135805	CCGAAGTGCAGGAGCAG	5-8-5	73	2304
623992	135790	135807	AACCGAAGTGCAGGAGC	5-8-5	73	2305
623993	135868	135885	TGCTCTTACTCCCATCAC	5-8-5	59	2306
623994	135869	135886	TTGCTCTTACTCCCATCA	5-8-5	85	2307
623995	135871	135888	ATTTGCTCTTACTCCCAT	5-8-5	77	2308
623996	135872	135889	AATTTGCTCTTACTCCCA	5-8-5	80	2309
625423	98879	98896	ACCTTCATTTACTGTCAG	5-8-5	90	2310
625424	98880	98897	CACCTTCATTTACTGTCA	5-8-5	94	2311
625425	98882	98899	CACACCTTCATTTACTGT	5-8-5	89	2312
	98919	98936		5-8-5		
625426	98883	98900	ACACACCTTCATTTACTG	5-8-5	87	2313
	98920	98937				
625427	98884	98901	AACACACCTTCATTTACT	5-8-5	86	2314
	98921	98938				
625428	98885	98902	AAACACACCTTCATTTAC	5-8-5	49	2315
	98922	98939				
625429	98886	98903	CAAACACACCTTCATTTA	5-8-5	66	2316
	98923	98940				
625430	98887	98904	TCAAACACACCTTCATTT	5-8-5	70	2317
	98924	98941				
625431	98888	98905	TTCAAACACACCTTCATT	5-8-5	74	2318
	98925	98942				
625432	98889	98906	TTTCAAACACACCTTCAT	5-8-5	81	2319
	98926	98943				
625433	98894	98911	TTGGTTTTCAAACACACC	5-8-5	92	2320
625434	75128	75145	AGCATTTAAAGAGAAAAG	5-8-5	13	2321
625435	75136	75153	TTATTTTTAGCATTAATA	5-8-5	0	2322
625436	75138	75155	TCTTATTTTTAGCATTA	5-8-5	52	2323
625437	75139	75156	TTCTTATTTTTAGCATTA	5-8-5	86	2324
625438	75140	75157	TTTCTTATTTTTAGCATT	5-8-5	40	2325

625439	75141	75158	TTTTCTTATTTTATAGCAT	5-8-5	0	2326
625440	75142	75159	GTTTTCTTATTTTATAGCA	5-8-5	82	2327
625441	75143	75160	TGTTTTCTTATTTTATAGC	5-8-5	68	2328
625442	75146	75163	AGGTGTTTTCTTATTTTT	5-8-5	83	2329
625443	75154	75171	GGGCTGCAAGGTGTTTTTC	5-8-5	69	2330
625444	98881	98898	ACACCTTCATTTACTGTC	4-8-6	90	897
	98918	98935				
625445	98882	98899	CACACCTTCATTTACTGT	4-8-6	82	2312
	98919	98936				
625446	98883	98900	ACACACCTTCATTTACTG	4-8-6	84	2313
	98920	98937				
625447	98884	98901	AACACACCTTCATTTACT	4-8-6	40	2314
	98921	98938				
625448	98889	98906	TTTCAAACACACCTTCAT	4-8-6	83	2319
	98926	98943				
625449	98890	98907	TTTTCAAACACACCTTCA	4-8-6	0	898
	98927	98944				
625450	98891	98908	GTTTTCAAACACACCTTC	4-8-6	94	665
	98928	98945				
625451	98892	98909	GGTTTTCAAACACACCTT	4-8-6	94	899
	98929	98946				
625452	98893	98910	TGGTTTTCAAACACACCT	4-8-6	94	900
	98930	98947				
625453	98881	98898	ACACCTTCATTTACTGTC	6-8-4	96	897
	98918	98935				
625454	98882	98899	CACACCTTCATTTACTGT	6-8-4	96	2312
	98919	98936				
625455	98883	98900	ACACACCTTCATTTACTG	6-8-4	93	2313
	98920	98937				
625456	98884	98901	AACACACCTTCATTTACT	6-8-4	88	2314
	98921	98938				
625457	98889	98906	TTTCAAACACACCTTCAT	6-8-4	85	2319
	98926	98943				
625458	98890	98907	TTTTCAAACACACCTTCA	6-8-4	90	898
	98927	98944				
625459	98891	98908	GTTTTCAAACACACCTTC	6-8-4	97	665
	98928	98945				
625460	98892	98909	GGTTTTCAAACACACCTT	6-8-4	97	899

	98929	98946				
625461	98893	98910	TGGTTTTCAAACACACCT	6-8-4	96	900
	98930	98947				

Example 13: Dose-dependent antisense inhibition of human tau in SH-SY5Y cells by MOE gapmers

Gapmers from studies described above exhibiting significant *in vitro* inhibition of tau mRNA were selected and tested at various doses in SH-SY5Y cells. 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. Cells were plated at a density of 20,000 cells per well and transfected using electroporation with 0.938 μ M, 0.1.875 μ M, 3.750 μ M, 7.500 μ M, and 15.00 μ M concentrations of antisense oligonucleotide, as specified in the Tables below. After a treatment period of approximately 16 hours, RNA was isolated from the cells and tau mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3104 was used to measure mRNA levels. Tau mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN[®]. Results are presented as percent inhibition of tau, relative to untreated control cells. Tau mRNA levels were significantly reduced in a dose-dependent manner in antisense oligonucleotide treated cells.

Table 50

ISIS No	0.938 μ M	1.875 μ M	3.750 μ M	7.500 μ M	15.00 μ M
613412	57	53	49	83	91
620887	68	84	95	95	97
620919	35	54	76	95	96
620930	32	49	76	86	92
620946	41	61	73	90	92
620971	61	63	75	88	96
620976	40	68	80	91	96
620978	49	49	78	93	94
620988	64	58	76	92	95
621031	51	72	90	89	92
621032	35	55	81	89	96
621041	48	73	80	88	95
621236	62	59	78	86	88
621239	46	62	63	94	94
621254	63	67	88	84	87

Table 51

ISIS No	0.938 μ M	1.875 μ M	3.750 μ M	7.500 μ M	15.00 μ M
613412	33	54	63	89	95
620887	72	90	95	96	96
620889	20	45	72	87	95
621417	52	68	81	88	92
621434	45	64	69	84	76
621440	58	72	77	88	87
621492	40	60	80	78	83
621599	43	73	83	91	95
621615	36	67	74	81	87
621620	48	74	88	95	98
621644	4	28	33	55	65
623685	30	48	73	87	93
623872	31	61	80	90	94
623879	22	50	74	88	95
623932	39	62	80	91	95

Table 52

ISIS No	0.938 μ M	1.875 μ M	3.750 μ M	7.500 μ M	15.00 μ M
613412	23	51	50	87	94
620887	64	82	92	95	96
620891	79	89	93	96	96
623757	38	58	73	85	95
623783	30	40	67	78	91
623804	51	70	81	87	92
623902	62	77	90	87	95
623936	46	70	84	91	94
623937	48	58	79	91	93
623938	39	63	76	90	93
623939	29	57	77	91	93
623962	44	68	78	87	91
625442	32	57	66	82	88
625459	74	87	95	96	98
625460	88	94	97	97	98

5

Table 53

ISIS No	0.938 μ M	1.875 μ M	3.750 μ M	7.500 μ M	15.00 μ M
613412	6	11	20	0	35
620887	71	86	92	95	96
620888	73	89	93	95	96

620890	82	90	94	95	96
623969	41	62	84	94	n.d.
623987	46	71	89	96	97
625424	50	73	88	94	96
625433	64	83	90	95	95
625450	69	84	91	96	97
625451	85	91	95	93	95
625452	67	83	91	93	95
625453	72	85	91	94	96
625454	73	86	93	95	96
625455	44	68	86	92	94
625461	75	84	94	95	97

Table 54

ISIS No	0.938 μ M	1.875 μ M	3.750 μ M	7.500 μ M	15.00 μ M
613412	11	30	65	82	83
620887	59	77	66	95	79
623968	43	57	72	86	93
623970	29	54	77	88	94
623973	48	65	80	93	94
623977	38	60	72	82	89
623986	45	53	80	91	96
625423	43	57	75	77	95
625425	39	49	78	88	93
625426	15	43	61	82	92
625427	16	35	64	81	93
625437	30	45	64	84	91
625444	28	45	67	84	92
625446	16	33	58	76	92
625456	27	43	57	86	91
625458	19	45	61	85	93

Table 55

ISIS No	0.938 μ M	1.875 μ M	3.750 μ M	7.500 μ M	15.00 μ M
613412	0	10	31	71	77
620887	33	58	74	82	92
621842	7	31	45	72	87
621846	0	0	28	62	90
623903	0	0	25	71	83
623985	0	17	41	74	84
623994	19	42	67	81	83
625457	0	5	57	69	80

Example 14: Design of 5-7-6 MOE, 5-8-5 MOE, 5-9-5 MOE, and 5-10-5 MOE gapmers with phosphorothioate and phosphodiester internucleoside linkages at a hot spot region of human Tau

Antisense oligonucleotides were designed targeting a tau nucleic acid at a region identified as a
5 ‘hotspot’ in the studies above.

The newly designed chimeric antisense oligonucleotides in the Table below were designed as 5-7-6 MOE, 5-8-5 MOE, 5-9-5 MOE, or 5-10-5 MOE gapmers. The 5-7-6 MOE gapmers are 18 nucleosides in length, wherein the central gap segment comprises of seven 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising five and six nucleosides respectively. The 5-8-5
10 MOE gapmers are 18 nucleosides in length, wherein the central gap segment comprises of eight 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising five nucleosides each. The 5-9-5 MOE gapmers are 19 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 five nucleosides each. The 5-10-5 MOE gapmers are 20 nucleosides in length, wherein
15 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'-MOE modification. The internucleoside linkages throughout each gapmer are either phosphorothioate linkages or phosphodiester linkages. The ‘Chemistry’ column describes the internucleoside linkages of each oligonucleotide. ‘s’ indicates phosphorothioate linkage and ‘o’
20 indicates phosphodiester linkage. All cytosine residues throughout each gapmer are 5-methylcytosines.

“Start site” indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. “Stop site” indicates the 3'-most nucleoside to which the gapmer is targeted in the human gene sequence. Each gapmer listed in the Table below is targeted to either the human tau genomic sequence, designated herein as SEQ ID NO: 1 (GENBANK Accession No. NT_010783.15 truncated from nucleotides
25 9240000 to 9381000) or to the human tau mRNA sequence, designated herein as SEQ ID NO: 2 (GENBANK Accession No. NM_001123066.3). ‘n/a’ indicates that the antisense oligonucleotide does not target that particular gene sequence with 100% complementarity.

Table 56
MOE gapmers targeting SEQ ID NOs: 1 and 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	Linkage chemistry	Motif	SEQ ID NO
664511	135820	135837	GACAAAAGCAGGTTAAGT	2783	2800	sooooooooooooo	5-8-5	2331
664714	135820	135838	TGACAAAAGCAGGTTAAGT	2783	2801	sooooooooooooo	5-9-5	2332

664661	135820	135839	GTGACAAAAGCAGGTTAAGT	2783	2802	SOOOSSSSSSSSSSOOSS	5-10-5	2333
664767	135820	135837	GACAAAAGCAGGTTAAGT	2783	2800	SOOOSSSSSSSSOOSS	5-7-6	2331
664512	135821	135838	TGACAAAAGCAGGTTAAG	2784	2801	SOOOSSSSSSSSSSOOSS	5-8-5	2334
664715	135821	135839	GTGACAAAAGCAGGTTAAG	2784	2802	SOOOSSSSSSSSSSOOSS	5-9-5	2335
664662	135821	135840	AGTGACAAAAGCAGGTTAAG	2784	2803	SOOOSSSSSSSSSSOOSS	5-10-5	2336
664768	135821	135838	TGACAAAAGCAGGTTAAG	2784	2801	SOOOSSSSSSSSOOSS	5-7-6	2334
622109	135822	135839	GTGACAAAAGCAGGTTAA	2785	2802	SOOOSSSSSSSSSSOOSS	5-8-5	2038
664716	135822	135840	AGTGACAAAAGCAGGTTAA	2785	2803	SOOOSSSSSSSSSSOOSS	5-9-5	2337
664663	135822	135841	GAGTGACAAAAGCAGGTTAA	2785	2804	SOOOSSSSSSSSSSOOSS	5-10-5	2338
664769	135822	135839	GTGACAAAAGCAGGTTAA	2785	2802	SOOOSSSSSSSSOOSS	5-7-6	2038
664513	135823	135840	AGTGACAAAAGCAGGTTA	2786	2803	SOOOSSSSSSSSSSOOSS	5-8-5	2339
664717	135823	135841	GAGTGACAAAAGCAGGTTA	2786	2804	SOOOSSSSSSSSSSOOSS	5-9-5	2340
664664	135823	135842	CGAGTGACAAAAGCAGGTTA	2786	2805	SOOOSSSSSSSSSSOOSS	5-10-5	2341
664770	135823	135840	AGTGACAAAAGCAGGTTA	2786	2803	SOOOSSSSSSSSOOSS	5-7-6	2339
664514	135824	135841	GAGTGACAAAAGCAGGTT	2787	2804	SOOOSSSSSSSSSSOOSS	5-8-5	2342
664718	135824	135842	CGAGTGACAAAAGCAGGTT	2787	2805	SOOOSSSSSSSSSSOOSS	5-9-5	2343
664665	135824	135843	CCGAGTGACAAAAGCAGGTT	2787	2806	SOOOSSSSSSSSSSOOSS	5-10-5	2344
664771	135824	135841	GAGTGACAAAAGCAGGTT	2787	2804	SOOOSSSSSSSSOOSS	5-7-6	2342
622110	135825	135842	CGAGTGACAAAAGCAGGT	2788	2805	SOOOSSSSSSSSSSOOSS	5-8-5	2039
664719	135825	135843	CCGAGTGACAAAAGCAGGT	2788	2806	SOOOSSSSSSSSSSOOSS	5-9-5	2345
664666	135825	135844	GCCGAGTGACAAAAGCAGGT	2788	2807	SOOOSSSSSSSSSSOOSS	5-10-5	2346
664772	135825	135842	CGAGTGACAAAAGCAGGT	2788	2805	SOOOSSSSSSSSOOSS	5-7-6	2039
664515	135826	135843	CCGAGTGACAAAAGCAGG	2789	2806	SOOOSSSSSSSSSSOOSS	5-8-5	2347
664720	135826	135844	GCCGAGTGACAAAAGCAGG	2789	2807	SOOOSSSSSSSSSSOOSS	5-9-5	2348
664667	135826	135845	AGCCGAGTGACAAAAGCAGG	2789	2808	SOOOSSSSSSSSSSOOSS	5-10-5	2349
664773	135826	135843	CCGAGTGACAAAAGCAGG	2789	2806	SOOOSSSSSSSSOOSS	5-7-6	2347
664516	135827	135844	GCCGAGTGACAAAAGCAG	2790	2807	SOOOSSSSSSSSSSOOSS	5-8-5	2350
664721	135827	135845	AGCCGAGTGACAAAAGCAG	2790	2808	SOOOSSSSSSSSSSOOSS	5-9-5	2351
664668	135827	135846	AAGCCGAGTGACAAAAGCAG	2790	2809	SOOOSSSSSSSSSSOOSS	5-10-5	2352
664774	135827	135844	GCCGAGTGACAAAAGCAG	2790	2807	SOOOSSSSSSSSOOSS	5-7-6	2350
622111	135828	135845	AGCCGAGTGACAAAAGCA	2791	2808	SOOOSSSSSSSSSSOOSS	5-8-5	2040
664722	135828	135846	AAGCCGAGTGACAAAAGCA	2791	2809	SOOOSSSSSSSSSSOOSS	5-9-5	2353
664669	135828	135847	AAAGCCGAGTGACAAAAGCA	2791	2810	SOOOSSSSSSSSSSOOSS	5-10-5	2354
664775	135828	135845	AGCCGAGTGACAAAAGCA	2791	2808	SOOOSSSSSSSSOOSS	5-7-6	2040
664517	135829	135846	AAGCCGAGTGACAAAAGC	2792	2809	SOOOSSSSSSSSSSOOSS	5-8-5	2355
664723	135829	135847	AAAGCCGAGTGACAAAAGC	2792	2810	SOOOSSSSSSSSSSOOSS	5-9-5	2356
664670	135829	135848	CAAAGCCGAGTGACAAAAGC	2792	2811	SOOOSSSSSSSSSSOOSS	5-10-5	2357

664776	135829	135846	AAGCCGAGTGACAAAAGC	2792	2809	sooooooooooooo	5-7-6	2355
664518	135830	135847	AAAGCCGAGTGACAAAAG	2793	2810	sooooooooooooo	5-8-5	2358
664724	135830	135848	CAAAGCCGAGTGACAAAAG	2793	2811	sooooooooooooo	5-9-5	2359
664671	135830	135849	CAAAGCCGAGTGACAAAAG	2793	2812	sooooooooooooo	5-10-5	2360
664777	135830	135847	AAAGCCGAGTGACAAAAG	2793	2810	sooooooooooooo	5-7-6	2358
622112	135831	135848	CAAAGCCGAGTGACAAA	2794	2811	sooooooooooooo	5-8-5	2041
664725	135831	135849	CAAAGCCGAGTGACAAA	2794	2812	sooooooooooooo	5-9-5	2361
664672	135831	135850	GCCAAAGCCGAGTGACAAA	2794	2813	sooooooooooooo	5-10-5	2362
664778	135831	135848	CAAAGCCGAGTGACAAA	2794	2811	sooooooooooooo	5-7-6	2041
664519	135832	135849	CAAAGCCGAGTGACAAA	2795	2812	sooooooooooooo	5-8-5	2363
664726	135832	135850	GCCAAAGCCGAGTGACAAA	2795	2813	sooooooooooooo	5-9-5	2364
664673	135832	135851	AGCCAAAGCCGAGTGACAAA	2795	2814	sooooooooooooo	5-10-5	2365
664779	135832	135849	CAAAGCCGAGTGACAAA	2795	2812	sooooooooooooo	5-7-6	2363
664520	135833	135850	GCCAAAGCCGAGTGACAA	2796	2813	sooooooooooooo	5-8-5	2366
664727	135833	135851	AGCCAAAGCCGAGTGACAA	2796	2814	sooooooooooooo	5-9-5	2367
664674	135833	135852	GAGCCAAAGCCGAGTGACAA	2796	2815	sooooooooooooo	5-10-5	2368
664780	135833	135850	GCCAAAGCCGAGTGACAA	2796	2813	sooooooooooooo	5-7-6	2366
622113	135834	135851	AGCCAAAGCCGAGTGACA	2797	2814	sooooooooooooo	5-8-5	2042
664728	135834	135852	GAGCCAAAGCCGAGTGACA	2797	2815	sooooooooooooo	5-9-5	2369
664675	135834	135853	CGAGCCAAAGCCGAGTGACA	2797	2816	sooooooooooooo	5-10-5	2419
664781	135834	135851	AGCCAAAGCCGAGTGACA	2797	2814	sooooooooooooo	5-7-6	2042
664521	135835	135852	GAGCCAAAGCCGAGTGAC	2798	2815	sooooooooooooo	5-8-5	2420
664729	135835	135853	CGAGCCAAAGCCGAGTGAC	2798	2816	sooooooooooooo	5-9-5	2421
664676	135835	135854	CCGAGCCAAAGCCGAGTGAC	2798	2817	sooooooooooooo	5-10-5	2422
664782	135835	135852	GAGCCAAAGCCGAGTGAC	2798	2815	sooooooooooooo	5-7-6	2420
664522	135836	135853	CGAGCCAAAGCCGAGTGA	2799	2816	sooooooooooooo	5-8-5	2423
664730	135836	135854	CCGAGCCAAAGCCGAGTGA	2799	2817	sooooooooooooo	5-9-5	2424
664677	135836	135855	CCCGAGCCAAAGCCGAGTGA	2799	2818	sooooooooooooo	5-10-5	2425
664783	135836	135853	CGAGCCAAAGCCGAGTGA	2799	2816	sooooooooooooo	5-7-6	2423
622114	135837	135854	CCGAGCCAAAGCCGAGTG	2800	2817	sooooooooooooo	5-8-5	2043
664731	135837	135855	CCCGAGCCAAAGCCGAGTG	2800	2818	sooooooooooooo	5-9-5	2426
664678	135837	135856	TCCCGAGCCAAAGCCGAGTG	2800	2819	sooooooooooooo	5-10-5	2427
664784	135837	135854	CCGAGCCAAAGCCGAGTG	2800	2817	sooooooooooooo	5-7-6	2043
664523	135838	135855	CCCGAGCCAAAGCCGAGT	2801	2818	sooooooooooooo	5-8-5	2428
664732	135838	135856	TCCCGAGCCAAAGCCGAGT	2801	2819	sooooooooooooo	5-9-5	2429
664679	135838	135857	GTCCCGAGCCAAAGCCGAGT	2801	2820	sooooooooooooo	5-10-5	2430
664785	135838	135855	CCCGAGCCAAAGCCGAGT	2801	2818	sooooooooooooo	5-7-6	2428

664524	135839	135856	TCCCGAGCCAAAGCCGAG	2802	2819	SOOOSSSSSSSSOOSS	5-8-5	2431
664733	135839	135857	GTCCCGAGCCAAAGCCGAG	2802	2820	SOOOSSSSSSSSSOOSS	5-9-5	2432
664680	135839	135858	AGTCCCGAGCCAAAGCCGAG	2802	2821	SOOOSSSSSSSSSSOOSS	5-10-5	2433
664786	135839	135856	TCCCGAGCCAAAGCCGAG	2802	2819	SOOOSSSSSSSSOOSS	5-7-6	2431
622115	135840	135857	GTCCCGAGCCAAAGCCGA	2803	2820	SOOOSSSSSSSSOOSS	5-8-5	2044
664734	135840	135858	AGTCCCGAGCCAAAGCCGA	2803	2821	SOOOSSSSSSSSSOOSS	5-9-5	2434
664681	135840	135859	AAGTCCCGAGCCAAAGCCGA	2803	2822	SOOOSSSSSSSSSSOOSS	5-10-5	2435
664787	135840	135857	GTCCCGAGCCAAAGCCGA	2803	2820	SOOOSSSSSSSSOOSS	5-7-6	2044
664525	135841	135858	AGTCCCGAGCCAAAGCCG	2804	2821	SOOOSSSSSSSSOOSS	5-8-5	2436
664735	135841	135859	AAGTCCCGAGCCAAAGCCG	2804	2822	SOOOSSSSSSSSSOOSS	5-9-5	2437
664682	135841	135860	GAAGTCCCGAGCCAAAGCCG	2804	2823	SOOOSSSSSSSSSSOOSS	5-10-5	2438
664788	135841	135858	AGTCCCGAGCCAAAGCCG	2804	2821	SOOOSSSSSSSSOOSS	5-7-6	2436
664526	135842	135859	AAGTCCCGAGCCAAAGCC	2805	2822	SOOOSSSSSSSSOOSS	5-8-5	2439
664736	135842	135860	GAAGTCCCGAGCCAAAGCC	2805	2823	SOOOSSSSSSSSSOOSS	5-9-5	2440
664683	135842	135861	TGAAGTCCCGAGCCAAAGCC	2805	2824	SOOOSSSSSSSSSSOOSS	5-10-5	2441
664789	135842	135859	AAGTCCCGAGCCAAAGCC	2805	2822	SOOOSSSSSSSSOOSS	5-7-6	2439
622116	135843	135860	GAAGTCCCGAGCCAAAGC	2806	2823	SOOOSSSSSSSSOOSS	5-8-5	2045
664737	135843	135861	TGAAGTCCCGAGCCAAAGC	2806	2824	SOOOSSSSSSSSSOOSS	5-9-5	2442
664684	135843	135862	TTGAAGTCCCGAGCCAAAGC	2806	2825	SOOOSSSSSSSSSSOOSS	5-10-5	2443
664790	135843	135860	GAAGTCCCGAGCCAAAGC	2806	2823	SOOOSSSSSSSSOOSS	5-7-6	2045
664527	135844	135861	TGAAGTCCCGAGCCAAAG	2807	2824	SOOOSSSSSSSSOOSS	5-8-5	2478
664738	135844	135862	TTGAAGTCCCGAGCCAAAG	2807	2825	SOOOSSSSSSSSSOOSS	5-9-5	2532
664685	135844	135863	TTTGAAGTCCCGAGCCAAAG	2807	2826	SOOOSSSSSSSSSSOOSS	5-10-5	2533
664791	135844	135861	TGAAGTCCCGAGCCAAAG	2807	2824	SOOOSSSSSSSSOOSS	5-7-6	2478
664528	135845	135862	TTGAAGTCCCGAGCCAAA	2808	2825	SOOOSSSSSSSSOOSS	5-8-5	2479
664739	135845	135863	TTTGAAGTCCCGAGCCAAA	2808	2826	SOOOSSSSSSSSSOOSS	5-9-5	2534
664686	135845	135864	TTTTGAAGTCCCGAGCCAAA	2808	2827	SOOOSSSSSSSSSSOOSS	5-10-5	2535
664792	135845	135862	TTGAAGTCCCGAGCCAAA	2808	2825	SOOOSSSSSSSSOOSS	5-7-6	2479
622117	135846	135863	TTTGAAGTCCCGAGCCAA	2809	2826	SOOOSSSSSSSSOOSS	5-8-5	2046
664740	135846	135864	TTTTGAAGTCCCGAGCCAA	2809	2827	SOOOSSSSSSSSSOOSS	5-9-5	2536
664687	135846	135865	ATTTTGAAGTCCCGAGCCAA	2809	2828	SOOOSSSSSSSSSSOOSS	5-10-5	2537
664793	135846	135863	TTTGAAGTCCCGAGCCAA	2809	2826	SOOOSSSSSSSSOOSS	5-7-6	2538
664529	135847	135864	TTTTGAAGTCCCGAGCCA	2810	2827	SOOOSSSSSSSSOOSS	5-8-5	2480
664741	135847	135865	ATTTTGAAGTCCCGAGCCA	2810	2828	SOOOSSSSSSSSSOOSS	5-9-5	2539
664688	135847	135866	GATTTTGAAGTCCCGAGCCA	2810	2829	SOOOSSSSSSSSSSOOSS	5-10-5	2540
664794	135847	135864	TTTTGAAGTCCCGAGCCA	2810	2827	SOOOSSSSSSSSOOSS	5-7-6	2480
664530	135848	135865	ATTTTGAAGTCCCGAGCC	2811	2828	SOOOSSSSSSSSOOSS	5-8-5	2481

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664742	135848	135866	GATTTTGAAGTCCCGAGCC	2811	2829	sooooooooooooo	5-9-5	2541
664689	135848	135867	TGATTTTGAAGTCCCGAGCC	1644	1663	sooooooooooooo	5-10-5	56
664795	135848	135865	ATTTTGAAGTCCCGAGCC	2811	2828	sooooooooooooo	5-7-6	2481
622118	135849	135866	GATTTTGAAGTCCCGAGC	2812	2829	sooooooooooooo	5-8-5	2047
664743	135849	135867	TGATTTTGAAGTCCCGAGC	2812	2830	sooooooooooooo	5-9-5	2542
664690	135849	135868	CTGATTTTGAAGTCCCGAGC	2812	2831	sooooooooooooo	5-10-5	464
664796	135849	135866	GATTTTGAAGTCCCGAGC	2812	2829	sooooooooooooo	5-7-6	2047
664531	135850	135867	TGATTTTGAAGTCCCGAG	2813	2830	sooooooooooooo	5-8-5	2482
664744	135850	135868	CTGATTTTGAAGTCCCGAG	2813	2831	sooooooooooooo	5-9-5	2543
664691	135850	135869	ACTGATTTTGAAGTCCCGAG	2813	2832	sooooooooooooo	5-10-5	2544
664797	135850	135867	TGATTTTGAAGTCCCGAG	2813	2830	sooooooooooooo	5-7-6	2482
664532	135851	135868	CTGATTTTGAAGTCCCGA	2814	2831	sooooooooooooo	5-8-5	2483
664745	135851	135869	ACTGATTTTGAAGTCCCGA	2814	2832	sooooooooooooo	5-9-5	2545
664692	135851	135870	CACTGATTTTGAAGTCCCGA	2814	2833	sooooooooooooo	5-10-5	2546
664798	135851	135868	CTGATTTTGAAGTCCCGA	2814	2831	sooooooooooooo	5-7-6	2483
622119	135852	135869	ACTGATTTTGAAGTCCCG	2815	2832	sooooooooooooo	5-8-5	2048
664746	135852	135870	CACTGATTTTGAAGTCCCG	2815	2833	sooooooooooooo	5-9-5	2547
664693	135852	135871	TCACTGATTTTGAAGTCCCG	2815	2834	sooooooooooooo	5-10-5	2548
664799	135852	135869	ACTGATTTTGAAGTCCCG	2815	2832	sooooooooooooo	5-7-6	2549
664533	135853	135870	CACTGATTTTGAAGTCCC	2816	2833	sooooooooooooo	5-8-5	2370
664747	135853	135871	TCACTGATTTTGAAGTCCC	2816	2834	sooooooooooooo	5-9-5	2371
664694	135853	135872	ATCACTGATTTTGAAGTCCC	1649	1668	sooooooooooooo	5-10-5	57
664800	135853	135870	CACTGATTTTGAAGTCCC	2816	2833	sooooooooooooo	5-7-6	2370
664534	135854	135871	TCACTGATTTTGAAGTCC	2817	2834	sooooooooooooo	5-8-5	2372
664748	135854	135872	ATCACTGATTTTGAAGTCC	2817	2835	sooooooooooooo	5-9-5	2373
664695	135854	135873	CATCACTGATTTTGAAGTCC	2817	2836	sooooooooooooo	5-10-5	2374
664801	135854	135871	TCACTGATTTTGAAGTCC	2817	2834	sooooooooooooo	5-7-6	2372
622120	135855	135872	ATCACTGATTTTGAAGTC	2818	2835	sooooooooooooo	5-8-5	1668
664749	135855	135873	CATCACTGATTTTGAAGTC	2818	2836	sooooooooooooo	5-9-5	2375
664696	135855	135874	CCATCACTGATTTTGAAGTC	2818	2837	sooooooooooooo	5-10-5	2376
664802	135855	135872	ATCACTGATTTTGAAGTC	2818	2835	sooooooooooooo	5-7-6	1668
664535	135856	135873	CATCACTGATTTTGAAGT	2819	2836	sooooooooooooo	5-8-5	2377
664750	135856	135874	CCATCACTGATTTTGAAGT	2819	2837	sooooooooooooo	5-9-5	2378
664697	135856	135875	CCCATCACTGATTTTGAAGT	2819	2838	sooooooooooooo	5-10-5	2379
664803	135856	135873	CATCACTGATTTTGAAGT	2819	2836	sooooooooooooo	5-7-6	2377
664536	135857	135874	CCATCACTGATTTTGAAG	2820	2837	sooooooooooooo	5-8-5	2380
664751	135857	135875	CCCATCACTGATTTTGAAG	2820	2838	sooooooooooooo	5-9-5	2381

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664698	135857	135876	TCCCATCACTGATTTTGAAG	2820	2839	SOOOSSSSSSSSSSOOSS	5-10-5	2382
664804	135857	135874	CCATCACTGATTTTGAAG	2820	2837	SOOOSSSSSSSSOOSS	5-7-6	2380
622121	135858	135875	CCCATCACTGATTTTGA	2821	2838	SOOOSSSSSSSSSSOOSS	5-8-5	1669
664752	135858	135876	TCCCATCACTGATTTTGA	2821	2839	SOOOSSSSSSSSSSOOSS	5-9-5	2383
664699	135858	135877	CTCCCATCACTGATTTTGA	2821	2840	SOOOSSSSSSSSSSOOSS	5-10-5	2384
664805	135858	135875	CCCATCACTGATTTTGA	2821	2838	SOOOSSSSSSSSOOSS	5-7-6	1669
664537	135859	135876	TCCCATCACTGATTTTGA	2822	2839	SOOOSSSSSSSSSSOOSS	5-8-5	2385
664753	135859	135877	CTCCCATCACTGATTTTGA	2822	2840	SOOOSSSSSSSSSSOOSS	5-9-5	2386
664700	135859	135878	ACTCCCATCACTGATTTTGA	2822	2841	SOOOSSSSSSSSSSOOSS	5-10-5	2387
664806	135859	135876	TCCCATCACTGATTTTGA	2822	2839	SOOOSSSSSSSSOOSS	5-7-6	2385
664538	135860	135877	CTCCCATCACTGATTTTG	2823	2840	SOOOSSSSSSSSSSOOSS	5-8-5	2388
664754	135860	135878	ACTCCCATCACTGATTTTG	2823	2841	SOOOSSSSSSSSSSOOSS	5-9-5	2389
664701	135860	135879	TACTCCCATCACTGATTTTG	2823	2842	SOOOSSSSSSSSSSOOSS	5-10-5	2390
664807	135860	135877	CTCCCATCACTGATTTTG	2823	2840	SOOOSSSSSSSSOOSS	5-7-6	2388
622122	135861	135878	ACTCCCATCACTGATTTT	2824	2841	SOOOSSSSSSSSSSOOSS	5-8-5	1670
664755	135861	135879	TACTCCCATCACTGATTTT	2824	2842	SOOOSSSSSSSSSSOOSS	5-9-5	2391
664702	135861	135880	TTACTCCCATCACTGATTTT	2824	2843	SOOOSSSSSSSSSSOOSS	5-10-5	2392
664808	135861	135878	ACTCCCATCACTGATTTT	2824	2841	SOOOSSSSSSSSOOSS	5-7-6	1670
664539	135862	135879	TACTCCCATCACTGATTT	2825	2842	SOOOSSSSSSSSSSOOSS	5-8-5	2393
664756	135862	135880	TTACTCCCATCACTGATTT	2825	2843	SOOOSSSSSSSSSSOOSS	5-9-5	2394
664703	135862	135881	CTTACTCCCATCACTGATTT	2825	2844	SOOOSSSSSSSSSSOOSS	5-10-5	2395
664809	135862	135879	TACTCCCATCACTGATTT	2825	2842	SOOOSSSSSSSSOOSS	5-7-6	2393
664540	135863	135880	TTACTCCCATCACTGATT	2826	2843	SOOOSSSSSSSSSSOOSS	5-8-5	2396
664757	135863	135881	CTTACTCCCATCACTGATT	2826	2844	SOOOSSSSSSSSSSOOSS	5-9-5	2397
664704	135863	135882	TCTTACTCCCATCACTGATT	2826	2845	SOOOSSSSSSSSSSOOSS	5-10-5	2398
664810	135863	135880	TTACTCCCATCACTGATT	2826	2843	SOOOSSSSSSSSOOSS	5-7-6	2396
622123	135864	135881	CTTACTCCCATCACTGAT	2827	2844	SOOOSSSSSSSSSSOOSS	5-8-5	1671
664758	135864	135882	TCTTACTCCCATCACTGAT	2827	2845	SOOOSSSSSSSSSSOOSS	5-9-5	2399
664705	135864	135883	CTCTTACTCCCATCACTGAT	2827	2846	SOOOSSSSSSSSSSOOSS	5-10-5	2400
664811	135864	135881	CTTACTCCCATCACTGAT	2827	2844	SOOOSSSSSSSSOOSS	5-7-6	1671
664541	135865	135882	TCTTACTCCCATCACTGA	2828	2845	SOOOSSSSSSSSSSOOSS	5-8-5	2401
664759	135865	135883	CTCTTACTCCCATCACTGA	2828	2846	SOOOSSSSSSSSSSOOSS	5-9-5	2402
664706	135865	135884	GCTCTTACTCCCATCACTGA	2828	2847	SOOOSSSSSSSSSSOOSS	5-10-5	2403
664812	135865	135882	TCTTACTCCCATCACTGA	2828	2845	SOOOSSSSSSSSOOSS	5-7-6	2401
664542	135866	135883	CTCTTACTCCCATCACTG	2829	2846	SOOOSSSSSSSSSSOOSS	5-8-5	2404
664760	135866	135884	GCTCTTACTCCCATCACTG	2829	2847	SOOOSSSSSSSSSSOOSS	5-9-5	2405
664707	135866	135885	TGCTCTTACTCCCATCACTG	2829	2848	SOOOSSSSSSSSSSOOSS	5-10-5	2406

664813	135866	135883	CTCTTACTCCCATCACTG	2829	2846	sooooooooooooo	5-7-6	2404
622124	135867	135884	GCTCTTACTCCCATCACT	2830	2847	sooooooooooooo	5-8-5	1672
664761	135867	135885	TGCTCTTACTCCCATCACT	2830	2848	sooooooooooooo	5-9-5	2407
664708	135867	135886	TTGCTCTTACTCCCATCACT	2830	2849	sooooooooooooo	5-10-5	2408
664814	135867	135884	GCTCTTACTCCCATCACT	2830	2847	sooooooooooooo	5-7-6	1672
623993	135868	135885	TGCTCTTACTCCCATCAC	2831	2848	sooooooooooooo	5-8-5	2306
664762	135868	135886	TTGCTCTTACTCCCATCAC	2831	2849	sooooooooooooo	5-9-5	2409
664709	135868	135887	TTTGCTCTTACTCCCATCAC	2831	2850	sooooooooooooo	5-10-5	2410
664815	135868	135885	TGCTCTTACTCCCATCAC	2831	2848	sooooooooooooo	5-7-6	2306
623994	135869	135886	TTGCTCTTACTCCCATCA	2832	2849	sooooooooooooo	5-8-5	2307
664763	135869	135887	TTTGCTCTTACTCCCATCA	2832	2850	sooooooooooooo	5-9-5	2411
664710	135869	135888	ATTTGCTCTTACTCCCATCA	2832	2851	sooooooooooooo	5-10-5	2412
664816	135869	135886	TTGCTCTTACTCCCATCA	2832	2849	sooooooooooooo	5-7-6	2307
622125	135870	135887	TTTGCTCTTACTCCCATC	2833	2850	sooooooooooooo	5-8-5	1673
664764	135870	135888	ATTTGCTCTTACTCCCATC	2833	2851	sooooooooooooo	5-9-5	2413
664711	135870	135889	AATTTGCTCTTACTCCCATC	2833	2852	sooooooooooooo	5-10-5	2414
664817	135870	135887	TTTGCTCTTACTCCCATC	2833	2850	sooooooooooooo	5-7-6	1673
623995	135871	135888	ATTTGCTCTTACTCCCAT	2834	2851	sooooooooooooo	5-8-5	2308
664765	135871	135889	AATTTGCTCTTACTCCCAT	2834	2852	sooooooooooooo	5-9-5	2415
664712	135871	135890	AAATTTGCTCTTACTCCCAT	2834	2853	sooooooooooooo	5-10-5	2416
664818	135871	135888	ATTTGCTCTTACTCCCAT	2834	2851	sooooooooooooo	5-7-6	2308
623996	135872	135889	AATTTGCTCTTACTCCCA	2835	2852	sooooooooooooo	5-8-5	2309
664766	135872	135890	AAATTTGCTCTTACTCCCA	2835	2853	sooooooooooooo	5-9-5	2417
664713	135872	135891	GAAATTTGCTCTTACTCCCA	2835	2854	sooooooooooooo	5-10-5	2418
664819	135872	135889	AATTTGCTCTTACTCCCA	2835	2852	sooooooooooooo	5-7-6	2309

Example 15: Intracerebroventricular administration of antisense oligonucleotides against human tau mRNA in htau mice

5 Selected compounds were tested for efficacy by ICV administration in human tau transgenic mice (Duff et al., Neurobiology of Disease 7:87-98, 2000).

Treatment and surgery

10 Groups of 4 mice each were administered ISIS 613255, ISIS 613329, ISIS 613344, ISIS 613361, ISIS 613369, ISIS 613370, ISIS 613397, ISIS 613045, ISIS 613099, ISIS 613118, ISIS 613136 with a 200 µg dose delivered by ICV bolus injection. A control group of 2 mice was similarly treated with ISIS 424880 and a control group of 4 mice was similarly treated with PBS. All procedures were performed under

isoflourane anesthesia and in accordance with IACUC regulations. For mouse ICV bolus injections, the antisense oligonucleotide was injected into the right lateral ventricle of human tau transgenic mice. Ten microliters of solution containing 300 µg of oligonucleotide in PBS was injected over approximately 10 seconds. Tissue was collected 14 days after oligonucleotide administration.

5

RNA Analysis

On day 14 after the oligonucleotide administration, RNA was extracted from the hippocampus, spinal cord and cortex for real-time PCR analysis of tau mRNA levels. Human tau mRNA levels were measured using the human primer probe set RTS3104. Results were calculated as percent inhibition of human tau mRNA expression compared to the control. All the antisense oligonucleotides effect significant inhibition of human tau mRNA levels.

10

Table 57

Percent reduction of human tau mRNA levels in hTau mice

ISIS No	Cortex	Hippocampus	Spinal Cord
613255	30	46	36
613329	20	69	67
613344	41	42	34
613361	69	57	72
613369	17	48	46
613370	42	61	63
613397	33	41	57
613045	12	38	47
613099	42	55	54
613118	64	73	58
613136	26	39	27
424880	50	53	55

15

Example 16: Antisense inhibition of human Tau in SH-SY5Y cells 5-7-6 MOE, 5-8-5 MOE, 5-9-5 MOE, and 5-10-5 MOE gapmers

The antisense oligonucleotides described in the Examples above, as well as newly designed antisense oligonucleotides targeting a human tau nucleic acid, were tested in a series of experiments that had similar culture conditions. The results for each experiment are presented in separate tables shown below. Cultured SH-SY5Y cells were transfected using electroporation with 8,000 nM antisense oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and tau mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3104 was used to measure

20

mRNA levels. Tau mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of tau, relative to untreated control cells.

The newly designed chimeric antisense oligonucleotides in the Tables below were designed as 5-7-6 MOE, 5-8-5 MOE, 5-9-5 MOE, or 5-10-5 MOE gapmers. The 5-7-6 MOE gapmers are 18 nucleosides in length, wherein the central gap segment comprises of seven 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising five and six nucleosides respectively. The 5-8-5 MOE gapmers are 18 nucleosides in length, wherein the central gap segment comprises of eight 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising five nucleosides each. The 5-9-5 MOE gapmers are 19 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 five nucleosides each. 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. Each nucleoside in the 5' wing segment and each nucleoside in the 3' wing segment has a 2'-MOE modification. The internucleoside linkages throughout each gapmer are either phosphorothioate linkages or phosphodiester linkages. The 'Linkage Chemistry' column describes the internucleoside linkages of each oligonucleotide. 's' indicates phosphorothioate linkage and 'o' indicates phosphodiester linkage. All cytosine residues throughout each gapmer are 5-methylcytosines.

"Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. "Stop site" indicates the 3'-most nucleoside to which the gapmer is targeted in the human gene sequence. Each gapmer listed in the Table below is targeted to either the human tau genomic sequence, designated herein as SEQ ID NO: 1 (GENBANK Accession No. NT_010783.15 truncated from nucleotides 9240000 to 9381000) or to the human tau mRNA sequence, designated herein as SEQ ID NO: 2 (GENBANK Accession No. NM_001123066.3). 'n/a' indicates that the antisense oligonucleotide does not target that particular gene sequence with 100% complementarity.

Table 58

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	SEQ ID NO: 2 start site	SEQ ID NO: 2 stop site	Linkage Chemistry	Motif	% inhibition	SEQ ID NO
623965	73880	73897	TGATCTTCCATCACTTCG	n/a	n/a	sooooooooooooo	5-8-5	52	2278
620887	98891	98908	GTTTCAAACACACCTTC	n/a	n/a	sooooooooooooo	5-8-5	91	665
	98928	98945							
664511	135820	135837	GACAAAAGCAGGTTAAGT	2783	2800	sooooooooooooo	5-8-5	65	2331
664767	135820	135837	GACAAAAGCAGGTTAAGT	2783	2800	sooooooooooooo	5-7-6	21	2331
664512	135821	135838	TGACAAAAGCAGGTTAAG	2784	2801	sooooooooooooo	5-8-5	60	2334

664768	135821	135838	TGACAAAAGCAGGTTAAG	2784	2801	SOOOSSSSSSSSOOSS	5-7-6	30	2334
622109	135822	135839	GTGACAAAAGCAGGTTAA	2785	2802	SOOOSSSSSSSSOOSS	5-8-5	72	2038
664769	135822	135839	GTGACAAAAGCAGGTTAA	2785	2802	SOOOSSSSSSSSOOSS	5-7-6	49	2038
664513	135823	135840	AGTGACAAAAGCAGGTTA	2786	2803	SOOOSSSSSSSSOOSS	5-8-5	56	2339
664770	135823	135840	AGTGACAAAAGCAGGTTA	2786	2803	SOOOSSSSSSSSOOSS	5-7-6	45	2339
664514	135824	135841	GAGTGACAAAAGCAGGTT	2787	2804	SOOOSSSSSSSSOOSS	5-8-5	84	2342
664771	135824	135841	GAGTGACAAAAGCAGGTT	2787	2804	SOOOSSSSSSSSOOSS	5-7-6	63	2342
622110	135825	135842	CGAGTGACAAAAGCAGGT	2788	2805	SOOOSSSSSSSSOOSS	5-8-5	77	2039
664772	135825	135842	CGAGTGACAAAAGCAGGT	2788	2805	SOOOSSSSSSSSOOSS	5-7-6	37	2039
664515	135826	135843	CCGAGTGACAAAAGCAGG	2789	2806	SOOOSSSSSSSSOOSS	5-8-5	70	2347
664773	135826	135843	CCGAGTGACAAAAGCAGG	2789	2806	SOOOSSSSSSSSOOSS	5-7-6	62	2347
664516	135827	135844	GCCGAGTGACAAAAGCAG	2790	2807	SOOOSSSSSSSSOOSS	5-8-5	79	2350
664774	135827	135844	GCCGAGTGACAAAAGCAG	2790	2807	SOOOSSSSSSSSOOSS	5-7-6	70	2350
622111	135828	135845	AGCCGAGTGACAAAAGCA	2791	2808	SOOOSSSSSSSSOOSS	5-8-5	75	2040
664775	135828	135845	AGCCGAGTGACAAAAGCA	2791	2808	SOOOSSSSSSSSOOSS	5-7-6	78	2040
664517	135829	135846	AAGCCGAGTGACAAAAGC	2792	2809	SOOOSSSSSSSSOOSS	5-8-5	67	2355
664776	135829	135846	AAGCCGAGTGACAAAAGC	2792	2809	SOOOSSSSSSSSOOSS	5-7-6	50	2355
664518	135830	135847	AAAGCCGAGTGACAAAAG	2793	2810	SOOOSSSSSSSSOOSS	5-8-5	47	2358
664777	135830	135847	AAAGCCGAGTGACAAAAG	2793	2810	SOOOSSSSSSSSOOSS	5-7-6	42	2358
622112	135831	135848	CAAAGCCGAGTGACAAA	2794	2811	SOOOSSSSSSSSOOSS	5-8-5	46	2041
664778	135831	135848	CAAAGCCGAGTGACAAA	2794	2811	SOOOSSSSSSSSOOSS	5-7-6	34	2041
664519	135832	135849	CCAAAGCCGAGTGACAAA	2795	2812	SOOOSSSSSSSSOOSS	5-8-5	57	2363
664779	135832	135849	CCAAAGCCGAGTGACAAA	2795	2812	SOOOSSSSSSSSOOSS	5-7-6	34	2363
664520	135833	135850	GCCAAAGCCGAGTGACAA	2796	2813	SOOOSSSSSSSSOOSS	5-8-5	63	2366
664780	135833	135850	GCCAAAGCCGAGTGACAA	2796	2813	SOOOSSSSSSSSOOSS	5-7-6	66	2366
622113	135834	135851	AGCCAAAGCCGAGTGACA	2797	2814	SOOOSSSSSSSSOOSS	5-8-5	70	2042
664781	135834	135851	AGCCAAAGCCGAGTGACA	2797	2814	SOOOSSSSSSSSOOSS	5-7-6	74	2042
664521	135835	135852	GAGCCAAAGCCGAGTGAC	2798	2815	SOOOSSSSSSSSOOSS	5-8-5	71	2420
664782	135835	135852	GAGCCAAAGCCGAGTGAC	2798	2815	SOOOSSSSSSSSOOSS	5-7-6	31	2420
664522	135836	135853	CGAGCCAAAGCCGAGTGA	2799	2816	SOOOSSSSSSSSOOSS	5-8-5	50	2423
664783	135836	135853	CGAGCCAAAGCCGAGTGA	2799	2816	SOOOSSSSSSSSOOSS	5-7-6	30	2423
622114	135837	135854	CCGAGCCAAAGCCGAGTG	2800	2817	SOOOSSSSSSSSOOSS	5-8-5	72	2043
664784	135837	135854	CCGAGCCAAAGCCGAGTG	2800	2817	SOOOSSSSSSSSOOSS	5-7-6	76	2043
664523	135838	135855	CCCGAGCCAAAGCCGAGT	2801	2818	SOOOSSSSSSSSOOSS	5-8-5	70	2428
664785	135838	135855	CCCGAGCCAAAGCCGAGT	2801	2818	SOOOSSSSSSSSOOSS	5-7-6	56	2428
664524	135839	135856	TCCCGAGCCAAAGCCGAG	2802	2819	SOOOSSSSSSSSOOSS	5-8-5	55	2431
664786	135839	135856	TCCCGAGCCAAAGCCGAG	2802	2819	SOOOSSSSSSSSOOSS	5-7-6	36	2431
622115	135840	135857	GTCCCGAGCCAAAGCCGA	2803	2820	SOOOSSSSSSSSOOSS	5-8-5	59	2044
664787	135840	135857	GTCCCGAGCCAAAGCCGA	2803	2820	SOOOSSSSSSSSOOSS	5-7-6	54	2044
664525	135841	135858	AGTCCCGAGCCAAAGCCG	2804	2821	SOOOSSSSSSSSOOSS	5-8-5	74	2436
664788	135841	135858	AGTCCCGAGCCAAAGCCG	2804	2821	SOOOSSSSSSSSOOSS	5-7-6	77	2436
664789	135842	135859	AAGTCCCGAGCCAAAGCC	2805	2822	SOOOSSSSSSSSOOSS	5-7-6	42	2439
664790	135843	135860	GAAGTCCCGAGCCAAAGC	2806	2823	SOOOSSSSSSSSOOSS	5-7-6	38	2045
664791	135844	135861	TGAAGTCCCGAGCCAAAG	2807	2824	SOOOSSSSSSSSOOSS	5-7-6	44	2478
664792	135845	135862	TTGAAGTCCCGAGCCAAA	2808	2825	SOOOSSSSSSSSOOSS	5-7-6	44	2479
664793	135846	135863	TTGAAGTCCCGAGCCAA	2809	2826	SOOOSSSSSSSSOOSS	5-7-6	29	2046

664794	135847	135864	TTTTGAAGTCCCGAGCCA	2810	2827	SOOOSSSSSSSSOOOSS	5-7-6	32	2480
664795	135848	135865	ATTTTGAAGTCCCGAGCC	2811	2828	SOOOSSSSSSSSOOOSS	5-7-6	15	2481
664796	135849	135866	GATTTTGAAGTCCCGAGC	2812	2829	SOOOSSSSSSSSOOOSS	5-7-6	76	2047
664797	135850	135867	TGATTTTGAAGTCCCGAG	2813	2830	SOOOSSSSSSSSOOOSS	5-7-6	70	2482
664798	135851	135868	CTGATTTTGAAGTCCCGA	2814	2831	SOOOSSSSSSSSOOOSS	5-7-6	75	2483
664799	135852	135869	ACTGATTTTGAAGTCCCG	2815	2832	SOOOSSSSSSSSOOOSS	5-7-6	79	2048
664800	135853	135870	CACTGATTTTGAAGTCCC	2816	2833	SOOOSSSSSSSSOOOSS	5-7-6	82	2370
664534	135854	135871	TCAGTATTTTGAAGTCC	2817	2834	SOOOSSSSSSSSOOOSS	5-8-5	78	2372
664801	135854	135871	TCAGTATTTTGAAGTCC	2817	2834	SOOOSSSSSSSSOOOSS	5-7-6	29	2372
664802	135855	135872	ATCACTGATTTTGAAGTC	2818	2835	SOOOSSSSSSSSOOOSS	5-7-6	52	1668
664803	135856	135873	CATCACTGATTTTGAAGT	2819	2836	SOOOSSSSSSSSOOOSS	5-7-6	55	2377
664804	135857	135874	CCATCACTGATTTTGAAG	2820	2837	SOOOSSSSSSSSOOOSS	5-7-6	38	2380
664805	135858	135875	CCCATCACTGATTTTGAA	2821	2838	SOOOSSSSSSSSOOOSS	5-7-6	62	1669
664806	135859	135876	TCCCATCACTGATTTTGA	2822	2839	SOOOSSSSSSSSOOOSS	5-7-6	72	2385
664807	135860	135877	CTCCCATCACTGATTTTG	2823	2840	SOOOSSSSSSSSOOOSS	5-7-6	55	2388
664808	135861	135878	ACTCCCATCACTGATTTT	2824	2841	SOOOSSSSSSSSOOOSS	5-7-6	38	1670
664809	135862	135879	TACTCCCATCACTGATTT	2825	2842	SOOOSSSSSSSSOOOSS	5-7-6	54	2393
664810	135863	135880	TTACTCCCATCACTGATT	2826	2843	SOOOSSSSSSSSOOOSS	5-7-6	39	2396
664811	135864	135881	CTTACTCCCATCACTGAT	2827	2844	SOOOSSSSSSSSOOOSS	5-7-6	39	1671
664812	135865	135882	TCTTACTCCCATCACTGA	2828	2845	SOOOSSSSSSSSOOOSS	5-7-6	45	2401
664813	135866	135883	CTTACTCCCATCACTG	2829	2846	SOOOSSSSSSSSOOOSS	5-7-6	61	2404
664814	135867	135884	GCTCTTACTCCCATCACT	2830	2847	SOOOSSSSSSSSOOOSS	5-7-6	14	1672
664815	135868	135885	TGCTCTTACTCCCATCAC	2831	2848	SOOOSSSSSSSSOOOSS	5-7-6	70	2306
664816	135869	135886	TTGCTCTTACTCCCATCA	2832	2849	SOOOSSSSSSSSOOOSS	5-7-6	72	2307
664817	135870	135887	TTTGCTCTTACTCCCATC	2833	2850	SOOOSSSSSSSSOOOSS	5-7-6	62	1673
664818	135871	135888	ATTTGCTCTTACTCCCAT	2834	2851	SOOOSSSSSSSSOOOSS	5-7-6	69	2308
664819	135872	135889	AATTTGCTCTTACTCCCA	2835	2852	SOOOSSSSSSSSOOOSS	5-7-6	67	2309

Table 59

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	SEQ ID NO: 2 start site	SEQ ID NO: 2 stop site	Linkage Chemistry	Motif	% inhibition	SEQ ID NO
665045	21592	21609	ACATCCAAATAACAATAT	n/a	n/a	SOOOSSSSSSSSOOOSS	5-8-5	1	2444
665046	21617	21634	TCCTGTCTCAAACACCTA	n/a	n/a	SOOOSSSSSSSSOOOSS	5-8-5	44	2445
665047	30083	30100	AGCTTATCACAGTAGGTG	n/a	n/a	SOOOSSSSSSSSOOOSS	5-8-5	94	2446
665048	30108	30125	CCTTTGCTTCACACACCA	n/a	n/a	SOOOSSSSSSSSOOOSS	5-8-5	67	2447
621013	30133	30150	AGCTCACTACAGCAGGCA	n/a	n/a	SOOOSSSSSSSSOOOSS	5-8-5	90	868
665049	30158	30175	TGGTTCTACAACCTGCCC	n/a	n/a	SOOOSSSSSSSSOOOSS	5-8-5	57	2448
665050	30183	30200	CCTTTGTAACCTTGAAC	n/a	n/a	SOOOSSSSSSSSOOOSS	5-8-5	25	2449
665051	33838	33855	AGTTAAAGATGGCAACC	n/a	n/a	SOOOSSSSSSSSOOOSS	5-8-5	32	2450
665052	33863	33880	CTGGGCATTTTGATAAAA	n/a	n/a	SOOOSSSSSSSSOOOSS	5-8-5	28	2451
621031	33888	33905	GGTATAATTTGTTTGGAC	n/a	n/a	SOOOSSSSSSSSOOOSS	5-8-5	85	886
665053	33913	33930	AGTGCCAGACATTTTCAA	n/a	n/a	SOOOSSSSSSSSOOOSS	5-8-5	20	2452

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665054	33938	33955	CTGGCACAACAGGCATTG	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	25	2453
621041	35721	35738	TTGCCATCTTGACAGGG	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	70	896
665055	35746	35763	GTGGTACAGAGGCTGTGT	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	47	2454
665056	35771	35788	TTGCAGATTCTGAATACC	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	78	2455
665057	64499	64516	TATGATTCCCAGGAGTCT	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	0	2456
621181	64543	64560	GTAGGTGTCATCATCATC	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	77	1113
665058	64568	64585	GTGACCCTTCAGGGCAAT	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	35	2457
665059	64593	64610	ATGCAGGTGCCTTGCAAG	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	36	2458
623965	73880	73897	TGATCTCCATCACTTCG	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	48	2278
665060	77364	77381	CCTGCTGCCAACAGTAGA	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	51	2459
665061	77389	77406	CCCTCACGGGCTGTTGTG	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	20	2460
621236	77414	77431	TCATCTGTGAAGCGGACG	73377	73394	SOOOSSSSSSSSOOSS	5-8-5	79	706
665062	77439	77456	ACGGTCTGAGCATGAGGC	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	77	2461
665063	77464	77481	AGCCATGGACCTGCTCTG	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	48	2462
665064	77731	77748	GACAGTATACCCACATC	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	48	2463
621238	77781	77798	GTTATTTTGAACAGTTT	73744	73761	SOOOSSSSSSSSOOSS	5-8-5	89	708
665065	78142	78159	AAGAGTGGTAAACCTAC	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	51	2464
665066	80259	80276	GCTCACCAGCAGGAACCT	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	56	2465
665067	80284	80301	AAGGGCCCCAGTGTAGCAC	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	66	2466
621251	80309	80326	AGTCATTATCATGTCACC	76272	76289	SOOOSSSSSSSSOOSS	5-8-5	73	721
665068	80334	80351	CCAATAAGTGGCAGTGAT	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	49	2467
665069	80359	80376	ACCATGCCTGGCAGATGA	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	66	2468
665070	80799	80816	CTTAGTCATCTTCCCTCA	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	64	2469
665071	80824	80841	ATTTCTGAATTCTTTGCC	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	69	2470
621254	80849	80866	GGTAACATGTAAAGCTTC	76812	76829	SOOOSSSSSSSSOOSS	5-8-5	76	724
665072	82508	82525	CTTACACTCTGGAAGGTT	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	74	2471
665073	82533	82550	TATCCAGGGCTGAGCAGG	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	38	2472
621263	82558	82575	ATGGGCTTATCAATGCAT	78521	78538	SOOOSSSSSSSSOOSS	5-8-5	80	733
665074	82583	82600	GGAGTCAATCTGCCCTGG	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	54	2473
665075	82608	82625	CTTCCCTGTGGCACTTTG	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	29	2474
665076	89600	89617	ATGCCTCACTCAACAAGG	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	26	2475
665077	89625	89642	CTCCACTTTGGGACCAGG	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	87	2476
621302	89650	89667	GCTATGACCTAGTAGGAA	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	68	772
665078	89675	89692	GGCACAGCACCCACATGC	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	66	2477
665079	89700	89717	GGTGATAAAAGTTCACTA	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	63	2531
620887	98891	98908	GTTTTCAAACACACCTTC	n/a	n/a	SOOOSSSSSSSSOOSS	5-8-5	91	665
	98928	98945							
664526	135842	135859	AAGTCCCGAGCCAAAGCC	2805	2822	SOOOSSSSSSSSOOSS	5-8-5	55	2439
622116	135843	135860	GAAGTCCCAGCCAAAGC	2806	2823	SOOOSSSSSSSSOOSS	5-8-5	63	2045
664527	135844	135861	TGAAGTCCCAGCCAAAG	2807	2824	SOOOSSSSSSSSOOSS	5-8-5	40	2478
664528	135845	135862	TTGAAGTCCCAGCCAAA	2808	2825	SOOOSSSSSSSSOOSS	5-8-5	61	2479
622117	135846	135863	TTTGAAGTCCCAGCCAA	2809	2826	SOOOSSSSSSSSOOSS	5-8-5	55	2046
664529	135847	135864	TTTTGAAGTCCCAGCCA	2810	2827	SOOOSSSSSSSSOOSS	5-8-5	25	2480

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664530	135848	135865	ATTTTGAAGTCCCGAGCC	2811	2828	sooooooooooooo	5-8-5	38	2481
622118	135849	135866	GATTTTGAAGTCCCGAGC	2812	2829	sooooooooooooo	5-8-5	63	2047
664531	135850	135867	TGATTTTGAAGTCCCGAG	2813	2830	sooooooooooooo	5-8-5	66	2482
664532	135851	135868	CTGATTTTGAAGTCCCGA	2814	2831	sooooooooooooo	5-8-5	73	2483
622119	135852	135869	ACTGATTTTGAAGTCCCG	2815	2832	sooooooooooooo	5-8-5	66	2048
664533	135853	135870	CACTGATTTTGAAGTCCC	2816	2833	sooooooooooooo	5-8-5	72	2370
664534	135854	135871	TCCTGATTTTGAAGTCC	2817	2834	sooooooooooooo	5-8-5	61	2372
622120	135855	135872	ATCACTGATTTTGAAGTC	2818	2835	sooooooooooooo	5-8-5	47	1668
664535	135856	135873	CATCACTGATTTTGAAGT	2819	2836	sooooooooooooo	5-8-5	59	2377
664536	135857	135874	CCATCACTGATTTTGAAG	2820	2837	sooooooooooooo	5-8-5	34	2380
622121	135858	135875	CCCATCACTGATTTTGAA	2821	2838	sooooooooooooo	5-8-5	49	1669
664537	135859	135876	TCCCATCACTGATTTTGA	2822	2839	sooooooooooooo	5-8-5	61	2385
664538	135860	135877	CTCCCATCACTGATTTTG	2823	2840	sooooooooooooo	5-8-5	76	2388
622122	135861	135878	ACTCCCATCACTGATTTT	2824	2841	sooooooooooooo	5-8-5	38	1670
664539	135862	135879	TACTCCCATCACTGATTT	2825	2842	sooooooooooooo	5-8-5	57	2393
664540	135863	135880	TTACTCCCATCACTGATT	2826	2843	sooooooooooooo	5-8-5	32	2396
622123	135864	135881	CTTACTCCCATCACTGAT	2827	2844	sooooooooooooo	5-8-5	33	1671
664541	135865	135882	TCTTACTCCCATCACTGA	2828	2845	sooooooooooooo	5-8-5	50	2401
664542	135866	135883	CTCTTACTCCCATCACTG	2829	2846	sooooooooooooo	5-8-5	58	2404
622124	135867	135884	GCTCTTACTCCCATCACT	2830	2847	sooooooooooooo	5-8-5	64	1672
623993	135868	135885	TGCTCTTACTCCCATCAC	n/a	n/a	sooooooooooooo	5-8-5	65	2306
623994	135869	135886	TTGCTCTTACTCCCATCA	n/a	n/a	sooooooooooooo	5-8-5	63	2307
622125	135870	135887	TTTGCTCTTACTCCCATC	2833	2850	sooooooooooooo	5-8-5	75	1673
623995	135871	135888	ATTTGCTCTTACTCCCAT	n/a	n/a	sooooooooooooo	5-8-5	60	2308
623996	135872	135889	AATTTGCTCTTACTCCCA	n/a	n/a	sooooooooooooo	5-8-5	72	2309

Table 60

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	SEQ ID NO: 2 start site	SEQ ID NO: 2 stop site	Linkage Chemistry	Motif	% inhibition	SEQ ID NO
665043	73879	73897	TGATCTTCCATCACTTCGA	345	364	sooooooooooooo	5-9-5	67	2484
665044	98890	98908	GTTTTCAAACACACCTTCA	n/a	n/a	sooooooooooooo	5-9-5	90	2485
	98927	98945							
665081	120039	120057	TTTTCTTACCACCCTAACA	n/a	n/a	sooooooooooooo	5-9-5	28	2486
665082	120041	120059	CGTTTTCTTACCACCCTAA	n/a	n/a	sooooooooooooo	5-9-5	86	2487
665083	120045	120063	AAACCGTTTTCTTACCACC	n/a	n/a	sooooooooooooo	5-9-5	86	2488
665084	120047	120065	AAAAACCGTTTTCTTACCA	n/a	n/a	sooooooooooooo	5-9-5	65	2489
665085	120060	120078	AGTCATCAAAGCAAAAAC	n/a	n/a	sooooooooooooo	5-9-5	65	2490
665086	120110	120128	TCAAAAGACTATGTATTTT	n/a	n/a	sooooooooooooo	5-9-5	54	2491
665087	120389	120407	TGTAAATAATTGCCAAGTG	n/a	n/a	sooooooooooooo	5-9-5	61	2492
665088	120439	120457	TAAGCCACCATGCCTGTAA	n/a	n/a	sooooooooooooo	5-9-5	61	2493
665089	121711	121729	TGGACCCGCCTACTTGCTC	n/a	n/a	sooooooooooooo	5-9-5	85	2494

665090	121736	121754	TTTCGATGAGTGACATGCG	n/a	n/a	sooooooooooooo	5-9-5	50	2495
665091	121761	121779	TGCTTGCTCGCAAGGACGC	n/a	n/a	sooooooooooooo	5-9-5	80	2496
665092	121765	121783	CGCCTGCTTGCTCGCAAGG	n/a	n/a	sooooooooooooo	5-9-5	82	2497
665093	121767	121785	CCCGCTGCTTGCTCGCAA	n/a	n/a	sooooooooooooo	5-9-5	92	2498
665094	121769	121787	GACCCGCTTGCTTGCTCGC	n/a	n/a	sooooooooooooo	5-9-5	91	2499
665095	121771	121789	TGGACCCGCTTGCTTGCTC	n/a	n/a	sooooooooooooo	5-9-5	83	2500
665096	121773	121791	CCTGGACCCGCTTGCTTG	n/a	n/a	sooooooooooooo	5-9-5	88	2501
665097	121775	121793	ACCCTGGACCCGCTTGCTT	n/a	n/a	sooooooooooooo	5-9-5	60	2502
665098	121786	121804	AGTGACACGCCACCCTGGA	n/a	n/a	sooooooooooooo	5-9-5	62	2503
665099	121811	121829	CCTTTGGTAGCCAGAAAAA	n/a	n/a	sooooooooooooo	5-9-5	53	2504
665100	121817	121835	TCTGCACCTTTGGTAGCCA	n/a	n/a	sooooooooooooo	5-9-5	84	2505
665101	121938	121956	ACAGCACGGCGCATGGGAC	n/a	n/a	sooooooooooooo	5-9-5	54	2506
665102	121940	121958	CCACAGCACGGCGCATGGG	n/a	n/a	sooooooooooooo	5-9-5	84	2507
665103	121942	121960	AGCCACAGCACGGCGCATG	n/a	n/a	sooooooooooooo	5-9-5	85	2508
664714	135820	135838	TGACAAAAGCAGGTTAAGT	2783	2801	sooooooooooooo	5-9-5	54	2332
664715	135821	135839	GTGACAAAAGCAGGTTAAG	2784	2802	sooooooooooooo	5-9-5	65	2335
664716	135822	135840	AGTGACAAAAGCAGGTTAA	2785	2803	sooooooooooooo	5-9-5	79	2337
664717	135823	135841	GAGTGACAAAAGCAGGTTA	2786	2804	sooooooooooooo	5-9-5	70	2340
664718	135824	135842	CGAGTGACAAAAGCAGGTT	2787	2805	sooooooooooooo	5-9-5	89	2343
664719	135825	135843	CCGAGTGACAAAAGCAGGT	2788	2806	sooooooooooooo	5-9-5	84	2345
664720	135826	135844	GCCGAGTGACAAAAGCAGG	2789	2807	sooooooooooooo	5-9-5	71	2348
664721	135827	135845	AGCCGAGTGACAAAAGCAG	2790	2808	sooooooooooooo	5-9-5	81	2351
664722	135828	135846	AAGCCGAGTGACAAAAGCA	2791	2809	sooooooooooooo	5-9-5	68	2353
664723	135829	135847	AAAGCCGAGTGACAAAAGC	2792	2810	sooooooooooooo	5-9-5	51	2356
664724	135830	135848	CAAAGCCGAGTGACAAAAG	2793	2811	sooooooooooooo	5-9-5	47	2359
664725	135831	135849	CCAAAGCCGAGTGACAAA	2794	2812	sooooooooooooo	5-9-5	69	2361
664726	135832	135850	GCCAAAGCCGAGTGACAAA	2795	2813	sooooooooooooo	5-9-5	76	2364
664727	135833	135851	AGCCAAAGCCGAGTGACAA	2796	2814	sooooooooooooo	5-9-5	64	2367
664728	135834	135852	GAGCCAAAGCCGAGTGACA	2797	2815	sooooooooooooo	5-9-5	78	2369
664729	135835	135853	CGAGCCAAAGCCGAGTGAC	2798	2816	sooooooooooooo	5-9-5	74	2421
664730	135836	135854	CCGAGCCAAAGCCGAGTGA	2799	2817	sooooooooooooo	5-9-5	76	2424
664731	135837	135855	CCCGAGCCAAAGCCGAGTG	2800	2818	sooooooooooooo	5-9-5	75	2426
664732	135838	135856	TCCCGAGCCAAAGCCGAGT	2801	2819	sooooooooooooo	5-9-5	80	2429
664733	135839	135857	GTCCCGAGCCAAAGCCGAG	2802	2820	sooooooooooooo	5-9-5	70	2432
664734	135840	135858	AGTCCCGAGCCAAAGCCGA	2803	2821	sooooooooooooo	5-9-5	59	2434
664735	135841	135859	AAGTCCCGAGCCAAAGCCG	2804	2822	sooooooooooooo	5-9-5	58	2437
664736	135842	135860	GAAGTCCCGAGCCAAAGCC	2805	2823	sooooooooooooo	5-9-5	76	2440
664737	135843	135861	TGAAGTCCCGAGCCAAAGC	2806	2824	sooooooooooooo	5-9-5	46	2442
664738	135844	135862	TTGAAGTCCCGAGCCAAAG	2807	2825	sooooooooooooo	5-9-5	46	2550
664739	135845	135863	TTTGAAGTCCCGAGCCAAA	2808	2826	sooooooooooooo	5-9-5	56	2551
664740	135846	135864	TTTTGAAGTCCCGAGCCAA	2809	2827	sooooooooooooo	5-9-5	44	2552
664741	135847	135865	ATTTTGAAGTCCCGAGCCA	2810	2828	sooooooooooooo	5-9-5	61	2553
664742	135848	135866	GATTTTGAAGTCCCGAGCC	2811	2829	sooooooooooooo	5-9-5	59	2554

664743	135849	135867	TGATTTTGAAGTCCCGAGC	2812	2830	sooooooooooooo	5-9-5	64	2555
664744	135850	135868	CTGATTTTGAAGTCCCGAG	2813	2831	sooooooooooooo	5-9-5	67	2556
664745	135851	135869	ACTGATTTTGAAGTCCCGA	2814	2832	sooooooooooooo	5-9-5	73	2557
664746	135852	135870	CACTGATTTTGAAGTCCCG	2815	2833	sooooooooooooo	5-9-5	86	2558
664747	135853	135871	TCACTGATTTTGAAGTCCC	2816	2834	sooooooooooooo	5-9-5	76	2371
664748	135854	135872	ATCACTGATTTTGAAGTCC	2817	2835	sooooooooooooo	5-9-5	74	2373
664749	135855	135873	CATCACTGATTTTGAAGTC	2818	2836	sooooooooooooo	5-9-5	50	2375
664750	135856	135874	CCATCACTGATTTTGAAGT	2819	2837	sooooooooooooo	5-9-5	57	2378
664751	135857	135875	CCCATCACTGATTTTGAAG	2820	2838	sooooooooooooo	5-9-5	64	2381
664752	135858	135876	TCCCATCACTGATTTGAA	2821	2839	sooooooooooooo	5-9-5	59	2383
664753	135859	135877	CTCCCATCACTGATTTGA	2822	2840	sooooooooooooo	5-9-5	73	2386
664754	135860	135878	ACTCCCATCACTGATTTG	2823	2841	sooooooooooooo	5-9-5	75	2389
664755	135861	135879	TACTCCCATCACTGATTT	2824	2842	sooooooooooooo	5-9-5	40	2391
664756	135862	135880	TTACTCCCATCACTGATT	2825	2843	sooooooooooooo	5-9-5	43	2394
664757	135863	135881	CTTACTCCCATCACTGAT	2826	2844	sooooooooooooo	5-9-5	70	2397
664758	135864	135882	TCTTACTCCCATCACTGA	2827	2845	sooooooooooooo	5-9-5	61	2399
664759	135865	135883	CTCTTACTCCCATCACTGA	2828	2846	sooooooooooooo	5-9-5	68	2402
664760	135866	135884	GCTCTTACTCCCATCACTG	2829	2847	sooooooooooooo	5-9-5	82	2405
664761	135867	135885	TGCTCTTACTCCCATCACT	2830	2848	sooooooooooooo	5-9-5	76	2407
664762	135868	135886	TTGCTCTTACTCCCATCAC	2831	2849	sooooooooooooo	5-9-5	77	2409
664763	135869	135887	TTTGCTCTTACTCCCATCA	2832	2850	sooooooooooooo	5-9-5	83	2411
664764	135870	135888	ATTTGCTCTTACTCCCATC	2833	2851	sooooooooooooo	5-9-5	82	2413
664765	135871	135889	AATTTGCTCTTACTCCCAT	2834	2852	sooooooooooooo	5-9-5	77	2415
664766	135872	135890	AAATTTGCTCTTACTCCCA	2835	2853	sooooooooooooo	5-9-5	69	2417

Table 61

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	SEQ ID NO: 2 start site	SEQ ID NO: 2 stop site	Linkage Chemistry	Motif	% inhibition	SEQ ID NO
665041	73879	73898	GTGATCTTCCATCACTTCGA	345	364	sooooooooooooo	5-10-5	86	25
665044	98890	98908	GTTTTCAAACACACCTTCA	n/a	n/a	sooooooooooooo	5-9-5	90	2485
	98927	98945							
665201	102119	102138	GGTTTGTTTTTTAAACAATT	n/a	n/a	sooooooooooooo	5-10-5	57	2509
665202	102144	102163	GAACCCAATGAGAGTAGCAA	n/a	n/a	sooooooooooooo	5-10-5	86	2510
665203	102169	102188	TTGCCAAAATCAGGAATGGG	n/a	n/a	sooooooooooooo	5-10-5	87	2511
665204	102194	102213	TCAGGGCAATCTGGAAGCAT	n/a	n/a	sooooooooooooo	5-10-5	79	2512
665205	102659	102678	ACTCTCCACTCCATGTCAAT	n/a	n/a	sooooooooooooo	5-10-5	26	2513
665206	102684	102703	CAGAGCTCACAGCAATGATC	n/a	n/a	sooooooooooooo	5-10-5	78	2514
665207	102709	102728	TCAGCATGAGTTGTGCCAAG	n/a	n/a	sooooooooooooo	5-10-5	91	2515
665208	102734	102753	CCAGAGGAACTGTGTGCATT	n/a	n/a	sooooooooooooo	5-10-5	79	2516
665209	102759	102778	CCAAGTTCCTGAGGACATT	n/a	n/a	sooooooooooooo	5-10-5	13	2517
665210	112934	112953	GTTGTGTTTTCTGGTTTATT	n/a	n/a	sooooooooooooo	5-10-5	96	2518

665211	112959	112978	TTTTTTTTTAAGTTAGGAGT	n/a	n/a	sooooooooooooo	5-10-5	20	2519
665212	112984	113003	TTTACTGGTTGTGTTTTCT	n/a	n/a	sooooooooooooo	5-10-5	90	2520
665213	113009	113028	CAGCTCTTAATGCTGTTATA	n/a	n/a	sooooooooooooo	5-10-5	90	2521
665214	113498	113517	TTCAGCTCCTGCACCCAGCA	n/a	n/a	sooooooooooooo	5-10-5	54	2522
665215	113548	113567	TTTTGCTTTTGCTCTGAAGA	n/a	n/a	sooooooooooooo	5-10-5	57	2523
665216	115105	115124	TTGCTATTAAATATAATGTA	n/a	n/a	sooooooooooooo	5-10-5	35	2524
665217	115130	115149	GCTTTTTAAAGTGACAACTG	n/a	n/a	sooooooooooooo	5-10-5	78	2525
665218	115155	115174	TTCCACATAAATGTTCTACA	n/a	n/a	sooooooooooooo	5-10-5	93	2526
665219	115205	115224	CCCTGATTGAGGAGAGGCAA	n/a	n/a	sooooooooooooo	5-10-5	77	2527
665220	116595	116614	ATGTTTTTTTCTGGCCGGGC	n/a	n/a	sooooooooooooo	5-10-5	85	2528
665221	116620	116639	TTCAGTATCTGCCACATACT	n/a	n/a	sooooooooooooo	5-10-5	64	2529
665222	116645	116664	TGAATCAAAGGACATTAAGC	n/a	n/a	sooooooooooooo	5-10-5	69	2530
664661	135820	135839	GTGACAAAAGCAGGTTAAGT	2783	2802	sooooooooooooo	5-10-5	78	2333
664662	135821	135840	AGTGACAAAAGCAGGTTAAG	2784	2803	sooooooooooooo	5-10-5	18	2336
664663	135822	135841	GAGTGACAAAAGCAGGTTAA	2785	2804	sooooooooooooo	5-10-5	79	2338
664664	135823	135842	CGAGTGACAAAAGCAGGTTA	2786	2805	sooooooooooooo	5-10-5	66	2341
664665	135824	135843	CCGAGTGACAAAAGCAGGTT	2787	2806	sooooooooooooo	5-10-5	94	2344
664666	135825	135844	GCCGAGTGACAAAAGCAGGT	2788	2807	sooooooooooooo	5-10-5	89	2346
664667	135826	135845	AGCCGAGTGACAAAAGCAGG	2789	2808	sooooooooooooo	5-10-5	29	2349
664668	135827	135846	AAGCCGAGTGACAAAAGCAG	2790	2809	sooooooooooooo	5-10-5	72	2352
664669	135828	135847	AAAGCCGAGTGACAAAAGCA	2791	2810	sooooooooooooo	5-10-5	53	2354
664670	135829	135848	CAAAGCCGAGTGACAAAAGC	2792	2811	sooooooooooooo	5-10-5	55	2357
664671	135830	135849	CCAAAGCCGAGTGACAAAAG	2793	2812	sooooooooooooo	5-10-5	58	2360
664672	135831	135850	GCCAAAGCCGAGTGACAAA	2794	2813	sooooooooooooo	5-10-5	80	2362
664673	135832	135851	AGCCAAAGCCGAGTGACAAA	2795	2814	sooooooooooooo	5-10-5	52	2365
664674	135833	135852	GAGCCAAAGCCGAGTGACAA	2796	2815	sooooooooooooo	5-10-5	71	2368
664675	135834	135853	CGAGCCAAAGCCGAGTGACA	2797	2816	sooooooooooooo	5-10-5	76	2419
664676	135835	135854	CCGAGCCAAAGCCGAGTGAC	2798	2817	sooooooooooooo	5-10-5	78	2422
664677	135836	135855	CCCGAGCCAAAGCCGAGTGA	2799	2818	sooooooooooooo	5-10-5	77	2425
664678	135837	135856	TCCCGAGCCAAAGCCGAGTG	2800	2819	sooooooooooooo	5-10-5	73	2427
664679	135838	135857	GTCCCGAGCCAAAGCCGAGT	2801	2820	sooooooooooooo	5-10-5	73	2430
664680	135839	135858	AGTCCCGAGCCAAAGCCGAG	2802	2821	sooooooooooooo	5-10-5	20	2433
664681	135840	135859	AAGTCCCGAGCCAAAGCCGA	2803	2822	sooooooooooooo	5-10-5	64	2435
664682	135841	135860	GAAGTCCCGAGCCAAAGCCG	2804	2823	sooooooooooooo	5-10-5	60	2438
664683	135842	135861	TGAAGTCCCGAGCCAAAGCC	2805	2824	sooooooooooooo	5-10-5	64	2441
664684	135843	135862	TTGAAGTCCCGAGCCAAAGC	2806	2825	sooooooooooooo	5-10-5	52	2443
664685	135844	135863	TTTGAAGTCCCGAGCCAAAG	2807	2826	sooooooooooooo	5-10-5	45	2559
664686	135845	135864	TTTTGAAGTCCCGAGCCAAA	2808	2827	sooooooooooooo	5-10-5	56	2560
664687	135846	135865	ATTTTGAAGTCCCGAGCCAA	2809	2828	sooooooooooooo	5-10-5	67	2561
664688	135847	135866	GATTTTGAAGTCCCGAGCCA	2810	2829	sooooooooooooo	5-10-5	73	2562
664689	135848	135867	TGATTTTGAAGTCCCGAGCC	1644	1663	sooooooooooooo	5-10-5	67	56
664690	135849	135868	CTGATTTTGAAGTCCCGAGC	2812	2831	sooooooooooooo	5-10-5	73	464
664691	135850	135869	ACTGATTTTGAAGTCCCGAG	2813	2832	sooooooooooooo	5-10-5	85	2563

664692	135851	135870	CACTGATTTTGAAGTCCCGA	2814	2833	sooooooooooooo	5-10-5	89	2564
664693	135852	135871	TCACTGATTTTGAAGTCCCG	2815	2834	sooooooooooooo	5-10-5	75	2565
424880	135853	135872	ATCACTGATTTTGAAGTCCC	2816	2835	sooooooooooooo	5-10-5	62	57
664694	135853	135872	ATCACTGATTTTGAAGTCCC	1649	1668	sooooooooooooo	5-10-5	85	57
664695	135854	135873	CATCACTGATTTTGAAGTCC	2817	2836	sooooooooooooo	5-10-5	83	2374
664696	135855	135874	CCATCACTGATTTTGAAGTC	2818	2837	sooooooooooooo	5-10-5	66	2376
664697	135856	135875	CCCATCACTGATTTTGAAGT	2819	2838	sooooooooooooo	5-10-5	58	2379
664698	135857	135876	TCCCATCACTGATTTTGAAG	2820	2839	sooooooooooooo	5-10-5	71	2382
664699	135858	135877	CTCCCATCACTGATTTTGAA	2821	2840	sooooooooooooo	5-10-5	32	2384
664700	135859	135878	ACTCCCATCACTGATTTTGA	2822	2841	sooooooooooooo	5-10-5	71	2387
664701	135860	135879	TACTCCCATCACTGATTTTG	2823	2842	sooooooooooooo	5-10-5	75	2390
664702	135861	135880	TTACTCCCATCACTGATTTT	2824	2843	sooooooooooooo	5-10-5	46	2392
664703	135862	135881	CTTACTCCCATCACTGATTT	2825	2844	sooooooooooooo	5-10-5	22	2395
664704	135863	135882	TCTTACTCCCATCACTGATT	2826	2845	sooooooooooooo	5-10-5	72	2398
664705	135864	135883	CTCTTACTCCCATCACTGAT	2827	2846	sooooooooooooo	5-10-5	70	2400
664706	135865	135884	GCTCTTACTCCCATCACTGA	2828	2847	sooooooooooooo	5-10-5	77	2403
664707	135866	135885	TGCTCTTACTCCCATCACTG	2829	2848	sooooooooooooo	5-10-5	88	2406
664708	135867	135886	TTGCTCTTACTCCCATCACT	2830	2849	sooooooooooooo	5-10-5	86	2408
664709	135868	135887	TTTGCTCTTACTCCCATCAC	2831	2850	sooooooooooooo	5-10-5	16	2410
664710	135869	135888	ATTTGCTCTTACTCCCATCA	2832	2851	sooooooooooooo	5-10-5	80	2412
664711	135870	135889	AATTTGCTCTTACTCCCATC	2833	2852	sooooooooooooo	5-10-5	65	2414
664712	135871	135890	AAATTTGCTCTTACTCCCAT	2834	2853	sooooooooooooo	5-10-5	60	2416
664713	135872	135891	GAAATTTGCTCTTACTCCCA	2835	2854	sooooooooooooo	5-10-5	85	2418

Example 17: Dose-dependent antisense inhibition of human Tau in SH-SY5Y cells

- Gapmers from studies described above exhibiting significant *in vitro* inhibition of tau mRNA
- 5 were selected and tested at various doses in SH-SY5Y cells. 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. Cells were plated at a density of 20,000 cells per well and transfected using electroporation with 0.247 μ M, 0.741 μ M, 2.22 μ M, 6.67 μ M, and 20.00 μ M concentrations of antisense oligonucleotide, as specified in the Tables below. After a treatment
- 10 period of approximately 16 hours, RNA was isolated from the cells and tau mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3104 was used to measure mRNA levels. Tau mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN[®]. Results are presented as percent inhibition of tau, relative to untreated control cells. Tau mRNA levels were significantly reduced in a dose-dependent manner in antisense
- 15 oligonucleotide treated cells.

Table 62

ISIS No	0.247 μM	0.741 μM	2.22 μM	6.67 μM	20.00 μM	IC ₅₀ (μM)
620887	18	39	71	88	95	1.2
664662	5	16	34	59	68	6.4
664665	16	41	69	89	96	1.2
664667	5	20	39	78	90	2.9
664680	7	11	21	56	81	5.9
664699	0	1	28	59	85	5.7
664709	8	16	48	66	89	3.1
665044	15	33	59	84	94	1.6
665205	0	7	35	51	86	5.3
665207	22	36	57	82	93	1.4
665210	15	47	74	94	97	1.0
665212	6	22	56	82	95	2.1
665213	0	18	57	78	93	2.5
665217	10	28	63	86	95	1.7
665218	10	31	64	85	93	1.7

Table 63

ISIS No	0.247 μM	0.741 μM	2.22 μM	6.67 μM	20.00 μM	IC ₅₀ (μM)
664718	26	34	60	88	86	1.3
664745	34	39	67	87	95	0.9
664746	15	37	60	87	92	1.5
664760	32	50	75	89	97	0.7
665044	21	44	75	92	97	0.9
665082	5	27	67	87	96	1.7
665083	17	34	67	85	97	1.4
665089	9	26	53	84	94	2.0
665093	11	57	81	93	95	0.9
665094	25	53	76	91	93	0.7
665095	20	33	63	89	95	1.4
665096	5	37	57	86	95	1.8
665102	8	36	61	90	96	1.6
665103	6	24	59	83	92	2.1

5

Table 64

ISIS No	0.247 μM	0.741 μM	2.22 μM	6.67 μM	20.00 μM	IC ₅₀ (μM)
620887	26	45	72	89	96	1.2
621013	26	49	82	93	97	0.7
621031	25	41	66	84	92	1.1

621041	26	55	70	89	92	0.7
621238	23	41	59	85	95	1.2
621251	33	56	74	88	92	0.5
664514	11	36	68	79	91	1.6
664516	16	36	64	82	94	1.5
664534	18	35	48	76	91	1.9
664775	24	30	59	79	92	1.6
664788	11	21	26	55	73	6.2
664799	26	37	63	79	90	1.3
664800	15	0	61	75	90	2.7
665047	43	65	82	95	98	0.2
665077	19	44	63	85	96	1.2

Example 18: Intracerebroventricular administration of antisense oligonucleotides against human tau mRNA in htau mice

- 5 Selected compounds were tested for efficacy by ICV administration in human tau transgenic mice (Duff et al., Neurobiology of Disease 7:87-98, 2000).

Treatment and surgery

- 10 Groups of 4 mice each were administered ISIS 613099, ISIS 613361, ISIS 613370, ISIS 623782, or ISIS 623996 with a 200 µg dose delivered by ICV bolus injection. A control group of 2 mice was similarly treated with ISIS 424880 and a control group of 4 mice was similarly treated with PBS. All procedures were performed under isoflurane anesthesia and in accordance with IACUC regulations. For mouse ICV bolus injections, the antisense oligonucleotide was injected into the right lateral ventricle of human tau transgenic mice. Ten microliters of solution containing 200 µg of oligonucleotide in PBS was injected over
- 15 approximately 10 seconds. Tissue was collected 14 days after oligonucleotide administration.

RNA Analysis

- 20 On day 14 after the oligonucleotide administration, RNA was extracted from the hippocampus, spinal cord and cortex for real-time PCR analysis of tau mRNA levels. Human tau mRNA levels were measured using the human primer probe set RTS3104. Results were calculated as percent inhibition of human tau mRNA expression compared to the control. All the antisense oligonucleotides effect significant inhibition of human tau mRNA levels in several tissues.

Table 65**Percent reduction of human tau mRNA levels in hTau mice**

ISIS No	Cortex	Hippocampus	Spinal Cord
613099	41.8	55.2	54.1
613361	69.4	57.3	72.5
613370	42.2	61.0	63.0
623782	62.2	79.1	70.8
623996	74.1	69.2	76.4
424880	50.3	53.1	55.2

5

Example 19: Design of oligonucleotides targeting human Tau

ISIS No. 603054 was designed to target human Tau. The nucleobase sequence and linkage chemistry of of ISIS No. 603054 is given in table 66 below. ISIS No. 603054 is a 5-10-5 MOE gapmer. ISIS No. 603054 is 20 nucleosides in length, wherein the central gap segment comprises 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'-MOE modification. All cytosine residues throughout each gapmer are 5-methylcytosines. "Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. "Stop site" indicates the 3'-most nucleoside to which the gapmer is targeted human gene sequence. Each gapmer listed in Table 1 below is targeted to either the human tau genomic sequence, designated herein as SEQ ID NO: 1 (GENBANK Accession No. NT_010783.15 truncated from nucleotides 9240000 to 9381000) or to the human tau mRNA sequence, designated herein as SEQ ID NO: 2 (GENBANK Accession No. NM_001123066.3).

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Table 66**ICV *in vivo* study in hTau mice and WT C57Bl6 mice**

ISIS NO	SEQ ID NO: 1 start site	SEQ ID NO: 1 stop site	Sequence	SEQ ID NO: 2 start site	SEQ ID NO: 2 stop site	Linkage Chemistry	SEQ ID NO.
603054	135853	135872	ATCACTGATTTTGAAGTCCC	2816	2835	SOOOSSSSSSSSSSOOS	57

Example 20: *In vivo* analysis in mice of oligonucleotides targeting human Tau

Oligonucleotides, shown in the table below, were designed to target Tau. Mice, either human tau transgenic mice “hTau” (Duff et al., *Neurobiology of Disease* 7:87-98, 2000; Davies et al. *J. Neurochem.* (2003) 86, 582–590) or wild-type WT C57Bl6 mice were separated into groups of 3 or 4 mice. Each mouse in each group of mice was administered a single ICV dose of either 300ug or 200ug each of the oligonucleotides in the table below. At 3 hours post injection, each mouse was evaluated according to 7 different criteria. The 7 criteria are (1) the mouse was bright, alert, and responsive; (2) the mouse was standing or hunched without stimuli; (3) the mouse shows any movement without stimuli (4) the mouse demonstrates forward movement after its lifted; (5) the mouse demonstrates any movement after its lifted; (6) the mouse responds to a tail pinch; (7) regular breathing. For each of the 7 different criteria, each mouse was given a sub-score of 0 if it met the criteria or 1 if it did not. After all of the 7 criteria were evaluated, the sub-scores were summed for each mouse and then averaged for each group. For example, if a mouse was bright, alert, and responsive 3 hours after the 300 µg ICV dose, and met all other other criteria, it would get a summed score of 0. If another mouse was not bright, alert, and responsive 3 hours after the 300 µg ICV dose but met all other criteria, it would receive a score of 1. Saline treated mice generally receive a score of 0. Results are presented as the average score for each treatment group in Table 67 below. “ND” means no data. These results demonstrate that ISIS 613099, ISIS 613361, ISIS 613370, ISIS 623782, ISIS 623996, ISIS 424880, and ISIS 603054 were well tolerated.

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Table 67
ICV *in vivo* study in hTau mice and WT C57Bl6 mice

Line:	hTau		WT C57Bl6
Dose:	300ug	200ug	300ug
613099	0	ND	ND
613361	0	ND	ND
613370	0	ND	ND
623782	0	ND	ND
623996	0	ND	ND
424880	ND	3	ND
603054	ND	ND	0.25

Example 20: *In vivo* analysis in rats of oligonucleotides targeting human Tau

Sprague Dawley rats were separated into groups of 4 rats each. Each rat in each group of rats was administered a single 1 mg intrathecal (IT) dose or a single 3 mg intrathecal (IT) dose of ISIS 613099, ISIS 613361, ISIS 613370, ISIS 623782, ISIS 623996, ISIS 424880, or ISIS 603054. At 3 hours after injection, the movement of 7 different parts of the body was evaluated for each rat. The 7 body parts are (1) the rat's tail; (2) the rat's posterior posture; (3) the rat's hind limbs; (4) the rat's hind paws; (5) the rat's forepaws; (6) the rat's anterior posture; and (7) the rat's head. For each of the 7 different body parts, each rat was given a sub-score of 0 if the body part was moving or 1 if the body part was paralyzed. After each of the 7 body parts were evaluated, the sub-scores were summed for each rat and then averaged for each group. For example, if a rat's tail, head, and all other evaluated body parts were moving 3 hours after the 3 mg IT dose, it would get a summed score of 0. If another rat was not moving its tail 3 hours after the 3 mg IT dose but all other evaluated body parts were moving, it would receive a score of 1. Saline treated rats generally receive a score of 0. A score of at the top end of the range would be suggestive of toxicity. Results are presented as the average score for each treatment group in Table 68 below.

Table 68**1 mg and 3 mg IT bolus *in vivo* study**

ISIS No.	Score 3 hours after injection	
	Dose	
	1mg	3mg
613099	0.25	3
613361	0	0.33
613370	0	0
623782	0.25	0.75
623996	0	2
424880	2.3	6
603054	1.25	2.75

CLAIMS:

1. A modified oligonucleotide, or a pharmaceutically acceptable salt thereof, consisting of 12 to 30 linked nucleosides, wherein the modified oligonucleotide has a nucleobase sequence comprising at least 8 consecutive nucleobases of the nucleobase sequence of SEQ ID NO: 1634, wherein the nucleobase sequence of the modified oligonucleotide is at least 90% complementary to SEQ ID NO: 1 and wherein the modified oligonucleotide is capable of reducing Tau expression.
2. The modified oligonucleotide or pharmaceutically acceptable salt thereof of claim 1, wherein the modified oligonucleotide:
 - (i) consists of 20 linked nucleosides;
 - (ii) consists of 19 linked nucleosides; or
 - (iii) consists of 18 linked nucleosides.
3. The modified oligonucleotide or pharmaceutically acceptable salt thereof of claim 1, wherein the nucleobase sequence of the modified oligonucleotide comprises the nucleobase sequence of SEQ ID NO: 1634.
4. The modified oligonucleotide or pharmaceutically acceptable salt thereof of claim 1, wherein the nucleobase sequence of the modified oligonucleotide consists of the nucleobase sequence of SEQ ID NO: 1634.
5. The modified oligonucleotide or pharmaceutically acceptable salt thereof of claim 1, wherein the nucleobase sequence of the modified oligonucleotide is at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% complementary to SEQ ID NO: 1.
6. The modified oligonucleotide or pharmaceutically acceptable salt thereof of any one of claims 1 to 5, which is a gapmer.
7. The modified oligonucleotide or pharmaceutically acceptable salt thereof of any one of claims 1 to 6, which is a single-stranded modified oligonucleotide.
8. The modified oligonucleotide or pharmaceutically acceptable salt thereof of any one of claims 1 to 7, wherein at least one internucleoside linkage of the modified oligonucleotide is a modified internucleoside linkage.
9. The modified oligonucleotide or pharmaceutically acceptable salt thereof of claim 8, wherein (a) at least one modified internucleoside linkage of the modified

oligonucleotide is a phosphorothioate internucleoside linkage; and/or (b) at least one internucleoside linkage of the modified oligonucleotide is a phosphodiester internucleoside linkage.

10. The modified oligonucleotide or pharmaceutically acceptable salt thereof of any one of claims 1 to 9, wherein at least one nucleoside of the modified oligonucleotide comprises a modified nucleobase.

11. The modified oligonucleotide or pharmaceutically acceptable salt thereof of claim 10, wherein the modified nucleobase is a 5-methylcytosine.

12. The modified oligonucleotide or pharmaceutically acceptable salt thereof of any one of claims 1 to 11, wherein at least one nucleoside of the modified oligonucleotide comprises a modified sugar.

13. The modified oligonucleotide or pharmaceutically acceptable salt thereof of claim 12, wherein (a) the at least one modified sugar is a bicyclic sugar; or (b) the at least one modified sugar comprises a 2'-O-methoxyethyl group or a 2'-O-methyl group.

14. The modified oligonucleotide or pharmaceutically acceptable salt thereof of claim 13, wherein the bicyclic sugar comprises:

(a) a 4'-CH₂-N(R)-O-2' chemical bridge wherein R is independently selected from H and C₁-C₆ alkyl; or

(b) a 4'-CH(R)-O-2' chemical bridge wherein R is methyl, H or -CH₂-O-CH₃.

15. The modified oligonucleotide or pharmaceutically acceptable salt thereof of any one of claims 1 to 14, wherein at least one nucleoside of the modified oligonucleotide comprises a sugar surrogate.

16. The modified oligonucleotide or pharmaceutically acceptable salt thereof of claim 15, wherein the at least one sugar surrogate is a morpholino or a peptide nucleic acid.

17. The modified oligonucleotide or pharmaceutically acceptable salt thereof of any one of claims 1 to 16, which comprises:

a) 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;

b) a gap segment consisting of 9 linked deoxynucleosides;

a 5' wing segment consisting of 5 linked nucleosides; and

a 3' wing segment consisting of 5 linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar;

c) a gap segment consisting of 7 linked deoxynucleosides;

a 5' wing segment consisting of 5 linked nucleosides; and

a 3' wing segment consisting of 6 linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar;

d) a gap segment consisting of 8 linked deoxynucleosides;

a 5' wing segment consisting of 5 linked nucleosides; and

a 3' wing segment consisting of 5 linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar;

e) a gap segment consisting of 8 linked deoxynucleosides;

a 5' wing segment consisting of 4 linked nucleosides; and

a 3' wing segment consisting of 6 linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar; or

f) a gap segment consisting of 8 linked deoxynucleosides;

a 5' wing segment consisting of 6 linked nucleosides; and

a 3' wing segment consisting of 4 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.

18. The pharmaceutically acceptable salt of the modified oligonucleotide of any one of claims 1 to 17, which is a sodium salt.

19. A single-stranded modified oligonucleotide, or a pharmaceutically acceptable salt thereof, consisting of 18 linked nucleosides and having a nucleobase sequence comprising 18 consecutive nucleobases of the nucleobase sequence of SEQ ID NO: 1634, and wherein the modified oligonucleotide comprises:

a gap segment consisting of 8 linked deoxynucleosides;

a 5' wing segment consisting of 5 linked nucleosides; and

a 3' wing segment consisting of 5 linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, wherein each nucleoside of each wing segment comprises a 2'-O-methoxyethyl sugar, wherein at least one internucleoside linkage is a phosphorothioate internucleoside linkage, at least one internucleoside linkage is a phosphodiester internucleoside linkage, and each cytosine is a 5-methylcytosine.

20. The pharmaceutically acceptable salt of the single-stranded modified oligonucleotide of claim 19, which is a sodium salt.

21. A conjugated antisense compound comprising the modified oligonucleotide or pharmaceutically acceptable salt thereof of any one of claims 1 to 18, or the single-stranded modified oligonucleotide or pharmaceutically acceptable salt thereof of claims 19 or 20.

22. A composition comprising the modified oligonucleotide or pharmaceutically acceptable salt thereof of any one of claims 1 to 18, or the single-stranded modified oligonucleotide or pharmaceutically acceptable salt thereof of claims 19 or 20, or the conjugated antisense compound of claim 21, and at least one of a pharmaceutically acceptable carrier or diluent.

23. The composition of claim 22, wherein the pharmaceutically acceptable diluent is phosphate-buffered saline (PBS).

24. The modified oligonucleotide or pharmaceutically acceptable salt thereof of any one of claims 1 to 18, or the single-stranded modified oligonucleotide or pharmaceutically acceptable salt thereof of claims 19 or 20, or the conjugated antisense compound of claim 21, or the composition of claim 22 or 23, for use in therapy.

25. The modified oligonucleotide or pharmaceutically acceptable salt thereof of any one of claims 1 to 18, or the single-stranded modified oligonucleotide or pharmaceutically acceptable salt thereof of claim 19 or 20, or the conjugated antisense compound of claim 21, or the composition of claim 22 or 23, for use in the treatment of a neurodegenerative disease, disorder or condition.

26. The modified oligonucleotide or pharmaceutically acceptable salt thereof, the single-stranded modified oligonucleotide or pharmaceutically acceptable salt thereof, the conjugated antisense compound, or the composition for use of claim 25, wherein the neurodegenerative disease, disorder or condition is a tauopathy.

27. The modified oligonucleotide or pharmaceutically acceptable salt thereof, the single-stranded modified oligonucleotide or pharmaceutically acceptable salt thereof, the conjugated antisense compound, or the composition for use of claim 25, wherein the neurodegenerative disease, disorder or condition is Alzheimer's disease, Frontotemporal Dementia, FTDP-17, Progressive Supranuclear Palsy, Chronic Traumatic Encephalopathy, Corticobasal Ganglionic Degeneration, Epilepsy, or Dravet's Syndrome.

28. The modified oligonucleotide or pharmaceutically acceptable salt thereof, the single-stranded modified oligonucleotide or pharmaceutically acceptable salt thereof, the conjugated antisense compound, or the composition for use of claim 25, wherein the neurodegenerative disease, disorder or condition is Alzheimer's disease.

29. The modified oligonucleotide or pharmaceutically acceptable salt thereof, the single-stranded modified oligonucleotide or pharmaceutically acceptable salt thereof, the conjugated antisense compound, or the composition for use of claim 25, wherein the neurodegenerative disease, disorder or condition is Frontotemporal Dementia.

30. The modified oligonucleotide or pharmaceutically acceptable salt thereof, the single-stranded modified oligonucleotide or pharmaceutically acceptable salt thereof, the conjugated antisense compound, or the composition for use of claim 25, wherein the neurodegenerative disease, disorder or condition is Progressive Supranuclear Palsy.

31. The modified oligonucleotide or pharmaceutically acceptable salt thereof, the single-stranded modified oligonucleotide or pharmaceutically acceptable salt thereof, the conjugated antisense compound, or the composition for use of any one of claims 24 to 30, wherein the modified oligonucleotide or pharmaceutically acceptable salt thereof, the single-stranded modified oligonucleotide or pharmaceutically acceptable salt thereof, the conjugated antisense compound, or the composition is formulated for intrathecal administration.