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RNA interference mediated treatment of alzheimer's disease using short interfering nucleic acid (siNA)
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(54) Title: RNA INTERFERENCE MEDIATED TREATMENT OF ALZHEIMER'S DISEASE USING SHORT INTERFERING NUCLEIC ACID (siNA)

(57) Abstract: The present invention concerns methods and reagents useful in modulating BACE gene expression in a variety of applications, including use in therapeutic, diagnostic, target validation, and genomic discovery applications. Specifically, the invention relates to small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules capable of mediating RNA interference (RNAi) against beta-secretase (BACE), amyloid precursor protein (APP), pin-1, presenilin 1 (PS-1) and/or presenilin 2 (PS-2) gene expression and/or activity. The small nucleic acid molecules are useful in the treatment of Alzheimer's disease and any other condition that responds to modulation of BACE, APP, pin-1, PS-1 and/or PS-2 expression or activity.

**RNA INTERFERENCE MEDIATED TREATMENT OF ALZHEIMER'S
DISEASE USING SHORT INTERFERING NUCLEIC ACID (siNA)**

Field Of The Invention

5 The present invention concerns methods and reagents useful in modulating gene expression associated with Alzheimer's disease in a variety of applications, including use in therapeutic, diagnostic, target validation, and genomic discovery applications. The present invention concerns compounds, compositions, and methods for the study, diagnosis, and treatment of conditions and diseases that respond to the modulation of
10 beta-secretase (BACE), amyloid precursor protein (APP), pin-1, presenillin 1 (PS-1) and/or presenillin 2 (PS-2) gene expression and/or activity. The present invention also concerns compounds, compositions, and methods relating to conditions and diseases that respond to the modulation of expression and/or activity of genes involved in beta-secretase (BACE), amyloid precursor protein (APP), pin-1, presenillin 1 (PS-1) and/or
15 presenillin 2 (PS-2) pathways. Specifically, the invention relates to small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules capable of mediating RNA interference (RNAi) against beta-secretase (BACE), amyloid precursor protein (APP), pin-1, presenillin 1 (PS-1) and/or presenillin 2
20 (PS-2) gene expression.

Background Of The Invention

The following is a discussion of relevant art pertaining to RNAi. The discussion is provided only for understanding of the invention that follows. The summary is not an
25 admission that any of the work described below is prior art to the claimed invention.

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RNA interference refers to the process of sequence-specific post-transcriptional gene silencing in animals mediated by short interfering RNAs (siRNAs) (Fire *et al.*, 1998, *Nature*, 391, 806). The corresponding process in plants is commonly referred to as post-transcriptional gene silencing or RNA silencing and is also referred to as quelling in
5 fungi. The process of post-transcriptional gene silencing is thought to be an evolutionarily-conserved cellular defense mechanism used to prevent the expression of foreign genes and is commonly shared by diverse flora and phyla (Fire *et al.*, 1999, *Trends Genet.*, 15, 358). Such protection from foreign gene expression may have evolved in response to the production of double-stranded RNAs (dsRNAs) derived from
10 viral infection or from the random integration of transposon elements into a host genome via a cellular response that specifically destroys homologous single-stranded RNA or viral genomic RNA. The presence of dsRNA in cells triggers the RNAi response through a mechanism that has yet to be fully characterized. This mechanism appears to be different from the interferon response that results from dsRNA-mediated activation of
15 protein kinase PKR and 2',5'-oligoadenylate synthetase resulting in non-specific cleavage of mRNA by ribonuclease L.

The presence of long dsRNAs in cells stimulates the activity of a ribonuclease III enzyme referred to as dicer. Dicer is involved in the processing of the dsRNA into short pieces of dsRNA known as short interfering RNAs (siRNAs) (Bernstein *et al.*, 2001,
20 *Nature*, 409, 363). Short interfering RNAs derived from dicer activity are typically about 21 to about 23 nucleotides in length and comprise about 19 base pair duplexes (Elbashir *et al.*, 2001, *Genes Dev.*, 15, 188). Dicer has also been implicated in the excision of 21- and 22-nucleotide small temporal RNAs (stRNAs) from precursor RNA of conserved structure that are implicated in translational control (Hutvagner *et al.*, 2001,
25 *Science*, 293, 834). The RNAi response also features an endonuclease complex, commonly referred to as an RNA-induced silencing complex (RISC), which mediates cleavage of single-stranded RNA having sequence complementary to the antisense strand of the siRNA duplex. Cleavage of the target RNA takes place in the middle of the region complementary to the antisense strand of the siRNA duplex (Elbashir *et al.*, 2001, *Genes*
30 *Dev.*, 15, 188).

RNAi has been studied in a variety of systems. Fire *et al.*, 1998, *Nature*, 391, 806, were the first to observe RNAi in *C. elegans*. Wianny and Goetz, 1999, *Nature Cell*

Biol., 2, 70, describe RNAi mediated by dsRNA in mouse embryos. Hammond *et al.*, 2000, *Nature*, 404, 293, describe RNAi in *Drosophila* cells transfected with dsRNA. Elbashir *et al.*, 2001, *Nature*, 411, 494, describe RNAi induced by introduction of duplexes of synthetic 21-nucleotide RNAs in cultured mammalian cells including human embryonic kidney and HeLa cells. Recent work in *Drosophila* embryonic lysates (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877) has revealed certain requirements for siRNA length, structure, chemical composition, and sequence that are essential to mediate efficient RNAi activity. These studies have shown that 21-nucleotide siRNA duplexes are most active when containing 3'-terminal dinucleotide overhangs. Furthermore, complete substitution of one or both siRNA strands with 2'-deoxy (2'-H) or 2'-O-methyl nucleotides abolishes RNAi activity, whereas substitution of the 3'-terminal siRNA overhang nucleotides with 2'-deoxy nucleotides (2'-H) was shown to be tolerated. Single mismatch sequences in the center of the siRNA duplex were also shown to abolish RNAi activity. In addition, these studies also indicate that the position of the cleavage site in the target RNA is defined by the 5'-end of the siRNA guide sequence rather than the 3'-end of the guide sequence (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877). Other studies have indicated that a 5'-phosphate on the target-complementary strand of a siRNA duplex is required for siRNA activity and that ATP is utilized to maintain the 5'-phosphate moiety on the siRNA (Nykanen *et al.*, 2001, *Cell*, 107, 309).

Studies have shown that replacing the 3'-terminal nucleotide overhanging segments of a 21-mer siRNA duplex having two-nucleotide 3'-overhangs with deoxyribonucleotides does not have an adverse effect on RNAi activity. Replacing up to four nucleotides on each end of the siRNA with deoxyribonucleotides has been reported to be well-tolerated, whereas complete substitution with deoxyribonucleotides results in no RNAi activity (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877). In addition, Elbashir *et al.*, *supra*, also report that substitution of siRNA with 2'-O-methyl nucleotides completely abolishes RNAi activity. Li *et al.*, International PCT Publication No. WO 00/44914, and Beach *et al.*, International PCT Publication No. WO 01/68836 preliminarily suggest that siRNA may include modifications to either the phosphate-sugar backbone or the nucleoside to include at least one of a nitrogen or sulfur heteroatom, however, neither application postulates to what extent such modifications would be tolerated in siRNA molecules, nor provides any further guidance or examples of such modified siRNA. Kreutzer *et al.*, Canadian Patent Application No. 2,359,180, also describe certain

chemical modifications for use in dsRNA constructs in order to counteract activation of double-stranded RNA-dependent protein kinase PKR, specifically 2'-amino or 2'-O-methyl nucleotides, and nucleotides containing a 2'-O or 4'-C methylene bridge. However, Kreutzer *et al.* similarly fails to provide examples or guidance as to what
5 extent these modifications would be tolerated in siRNA molecules.

Parrish *et al.*, 2000, *Molecular Cell*, 6, 1977-1087, tested certain chemical modifications targeting the *unc-22* gene in *C. elegans* using long (>25 nt) siRNA transcripts. The authors describe the introduction of thiophosphate residues into these siRNA transcripts by incorporating thiophosphate nucleotide analogs with T7 and T3
10 RNA polymerase and observed that RNAs with two phosphorothioate modified bases also had substantial decreases in effectiveness as RNAi. Further, Parrish *et al.* reported that phosphorothioate modification of more than two residues greatly destabilized the RNAs *in vitro* such that interference activities could not be assayed. *Id.* at 1081. The authors also tested certain modifications at the 2'-position of the nucleotide sugar in the
15 long siRNA transcripts and found that substituting deoxynucleotides for ribonucleotides produced a substantial decrease in interference activity, especially in the case of Uridine to Thymidine and/or Cytidine to deoxy-Cytidine substitutions. *Id.* In addition, the authors tested certain base modifications, including substituting, in sense and antisense strands of the siRNA, 4-thiouracil, 5-bromouracil, 5-iodouracil, and 3-(aminoallyl)uracil
20 for uracil, and inosine for guanosine. Whereas 4-thiouracil and 5-bromouracil substitution appeared to be tolerated, Parrish reported that inosine produced a substantial decrease in interference activity when incorporated in either strand. Parrish also reported that incorporation of 5-iodouracil and 3-(aminoallyl)uracil in the antisense strand resulted in a substantial decrease in RNAi activity as well.

25 The use of longer dsRNA has been described. For example, Beach *et al.*, International PCT Publication No. WO 01/68836, describes specific methods for attenuating gene expression using endogenously-derived dsRNA. Tuschl *et al.*, International PCT Publication No. WO 01/75164, describe a *Drosophila in vitro* RNAi system and the use of specific siRNA molecules for certain functional genomic and
30 certain therapeutic applications; although Tuschl, 2001, *Chem. Biochem.*, 2, 239-245, doubts that RNAi can be used to cure genetic diseases or viral infection due to the danger of activating interferon response. Li *et al.*, International PCT Publication No. WO

00/44914, describe the use of specific dsRNAs for attenuating the expression of certain target genes. Zernicka-Goetz *et al.*, International PCT Publication No. WO 01/36646, describe certain methods for inhibiting the expression of particular genes in mammalian cells using certain dsRNA molecules. Fire *et al.*, International PCT Publication No. WO 5 99/32619, describe particular methods for introducing certain dsRNA molecules into cells for use in inhibiting gene expression. Plaetinck *et al.*, International PCT Publication No. WO 00/01846, describe certain methods for identifying specific genes responsible for conferring a particular phenotype in a cell using specific dsRNA molecules. Mello *et al.*, International PCT Publication No. WO 01/29058, describe the 10 identification of specific genes involved in dsRNA-mediated RNAi. Deschamps Depaillette *et al.*, International PCT Publication No. WO 99/07409, describe specific compositions consisting of particular dsRNA molecules combined with certain anti-viral agents. Waterhouse *et al.*, International PCT Publication No. 99/53050, describe certain methods for decreasing the phenotypic expression of a nucleic acid in plant cells using 15 certain dsRNAs. Driscoll *et al.*, International PCT Publication No. WO 01/49844, describe specific DNA constructs for use in facilitating gene silencing in targeted organisms.

Others have reported on various RNAi and gene-silencing systems. For example, Parrish *et al.*, 2000, *Molecular Cell*, 6, 1977-1087, describe specific chemically-modified 20 siRNA constructs targeting the unc-22 gene of *C. elegans*. Grossniklaus, International PCT Publication No. WO 01/38551, describes certain methods for regulating polycomb gene expression in plants using certain dsRNAs. Churikov *et al.*, International PCT Publication No. WO 01/42443, describe certain methods for modifying genetic characteristics of an organism using certain dsRNAs. Cogoni *et al.*, International PCT 25 Publication No. WO 01/53475, describe certain methods for isolating a Neurospora silencing gene and uses thereof. Reed *et al.*, International PCT Publication No. WO 01/68836, describe certain methods for gene silencing in plants. Honer *et al.*, International PCT Publication No. WO 01/70944, describe certain methods of drug screening using transgenic nematodes as Parkinson's Disease models using certain 30 dsRNAs. Deak *et al.*, International PCT Publication No. WO 01/72774, describe certain *Drosophila*-derived gene products that may be related to RNAi in *Drosophila*. Arndt *et al.*, International PCT Publication No. WO 01/92513 describe certain methods for mediating gene suppression by using factors that enhance RNAi. Tuschl *et al.*,

International PCT Publication No. WO 02/44321, describe certain synthetic siRNA constructs. Pachuk *et al.*, International PCT Publication No. WO 00/63364, and Satishchandran *et al.*, International PCT Publication No. WO 01/04313, describe certain methods and compositions for inhibiting the function of certain polynucleotide sequences using certain dsRNAs. Echeverri *et al.*, International PCT Publication No. WO 02/38805, describe certain *C. elegans* genes identified via RNAi. Kreutzer *et al.*, International PCT Publications Nos. WO 02/055692, WO 02/055693, and EP 1144623 B1 describes certain methods for inhibiting gene expression using RNAi. Graham *et al.*, International PCT Publications Nos. WO 99/49029 and WO 01/70949, and AU 4037501 describe certain vector expressed siRNA molecules. Fire *et al.*, US 6,506,559, describe certain methods for inhibiting gene expression in vitro using certain siRNA constructs that mediate RNAi.

McSwiggen *et al.*, International PCT Publication No. WO 01/16312, describes nucleic acid mediated inhibition of BACE, PS-1, and PS-2 expression.

15

SUMMARY OF THE INVENTION

This invention relates to compounds, compositions, and methods useful for modulating BACE expression by RNA interference (RNAi) using small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules. This invention also relates to compounds, compositions, and methods useful for modulating the expression and activity of BACE genes, or genes involved in BACE pathways of gene expression and/or BACE activity by RNA interference (RNAi) using small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules. In particular, the instant invention features small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules and methods used to modulate the expression of BACE genes. A siNA of the invention can be unmodified or chemically-modified. A siNA of the instant invention can be chemically synthesized, expressed from a vector or enzymatically synthesized. The instant invention also features various chemically-

modified synthetic short interfering nucleic acid (siNA) molecules capable of modulating BACE gene expression or activity in cells by RNA interference (RNAi). The use of chemically-modified siNA improves various properties of native siNA molecules through increased resistance to nuclease degradation *in vivo* and/or through improved cellular uptake. Further, contrary to earlier published studies, siNA having multiple chemical modifications retains its RNAi activity. The siNA molecules of the instant invention provide useful reagents and methods for a variety of therapeutic, diagnostic, target validation, genomic discovery, genetic engineering, and pharmacogenomic applications.

Accordingly, in one aspect there is provided a chemically synthesized double stranded short interfering nucleic acid (siNA) molecule that directs cleavage of a beta secretase (BACE) RNA via RNA interference (RNAi), wherein:

- (a) each strand of said siNA molecule is about 19 to about 23 nucleotides in length;
- (b) one strand of said siNA molecule comprises nucleotide sequence that is complementary to said BACE RNA such that the siNA molecule directs cleavage of the BACE RNA via RNA interference; and
- (c) said siNA molecule comprises at least one chemically modified nucleotide or non-nucleotide.

In one embodiment, the invention features one or more siNA molecules and methods that independently or in combination modulate the expression of gene(s) encoding proteins, such as BACE proteins, associated with the maintenance and/or development of Alzheimer's disease and other neurodegenerative disorders or conditions such as dementia, and stroke/cardiovascular accident (CVA), such as genes encoding sequences comprising those sequences referred to by GenBank Accession Nos. shown in Table I, referred to herein generally as BACE. The description below of the various aspects and embodiments is provided with reference to the exemplary BACE gene and BACE protein, including components or subunits thereof. However, the various aspects and embodiments are also directed to other genes which express other BACE related proteins or other proteins associated with Alzheimer's disease, such as APP, PIN-1, PS-1 and PS-2, including mutant genes and splice variant genes thereof. The various aspects and embodiments are also directed to other genes that are involved in BACE, APP, PIN-1, PS-1 and PS-2 mediated pathways of signal transduction or gene expression that are involved in the progression, development, or maintenance of disease (e.g., Alzheimer's disease). Those additional genes can be analysed for target sites using the methods

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described for BACEs herein. Thus, the inhibition and the effects of such inhibition of the other genes can be performed as described herein.

In one embodiment, the invention features a siNA molecule that down-regulates expression of a BACE gene, for example, wherein the BACE gene comprises BACE
5 encoding sequence.

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In one embodiment, the invention features a siNA molecule having RNAi activity against BACE RNA, wherein the siNA molecule comprises a sequence complementary to any RNA having BACE or other BACE encoding sequence, such as those sequences having GenBank Accession Nos. shown in **Table I**. Chemical modifications as shown in **Tables III and IV** or otherwise described herein can be applied to any siNA construct of the invention. Furthermore, the chemically modified constructs described in **Table IV** can be applied to any siNA sequence of the invention.

In another embodiment, the invention features a siNA molecule having RNAi activity against a BACE gene, wherein the siNA molecule comprises nucleotide sequence complementary to nucleotide sequence of a BACE gene, such as those BACE sequences having GenBank Accession Nos. shown in **Table I**. In another embodiment, a siNA molecule of the invention includes nucleotide sequence that can interact with nucleotide sequence of a BACE gene and thereby mediate silencing of BACE gene expression, for example, wherein the siNA mediates regulation of BACE gene expression by cellular processes that modulate the chromatin structure of the BACE gene and prevent transcription of the BACE gene.

In another embodiment, the invention features a siNA molecule comprising nucleotide sequence, for example, nucleotide sequence in the antisense region of the siNA molecule that is complementary to a nucleotide sequence or portion of sequence of a BACE gene. In another embodiment, the invention features a siNA molecule comprising a region, for example, the antisense region of the siNA construct, complementary to a sequence or portion of sequence comprising a BACE gene sequence.

In one embodiment, the antisense region of BACE siNA constructs can comprise a sequence complementary to sequence having any of SEQ ID NOs. 1-325 or 651-654. The antisense region can also comprise sequence having any of SEQ ID NOs. 326-650, 659-662, 667-670, 675-678, 695, 697, 699, 701, 703, or 704. In another embodiment, the sense region of BACE constructs can comprise sequence having any of SEQ ID NOs. 1-325, 651-658, 663-666, 671-674, 694, 696, 698, 700, or 702. The sense region can comprise a sequence of SEQ ID NO. 683 and the antisense region can comprise a sequence of SEQ ID NO. 684. The sense region can comprise a sequence of SEQ ID NO. 685 and the antisense region can comprise a sequence of SEQ ID NO. 686. The

sense region can comprise a sequence of SEQ ID NO. 687 and the antisense region can comprise a sequence of SEQ ID NO. 688. The sense region can comprise a sequence of SEQ ID NO. 689 and the antisense region can comprise a sequence of SEQ ID NO. 690. The sense region can comprise a sequence of SEQ ID NO. 691 and the antisense region
5 can comprise a sequence of SEQ ID NO. 692. The sense region can comprise a sequence of SEQ ID NO. 689 and the antisense region can comprise a sequence of SEQ ID NO. 693.

In one embodiment, a siNA molecule of the invention comprises any of SEQ ID NOs. 1-704. The sequences shown in SEQ ID NOs: 1-704 are not limiting. A siNA
10 molecule of the invention can comprise any contiguous BACE sequence (e.g., about 19 to about 25, or about 19, 20, 21, 22, 23, 24 or 25 contiguous BACE nucleotides).

In yet another embodiment, the invention features a siNA molecule comprising a sequence, for example, the antisense sequence of the siNA construct, complementary to a sequence or portion of sequence comprising sequence represented by GenBank
15 Accession Nos. shown in **Table I**. Chemical modifications in **Tables III and IV** and described herein can be applied to any siRNA construct of the invention. Furthermore, the chemically modified constructs described in **Table IV** can be applied to any siNA sequence of the invention.

In one embodiment of the invention a siNA molecule comprises an antisense
20 strand having about 19 to about 29 nucleotides, wherein the antisense strand is complementary to a RNA sequence encoding a BACE protein, and wherein said siNA further comprises a sense strand having about 19 to about 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28 or 29) nucleotides, and wherein said sense strand and said antisense strand are distinct nucleotide sequences with at least about 19 complementary
25 nucleotides.

In another embodiment of the invention a siNA molecule of the invention comprises an antisense region having about 19 to about 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28 or 29) nucleotides, wherein the antisense region is complementary to a RNA sequence encoding a BACE protein, and wherein said siNA further comprises a
30 sense region having about 19 to about 29 nucleotides, wherein said sense region and said

antisense region comprise a linear molecule with at least about 19 complementary nucleotides.

5 In one embodiment of the invention a siNA molecule comprises an antisense strand comprising a nucleotide sequence that is complementary to a nucleotide sequence or a portion thereof encoding a BACE protein. The siNA further comprises a sense strand, wherein said sense strand comprises a nucleotide sequence of a BACE gene or a portion thereof.

10 In another embodiment, a siNA molecule comprises an antisense region comprising a nucleotide sequence that is complementary to a nucleotide sequence or a portion thereof encoding a BACE protein. The siNA molecule further comprises a sense region, wherein said sense region comprises a nucleotide sequence of a BACE gene or a portion thereof.

In one embodiment, a siNA molecule of the invention has RNAi activity that modulates expression of RNA encoded by a BACE gene. Because BACE genes can share some degree of sequence homology with each other, siNA molecules can be designed to target a class of BACE genes (and associated receptor or ligand genes) or alternately specific BACE genes by selecting sequences that are either shared amongst different BACE targets or alternatively that are unique for a specific BACE target. Therefore, in one embodiment, the siNA molecule can be designed to target conserved regions of BACE RNA sequence having homology between several BACE genes so as to target several BACE genes (e.g., different BACE isoforms, splice variants, mutant genes etc.) with one siNA molecule. In another embodiment, the siNA molecule can be designed to target a sequence that is unique to a specific BACE RNA sequence due to the high degree of specificity that the siNA molecule requires to mediate RNAi activity.

25 In one embodiment, nucleic acid molecules of the invention that act as mediators of the RNA interference gene silencing response are double-stranded nucleic acid molecules. In another embodiment, the siNA molecules of the invention consist of duplexes containing about 19 base pairs between oligonucleotides comprising about 19 to about 25 (e.g., about 19, 20, 21, 22, 23, 24 or 25) nucleotides. In yet another embodiment, siNA molecules of the invention comprise duplexes with overhanging ends of about about 1 to about 3 (e.g., about 1, 2, or 3) nucleotides, for example, about 21-

nucleotide duplexes with about 19 base pairs and 3'-terminal mononucleotide, dinucleotide, or trinucleotide overhangs.

In one embodiment, the invention features one or more chemically-modified siNA constructs having specificity for BACE expressing nucleic acid molecules, such as RNA
5 encoding a BACE protein. Non-limiting examples of such chemical modifications include without limitation phosphorothioate internucleotide linkages, 2'-deoxyribonucleotides, 2'-O-methyl ribonucleotides, 2'-deoxy-2'-fluoro ribonucleotides, "universal base" nucleotides, "acyclic" nucleotides, 5-C-methyl nucleotides, and terminal glyceryl and/or inverted deoxy abasic residue incorporation. These chemical
10 modifications, when used in various siNA constructs, are shown to preserve RNAi activity in cells while at the same time, dramatically increasing the serum stability of these compounds. Furthermore, contrary to the data published by Parrish *et al.*, *supra*, applicant demonstrates that multiple (greater than one) phosphorothioate substitutions are well-tolerated and confer substantial increases in serum stability for modified siNA
15 constructs.

In one embodiment, a siNA molecule of the invention comprises modified nucleotides while maintaining the ability to mediate RNAi. The modified nucleotides can be used to improve *in vitro* or *in vivo* characteristics such as stability, activity, and/or bioavailability. For example, a siNA molecule of the invention can comprise modified
20 nucleotides as a percentage of the total number of nucleotides present in the siNA molecule. As such, a siNA molecule of the invention can generally comprise about 5% to about 100% modified nucleotides (e.g., about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 100% modified nucleotides). The actual percentage of modified nucleotides present in a given siNA
25 molecule will depend on the total number of nucleotides present in the siNA. If the siNA molecule is single stranded, the percent modification can be based upon the total number of nucleotides present in the single stranded siNA molecules. Likewise, if the siNA molecule is double stranded, the percent modification can be based upon the total number of nucleotides present in the sense strand, antisense strand, or both the sense and
30 antisense strands.

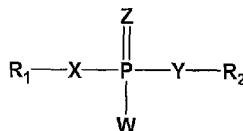
In a non-limiting example, the introduction of chemically-modified nucleotides into nucleic acid molecules provides a powerful tool in overcoming potential limitations of *in vivo* stability and bioavailability inherent to native RNA molecules that are delivered exogenously. For example, the use of chemically-modified nucleic acid molecules can enable a lower dose of a particular nucleic acid molecule for a given therapeutic effect since chemically-modified nucleic acid molecules tend to have a longer half-life in serum. Furthermore, certain chemical modifications can improve the bioavailability of nucleic acid molecules by targeting particular cells or tissues and/or improving cellular uptake of the nucleic acid molecule. Therefore, even if the activity of a chemically-modified nucleic acid molecule is reduced as compared to a native nucleic acid molecule, for example, when compared to an all-RNA nucleic acid molecule, the overall activity of the modified nucleic acid molecule can be greater than that of the native molecule due to improved stability and/or delivery of the molecule. Unlike native unmodified siNA, chemically-modified siNA can also minimize the possibility of activating interferon activity in humans.

The antisense region of a siNA molecule of the invention can comprise a phosphorothioate internucleotide linkage at the 3'-end of said antisense region. The antisense region can comprise about one to about five phosphorothioate internucleotide linkages at the 5'-end of said antisense region. The 3'-terminal nucleotide overhangs of a siNA molecule of the invention can comprise ribonucleotides or deoxyribonucleotides that are chemically-modified at a nucleic acid sugar, base, or backbone. The 3'-terminal nucleotide overhangs can comprise one or more universal base ribonucleotides. The 3'-terminal nucleotide overhangs can comprise one or more acyclic nucleotides.

One embodiment of the invention provides an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the invention in a manner that allows expression of the nucleic acid molecule. Another embodiment of the invention provides a mammalian cell comprising such an expression vector. The mammalian cell can be a human cell. The siNA molecule of the expression vector can comprise a sense region and an antisense region. The antisense region can comprise sequence complementary to a RNA or DNA sequence encoding BACE and the sense region can comprise sequence complementary to the antisense region. The siNA molecule can comprise two distinct strands having complementary sense and antisense

regions. The siNA molecule can comprise a single strand having complementary sense and antisense regions.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a BACE inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides comprising a backbone modified internucleotide linkage having Formula I:

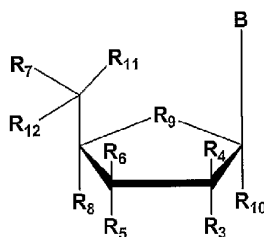


wherein each R1 and R2 is independently any nucleotide, non-nucleotide, or polynucleotide which can be naturally-occurring or chemically-modified, each X and Y is independently O, S, N, alkyl, or substituted alkyl, each Z and W is independently O, S, N, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, or aralkyl, and wherein W, X, Y, and Z are optionally not all O.

The chemically-modified internucleotide linkages having Formula I, for example, wherein any Z, W, X, and/or Y independently comprises a sulfur atom, can be present in one or both oligonucleotide strands of the siNA duplex, for example, in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) chemically-modified internucleotide linkages having Formula I at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (e.g., about 1, 2, 3, 4, 5, or more) chemically-modified internucleotide linkages having Formula I at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) pyrimidine nucleotides with chemically-modified internucleotide linkages having Formula I in the sense strand, the antisense strand, or both strands. In yet another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (e.g., about 1, 2,

3, 4, 5, 6, 7, 8, 9, 10, or more) purine nucleotides with chemically-modified internucleotide linkages having Formula I in the sense strand, the antisense strand, or both strands. In another embodiment, a siNA molecule of the invention having internucleotide linkage(s) of Formula I also comprises a chemically-modified nucleotide
 5 or non-nucleotide having any of Formulae I-VII.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a BACE inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides or
 10 non-nucleotides having Formula II:

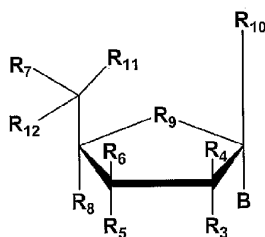


wherein each R3, R4, R5, R6, R7, R8, R10, R11 and R12 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3,
 15 NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I; R9 is O, S, CH2, S=O, CHF, or CF2, and B is a nucleosidic base such as adenine, guanine, uracil, cytosine, thymine, 2-aminoadenosine, 5-methylcytosine, 2,6-diaminopurine, or any other non-naturally
 20 occurring base that can be complementary or non-complementary to target RNA or a non-nucleosidic base such as phenyl, naphthyl, 3-nitropyrrole, 5-nitroindole, nebularine, pyridone, pyridinone, or any other non-naturally occurring universal base that can be complementary or non-complementary to target RNA.

25 The chemically-modified nucleotide or non-nucleotide of Formula II can be present in one or both oligonucleotide strands of the siNA duplex, for example in the

sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more chemically-modified nucleotide or non-nucleotide of Formula II at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can
 5 comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotides or non-nucleotides of Formula II at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotides or non-nucleotides of Formula II at the 3'-
 10 end of the sense strand, the antisense strand, or both strands.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a BACE inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides or
 15 non-nucleotides having Formula III:



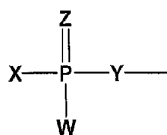
wherein each R3, R4, R5, R6, R7, R8, R10, R11 and R12 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH,
 20 O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I; R9 is O, S, CH2, S=O, CHF, or CF2, and B is a nucleosidic base such as adenine, guanine, uracil, cytosine, thymine, 2-
 25 aminoadenosine, 5-methylcytosine, 2,6-diaminopurine, or any other non-naturally occurring base that can be employed to be complementary or non-complementary to

target RNA or a non-nucleosidic base such as phenyl, naphthyl, 3-nitropyrrole, 5-nitroindole, nebularine, pyridone, pyridinone, or any other non-naturally occurring universal base that can be complementary or non-complementary to target RNA.

The chemically-modified nucleotide or non-nucleotide of Formula III can be present in one or both oligonucleotide strands of the siNA duplex, for example, in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more chemically-modified nucleotide or non-nucleotide of Formula III at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotide(s) or non-nucleotide(s) of Formula III at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotide or non-nucleotide of Formula III at the 3'-end of the sense strand, the antisense strand, or both strands.

In another embodiment, a siNA molecule of the invention comprises a nucleotide having Formula II or III, wherein the nucleotide having Formula II or III is in an inverted configuration. For example, the nucleotide having Formula II or III is connected to the siNA construct in a 3'-3', 3'-2', 2'-3', or 5'-5' configuration, such as at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both siNA strands.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a BACE inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises a 5'-terminal phosphate group having Formula IV:



25

wherein each X and Y is independently O, S, N, alkyl, substituted alkyl, or alkylhalo; wherein each Z and W is independently O, S, N, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, aralkyl, or alkylhalo; and wherein W, X, Y and Z are not all O.

In one embodiment, the invention features a siNA molecule having a 5'-terminal phosphate group having Formula IV on the target-complementary strand, for example, a strand complementary to a target RNA, wherein the siNA molecule comprises an all RNA siNA molecule. In another embodiment, the invention features a siNA molecule having a 5'-terminal phosphate group having Formula IV on the target-complementary strand wherein the siNA molecule also comprises about 1 to about 3 (*e.g.*, about 1, 2, or 3) nucleotide 3'-terminal nucleotide overhangs having about 1 to about 4 (*e.g.*, about 1, 2, 3, or 4) deoxyribonucleotides on the 3'-end of one or both strands. In another embodiment, a 5'-terminal phosphate group having Formula IV is present on the target-complementary strand of a siNA molecule of the invention, for example a siNA molecule having chemical modifications having any of Formulae I-VII.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a BACE inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more phosphorothioate internucleotide linkages. For example, in a non-limiting example, the invention features a chemically-modified short interfering nucleic acid (siNA) having about 1, 2, 3, 4, 5, 6, 7, 8 or more phosphorothioate internucleotide linkages in one siNA strand. In yet another embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) individually having about 1, 2, 3, 4, 5, 6, 7, 8 or more phosphorothioate internucleotide linkages in both siNA strands. The phosphorothioate internucleotide linkages can be present in one or both oligonucleotide strands of the siNA duplex, for example in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more phosphorothioate internucleotide linkages at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) consecutive phosphorothioate internucleotide linkages at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*,

about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) pyrimidine phosphorothioate internucleotide linkages in the sense strand, the antisense strand, or both strands. In yet another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) purine phosphorothioate
5 internucleotide linkages in the sense strand, the antisense strand, or both strands.

In one embodiment, the invention features a siNA molecule, wherein the sense strand comprises one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or about one or more
10 (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 10 or more, specifically about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (e.g., about 1, 2, 3,
15 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides,
20 with or without one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

In another embodiment, the invention features a siNA molecule, wherein the sense
25 strand comprises about 1 to about 5, specifically about 1, 2, 3, 4, or 5 phosphorothioate internucleotide linkages, and/or one or more (e.g., about 1, 2, 3, 4, 5, or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (e.g., about 1, 2, 3, 4, 5, or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense
30 strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5, or more phosphorothioate internucleotide linkages, and/or one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (e.g.,

about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without about 1 to about 5 or more, for example about 1, 2, 3, 4, 5, or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

10 In one embodiment, the invention features a siNA molecule, wherein the antisense strand comprises one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or about one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 10 or more, specifically about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3' and 5'-ends, being present in the same or different strand.

In another embodiment, the invention features a siNA molecule, wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and

optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without about 1 to about 5 or more, for example about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule having about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages in each strand of the siNA molecule.

In another embodiment, the invention features a siNA molecule comprising 2'-5' internucleotide linkages. The 2'-5' internucleotide linkage(s) can be at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of one or both siNA sequence strands. In addition, the 2'-5' internucleotide linkage(s) can be present at various other positions within one or both siNA sequence strands, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more including every internucleotide linkage of a pyrimidine nucleotide in one or both strands of the siNA molecule can comprise a 2'-5' internucleotide linkage, or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more including every internucleotide linkage of a purine nucleotide in one or both strands of the siNA molecule can comprise a 2'-5' internucleotide linkage.

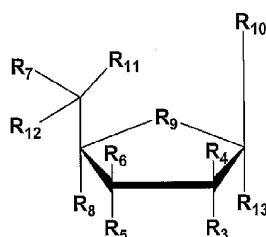
In another embodiment, a chemically-modified siNA molecule of the invention comprises a duplex having two strands, one or both of which can be chemically-modified, wherein each strand is about 18 to about 27 (*e.g.*, about 18, 19, 20, 21, 22, 23, 24, 25, 26, or 27) nucleotides in length, wherein the duplex has about 18 to about 23 (*e.g.*, about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the chemical modification

comprises a structure having any of Formulae I-VII. For example, an exemplary chemically-modified siNA molecule of the invention comprises a duplex having two strands, one or both of which can be chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein each strand consists of about 21 nucleotides, each having a 2-nucleotide 3'-terminal nucleotide overhang, and wherein the duplex has about 19 base pairs. In another embodiment, a siNA molecule of the invention comprises a single stranded hairpin structure, wherein the siNA is about 36 to about 70 (*e.g.*, about 36, 40, 45, 50, 55, 60, 65, or 70) nucleotides in length having about 18 to about 23 (*e.g.*, about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the siNA can include a chemical modification comprising a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a linear oligonucleotide having about 42 to about 50 (*e.g.*, about 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides that is chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein the linear oligonucleotide forms a hairpin structure having about 19 base pairs and a 2-nucleotide 3'-terminal nucleotide overhang. In another embodiment, a linear hairpin siNA molecule of the invention contains a stem loop motif, wherein the loop portion of the siNA molecule is biodegradable. For example, a linear hairpin siNA molecule of the invention is designed such that degradation of the loop portion of the siNA molecule *in vivo* can generate a double-stranded siNA molecule with 3'-terminal overhangs, such as 3'-terminal nucleotide overhangs comprising about 2 nucleotides.

In another embodiment, a siNA molecule of the invention comprises a circular nucleic acid molecule, wherein the siNA is about 38 to about 70 (*e.g.*, about 38, 40, 45, 50, 55, 60, 65, or 70) nucleotides in length having about 18 to about 23 (*e.g.*, about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the siNA can include a chemical modification, which comprises a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a circular oligonucleotide having about 42 to about 50 (*e.g.*, about 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides that is chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein the circular oligonucleotide forms a dumbbell shaped structure having about 19 base pairs and 2 loops.

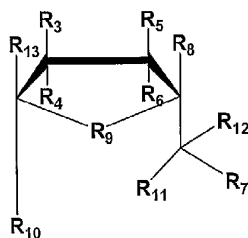
In another embodiment, a circular siNA molecule of the invention contains two loop motifs, wherein one or both loop portions of the siNA molecule is biodegradable. For example, a circular siNA molecule of the invention is designed such that degradation of the loop portions of the siNA molecule *in vivo* can generate a double-stranded siNA molecule with 3'-terminal overhangs, such as 3'-terminal nucleotide overhangs comprising about 2 nucleotides.

In one embodiment, a siNA molecule of the invention comprises at least one (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) abasic moiety, for example a compound having Formula V:



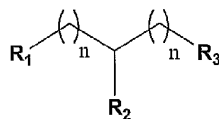
wherein each R3, R4, R5, R6, R7, R8, R10, R11, R12, and R13 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF₃, OCF₃, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO₂, NO₂, N₃, NH₂, aminoalkyl, aminoacid, aminoacyl, ONH₂, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I; R9 is O, S, CH₂, S=O, CHF, or CF₂.

In one embodiment, a siNA molecule of the invention comprises at least one (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) inverted abasic moiety, for example a compound having Formula VI:



wherein each R3, R4, R5, R6, R7, R8, R10, R11, R12, and R13 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I; R9 is O, S, CH2, S=O, CHF, or CF2, and either R2, R3, R8 or R13 serve as points of attachment to the siNA molecule of the invention.

In another embodiment, a siNA molecule of the invention comprises at least one (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) substituted polyalkyl moieties, for example a compound having Formula VII:



wherein each n is independently an integer from 1 to 12, each R1, R2 and R3 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or a group having Formula I, and R1, R2 or R3 serves as points of attachment to the siNA molecule of the invention.

In another embodiment, the invention features a compound having Formula VII, wherein R1 and R2 are hydroxyl (OH) groups, $n = 1$, and R3 comprises O and is the point of attachment to the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both strands of a double-stranded siNA molecule of the invention or to a single-stranded siNA molecule of the invention. This modification is referred to herein as "glyceryl" (for example modification 6 in **Figure 10**).

In another embodiment, a moiety having any of Formula V, VI or VII of the invention is at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of a siNA molecule of the invention. For example, a moiety having Formula V, VI or VII can be present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense strand, the sense strand, or both antisense and sense strands of the siNA molecule. In addition, a moiety having Formula VII can be present at the 3'-end or the 5'-end of a hairpin siNA molecule as described herein.

In another embodiment, a siNA molecule of the invention comprises an abasic residue having Formula V or VI, wherein the abasic residue having Formula VI or VI is connected to the siNA construct in a 3'-3', 3'-2', 2'-3', or 5'-5' configuration, such as at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both siNA strands.

In one embodiment, a siNA molecule of the invention comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) locked nucleic acid (LNA) nucleotides, for example at the 5'-end, the 3'-end, both of the 5' and 3'-ends, or any combination thereof, of the siNA molecule.

In another embodiment, a siNA molecule of the invention comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) acyclic nucleotides, for example at the 5'-end, the 3'-end, both of the 5' and 3'-ends, or any combination thereof, of the siNA molecule.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention, wherein the chemically-modified siNA comprises a sense region, where any (*e.g.*, one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a

plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and where any (*e.g.*, one or more or all) purine nucleotides present in the sense region are 2'-deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention, wherein the chemically-modified siNA comprises a sense region, where any (*e.g.*, one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and where any (*e.g.*, one or more or all) purine nucleotides present in the sense region are 2'-deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides), wherein any nucleotides comprising a 3'-terminal nucleotide overhang that are present in said sense region are 2'-deoxy nucleotides.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention, wherein the chemically-modified siNA comprises an antisense region, where any (*e.g.*, one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.*, one or more or all) purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention, wherein the chemically-modified siNA comprises an antisense region, where any (*e.g.*, one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or

alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.*, one or more or all) purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides), wherein any nucleotides comprising a 3'-terminal nucleotide overhang that are present in said antisense region are 2'-deoxy nucleotides.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention, wherein the chemically-modified siNA comprises an antisense region, where any (*e.g.*, one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and where any (*e.g.*, one or more or all) purine nucleotides present in the antisense region are 2'-deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention capable of mediating RNA interference (RNAi) against a BACE inside a cell or reconstituted *in vitro* system, wherein the chemically-modified siNA comprises a sense region, where one or more pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and where one or more purine nucleotides present in the sense region are 2'-deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides), and inverted deoxy abasic modifications that are optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense region, the sense region optionally further comprising a 3'-terminal overhang having about 1 to about 4 (*e.g.*, about 1, 2, 3, or 4) 2'-deoxyribonucleotides; and wherein the chemically-modified short interfering nucleic acid molecule comprises an antisense region, where one or more pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine

nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein one or more purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides), and a terminal cap modification, such as any modification described herein or shown in **Figure 10**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the antisense region optionally further comprising a 3'-terminal nucleotide overhang having about 1 to about 4 (e.g., about 1, 2, 3, or 4) 2'-deoxynucleotides, wherein the overhang nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages. Non-limiting examples of these chemically-modified siNAs are shown in **Figures 4 and 5** and **Table III** herein.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention capable of mediating RNA interference (RNAi) against a BACE inside a cell or reconstituted *in vitro* system, wherein the siNA comprises a sense region, where one or more pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and where one or more purine nucleotides present in the sense region are purine ribonucleotides (e.g., wherein all purine nucleotides are purine ribonucleotides or alternately a plurality of purine nucleotides are purine ribonucleotides), and inverted deoxy abasic modifications that are optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense region, the sense region optionally further comprising a 3'-terminal overhang having about 1 to about 4 (e.g., about 1, 2, 3, or 4) 2'-deoxyribonucleotides; and wherein the siNA comprises an antisense region, where one or more pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine

nucleotides), and a terminal cap modification, such as any modification described herein or shown in **Figure 10**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the antisense region optionally further comprising a 3'-terminal nucleotide overhang having about 1 to about 4 (e.g., about 1, 2, 3, or 4) 2'-deoxynucleotides, wherein the overhang nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages. Non-limiting examples of these chemically-modified siNAs are shown in **Figures 4 and 5** and **Table III** herein.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention capable of mediating RNA interference (RNAi) against a BACE inside a cell or reconstituted *in vitro* system, wherein the chemically-modified siNA comprises a sense region, where one or more pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and for example where one or more purine nucleotides present in the sense region are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides (e.g., wherein all purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides or alternately a plurality of purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides), and wherein inverted deoxy abasic modifications are optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense region, the sense region optionally further comprising a 3'-terminal overhang having about 1 to about 4 (e.g., about 1, 2, 3, or 4) 2'-deoxyribonucleotides; and wherein the chemically-modified short interfering nucleic acid molecule comprises an antisense region, where one or more pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein one or more purine nucleotides present in the antisense region are selected from the group consisting

of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides (e.g., wherein all purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides or alternately a plurality of purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides), and a terminal cap modification, such as any modification described herein or shown in Figure 10, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the antisense region optionally further comprising a 3'-terminal nucleotide overhang having about 1 to about 4 (e.g., about 1, 2, 3, or 4) 2'-deoxynucleotides, wherein the overhang nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages.

In another embodiment, any modified nucleotides present in the siNA molecules of the invention, preferably in the antisense strand of the siNA molecules of the invention, but also optionally in the sense and/or both antisense and sense strands, comprise modified nucleotides having properties or characteristics similar to naturally occurring ribonucleotides. For example, the invention features siNA molecules including modified nucleotides having a Northern conformation (e.g., Northern pseudorotation cycle, see for example Saenger, *Principles of Nucleic Acid Structure*, Springer-Verlag ed., 1984). As such, chemically modified nucleotides present in the siNA molecules of the invention, preferably in the antisense strand of the siNA molecules of the invention, but also optionally in the sense and/or both antisense and sense strands, are resistant to nuclease degradation while at the same time maintaining the capacity to mediate RNAi. Non-limiting examples of nucleotides having a northern configuration include locked nucleic acid (LNA) nucleotides (e.g., 2'-O,4'-C-methylene-(D-ribofuranosyl) nucleotides); 2'-methoxyethoxy (MOE) nucleotides; 2'-methyl-thio-ethyl, 2'-deoxy-2'-fluoro nucleotides, 2'-deoxy-2'-chloro nucleotides, 2'-azido nucleotides, and 2'-O-methyl nucleotides.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid molecule (siNA) capable of mediating RNA interference (RNAi) against a BACE inside a cell or reconstituted *in vitro* system, wherein the chemical modification

comprises a conjugate covalently attached to the chemically-modified siNA molecule. In another embodiment, the conjugate is covalently attached to the chemically-modified siNA molecule via a biodegradable linker. In one embodiment, the conjugate molecule is attached at the 3'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule. In another embodiment, the conjugate molecule is attached at the 5'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule. In yet another embodiment, the conjugate molecule is attached both the 3'-end and 5'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule, or any combination thereof. In one embodiment, a conjugate molecule of the invention comprises a molecule that facilitates delivery of a chemically-modified siNA molecule into a biological system, such as a cell. In another embodiment, the conjugate molecule attached to the chemically-modified siNA molecule is a poly ethylene glycol, human serum albumin, or a ligand for a cellular receptor that can mediate cellular uptake. Examples of specific conjugate molecules contemplated by the instant invention that can be attached to chemically-modified siNA molecules are described in Vargeese *et al.*, U.S. Serial No. 10/201,394, incorporated by reference herein. The type of conjugates used and the extent of conjugation of siNA molecules of the invention can be evaluated for improved pharmacokinetic profiles, bioavailability, and/or stability of siNA constructs while at the same time maintaining the ability of the siNA to mediate RNAi activity. As such, one skilled in the art can screen siNA constructs that are modified with various conjugates to determine whether the siNA conjugate complex possesses improved properties while maintaining the ability to mediate RNAi, for example in animal models as are generally known in the art.

In one embodiment, the invention features a short interfering nucleic acid (siNA) molecule of the invention, wherein the siNA further comprises a nucleotide, non-nucleotide, or mixed nucleotide/non-nucleotide linker that joins the sense region of the siNA to the antisense region of the siNA. In one embodiment, a nucleotide linker of the invention can be a linker of ≥ 2 nucleotides in length, for example 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides in length. In another embodiment, the nucleotide linker can be a nucleic acid aptamer. By "aptamer" or "nucleic acid aptamer" as used herein is meant a nucleic acid molecule that binds specifically to a target molecule wherein the nucleic acid molecule has sequence that comprises a sequence recognized by the target molecule in its natural

setting. Alternately, an aptamer can be a nucleic acid molecule that binds to a target molecule where the target molecule does not naturally bind to a nucleic acid. The target molecule can be any molecule of interest. For example, the aptamer can be used to bind to a ligand-binding domain of a protein, thereby preventing interaction of the naturally occurring ligand with the protein. This is a non-limiting example and those in the art will recognize that other embodiments can be readily generated using techniques generally known in the art. (See, for example, Gold *et al.*, 1995, *Annu. Rev. Biochem.*, 64, 763; Brody and Gold, 2000, *J. Biotechnol.*, 74, 5; Sun, 2000, *Curr. Opin. Mol. Ther.*, 2, 100; Kusser, 2000, *J. Biotechnol.*, 74, 27; Hermann and Patel, 2000, *Science*, 287, 820; and Jayasena, 1999, *Clinical Chemistry*, 45, 1628.)

In yet another embodiment, a non-nucleotide linker of the invention comprises abasic nucleotide, polyether, polyamine, polyamide, peptide, carbohydrate, lipid, polyhydrocarbon, or other polymeric compounds (e.g. polyethylene glycols such as those having about 2 to about 100 ethylene glycol units). Specific examples include those described by Seela and Kaiser, *Nucleic Acids Res.* 1990, 18:6353 and *Nucleic Acids Res.* 1987, 15:3113; Cload and Schepartz, *J. Am. Chem. Soc.* 1991, 113:6324; Richardson and Schepartz, *J. Am. Chem. Soc.* 1991, 113:5109; Ma *et al.*, *Nucleic Acids Res.* 1993, 21:2585 and *Biochemistry* 1993, 32:1751; Durand *et al.*, *Nucleic Acids Res.* 1990, 18:6353; McCurdy *et al.*, *Nucleosides & Nucleotides* 1991, 10:287; Jschke *et al.*, *Tetrahedron Lett.* 1993, 34:301; Ono *et al.*, *Biochemistry* 1991, 30:9914; Arnold *et al.*, International Publication No. WO 89/02439; Usman *et al.*, International Publication No. WO 95/06731; Dudycz *et al.*, International Publication No. WO 95/11910 and Ferentz and Verdine, *J. Am. Chem. Soc.* 1991, 113:4000, all hereby incorporated by reference herein. A "non-nucleotide" further means any group or compound that can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound can be abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine, for example at the C1 position of the sugar.

In one embodiment, the invention features a short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) inside a cell or reconstituted in vitro system, wherein one or both strands of the siNA molecule that are assembled

from two separate oligonucleotides do not comprise any ribonucleotides. All positions within the siNA can include chemically modified nucleotides and/or non-nucleotides such as nucleotides and or non-nucleotides having Formula I, II, III, IV, V, VI, or VII or any combination thereof to the extent that the ability of the siNA molecule to support RNAi activity in a cell is maintained.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system, wherein the siNA molecule comprises a single stranded polynucleotide having complementarity to a target nucleic acid sequence. In another embodiment, the single stranded siNA molecule of the invention comprises a 5'-terminal phosphate group. In another embodiment, the single stranded siNA molecule of the invention comprises a 5'-terminal phosphate group and a 3'-terminal phosphate group (e.g., a 2',3'-cyclic phosphate). In another embodiment, the single stranded siNA molecule of the invention comprises about 19 to about 29 nucleotides. In yet another embodiment, the single stranded siNA molecule of the invention comprises one or more chemically modified nucleotides or non-nucleotides described herein. For example, all the positions within the siNA molecule can include chemically-modified nucleotides such as nucleotides having any of Formulae I-VII, or any combination thereof to the extent that the ability of the siNA molecule to support RNAi activity in a cell is maintained.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system, wherein the siNA molecule comprises a single stranded polynucleotide having complementarity to a target nucleic acid sequence, and wherein one or more pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides), and a terminal cap modification, such as any modification described herein or shown in Figure 10, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the siNA optionally further comprising about 1 to about 4 (e.g.,

about 1, 2, 3, or 4) terminal 2'-deoxynucleotides at the 3'-end of the siNA molecule, wherein the terminal nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages, and wherein the siNA optionally further comprises a terminal phosphate group, such as a 5'-terminal phosphate group.

5 In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system, wherein the siNA molecule comprises a single stranded polynucleotide having complementarity to a target nucleic acid sequence, and wherein one or more pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all
10 pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any purine nucleotides present in the antisense region are 2'-deoxy purine nucleotides (e.g., wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides), and a
15 terminal cap modification, such as any modification described herein or shown in **Figure 10**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the siNA optionally further comprising about 1 to about 4 (e.g., about 1, 2, 3, or 4) terminal 2'-deoxynucleotides at the 3'-end of the siNA molecule, wherein the terminal nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4)
20 phosphorothioate internucleotide linkages, and wherein the siNA optionally further comprises a terminal phosphate group, such as a 5'-terminal phosphate group.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system, wherein the siNA molecule comprises a single stranded polynucleotide having complementarity
25 to a target nucleic acid sequence, and wherein one or more pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any purine nucleotides present in the antisense region are locked nucleic acid
30 (LNA) nucleotides (e.g., wherein all purine nucleotides are LNA nucleotides or alternately a plurality of purine nucleotides are LNA nucleotides), and a terminal cap modification, such as any modification described herein or shown in **Figure 10**, that is

optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the siNA optionally further comprising about 1 to about 4 (e.g., about 1, 2, 3, or 4) terminal 2'-deoxynucleotides at the 3'-end of the siNA molecule, wherein the terminal nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4)
 5 phosphorothioate internucleotide linkages, and wherein the siNA optionally further comprises a terminal phosphate group, such as a 5'-terminal phosphate group.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system, wherein the siNA molecule comprises a single stranded polynucleotide having complementarity
 10 to a target nucleic acid sequence, and wherein one or more pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any purine nucleotides present in the antisense region are 2'-methoxyethyl
 15 purine nucleotides (e.g., wherein all purine nucleotides are 2'-methoxyethyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-methoxyethyl purine nucleotides), and a terminal cap modification, such as any modification described herein or shown in **Figure 10**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the siNA optionally further comprising about 1
 20 to about 4 (e.g., about 1, 2, 3, or 4) terminal 2'-deoxynucleotides at the 3'-end of the siNA molecule, wherein the terminal nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages, and wherein the siNA optionally further comprises a terminal phosphate group, such as a 5'-terminal phosphate group.

In another embodiment, any modified nucleotides present in the single stranded
 25 siNA molecules of the invention comprise modified nucleotides having properties or characteristics similar to naturally occurring ribonucleotides. For example, the invention features siNA molecules including modified nucleotides having a Northern conformation (e.g., Northern pseudorotation cycle, see for example Saenger, *Principles of Nucleic Acid Structure*, Springer-Verlag ed., 1984). As such, chemically modified nucleotides present
 30 in the single stranded siNA molecules of the invention are preferably resistant to nuclease degradation while at the same time maintaining the capacity to mediate RNAi.

In one embodiment, the invention features a method for modulating the expression of a BACE gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the BACE gene; and (b) introducing
5 the siNA molecule into a cell under conditions suitable to modulate the expression of the BACE gene in the cell.

In one embodiment, the invention features a method for modulating the expression of a BACE gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands
10 comprises a sequence complementary to RNA of the BACE gene and wherein the sense strand sequence of the siNA comprises a sequence identical to the sequence of the target RNA; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the BACE gene in the cell.

In another embodiment, the invention features a method for modulating the expression of more than one BACE gene within a cell comprising: (a) synthesizing
15 siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the BACE genes; and (b) introducing the siNA molecules into a cell under conditions suitable to modulate the expression of the BACE genes in the cell.

In another embodiment, the invention features a method for modulating the expression of more than one BACE gene within a cell comprising: (a) synthesizing a
20 siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the BACE gene and wherein the sense strand sequence of the siNA comprises a sequence identical to the sequence of the target RNA; and (b) introducing the siNA molecules into a cell under
25 conditions suitable to modulate the expression of the BACE genes in the cell.

In one embodiment, the invention features a method of modulating the expression of a BACE gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands
30 comprises a sequence complementary to RNA of the BACE gene; and (b) introducing the siNA molecule into a cell of the tissue explant derived from a particular organism

under conditions suitable to modulate the expression of the BACE gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the BACE gene in that organism.

5 In one embodiment, the invention features a method of modulating the expression of a BACE gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the BACE gene and wherein the sense strand sequence of the siNA comprises a sequence identical to the sequence of the target
10 RNA; and (b) introducing the siNA molecule into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the BACE gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the BACE
15 gene in that organism.

In another embodiment, the invention features a method of modulating the expression of more than one BACE gene in a tissue explant comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the BACE genes; and (b)
20 introducing the siNA molecules into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the BACE genes in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the BACE genes in that
25 organism.

In one embodiment, the invention features a method of modulating the expression of a BACE gene in an organism comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the BACE gene; and (b) introducing
30 the siNA molecule into the organism under conditions suitable to modulate the expression of the BACE gene in the organism.

In another embodiment, the invention features a method of modulating the expression of more than one BACE gene in an organism comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the BACE genes; and (b) introducing the siNA molecules into the organism under conditions suitable to modulate the expression of the BACE genes in the organism.

In one embodiment, the invention features a method for modulating the expression of a BACE gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the BACE gene; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the BACE gene in the cell.

In another embodiment, the invention features a method for modulating the expression of more than one BACE gene within a cell comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the BACE gene; and (b) contacting the siNA molecule with a cell in vitro or in vivo under conditions suitable to modulate the expression of the BACE genes in the cell.

In one embodiment, the invention features a method of modulating the expression of a BACE gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the BACE gene; and (b) contacting the siNA molecule with a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the BACE gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the BACE gene in that organism.

In another embodiment, the invention features a method of modulating the expression of more than one BACE gene in a tissue explant comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA

comprises a single stranded sequence having complementarity to RNA of the BACE gene; and (b) introducing the siNA molecules into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the BACE genes in the tissue explant. In another embodiment, the method further comprises
5 introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the BACE genes in that organism.

In one embodiment, the invention features a method of modulating the expression of a BACE gene in an organism comprising: (a) synthesizing a siNA molecule of the
10 invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the BACE gene; and (b) introducing the siNA molecule into the organism under conditions suitable to modulate the expression of the BACE gene in the organism.

In another embodiment, the invention features a method of modulating the expression of more than one BACE gene in an organism comprising: (a) synthesizing
15 siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the BACE gene; and (b) introducing the siNA molecules into the organism under conditions suitable to modulate the expression of the BACE genes in the organism.

In one embodiment, the invention features a method of modulating the expression of a BACE gene in an organism comprising contacting the organism with a siNA molecule of the invention under conditions suitable to modulate the expression of the
20 BACE gene in the organism.

In another embodiment, the invention features a method of modulating the expression of more than one BACE gene in an organism comprising contacting the
25 organism with one or more siNA molecules of the invention under conditions suitable to modulate the expression of the BACE genes in the organism.

The siNA molecules of the invention can be designed to inhibit target (BACE) gene expression through RNAi targeting of a variety of RNA molecules. In one
30 embodiment, the siNA molecules of the invention are used to target various RNAs

corresponding to a target gene. Non-limiting examples of such RNAs include messenger RNA (mRNA), alternate RNA splice variants of target gene(s), post-transcriptionally modified RNA of target gene(s), pre-mRNA of target gene(s), and/or RNA templates. If alternate splicing produces a family of transcripts that are distinguished by usage of
5 appropriate exons, the instant invention can be used to inhibit gene expression through the appropriate exons to specifically inhibit or to distinguish among the functions of gene family members. For example, a protein that contains an alternatively spliced transmembrane domain can be expressed in both membrane bound and secreted forms. Use of the invention to target the exon containing the transmembrane domain can be
10 used to determine the functional consequences of pharmaceutical targeting of membrane bound as opposed to the secreted form of the protein. Non-limiting examples of applications of the invention relating to targeting these RNA molecules include therapeutic pharmaceutical applications, pharmaceutical discovery applications, molecular diagnostic and gene function applications, and gene mapping, for example
15 using single nucleotide polymorphism mapping with siNA molecules of the invention. Such applications can be implemented using known gene sequences or from partial sequences available from an expressed sequence tag (EST).

In another embodiment, the siNA molecules of the invention are used to target conserved sequences corresponding to a gene family or gene families such as BACE
20 family genes. As such, siNA molecules targeting multiple BACE targets can provide increased therapeutic effect. In addition, siNA can be used to characterize pathways of gene function in a variety of applications. For example, the present invention can be used to inhibit the activity of target gene(s) in a pathway to determine the function of uncharacterized gene(s) in gene function analysis, mRNA function analysis, or
25 translational analysis. The invention can be used to determine potential target gene pathways involved in various diseases and conditions toward pharmaceutical development. The invention can be used to understand pathways of gene expression involved in, for example, the progression and/or maintenance of Alzheimer's disease.

In one embodiment, siNA molecule(s) and/or methods of the invention are used to
30 inhibit the expression of gene(s) that encode RNA referred to by Genbank Accession, for example BACE genes encoding RNA sequence(s) referred to herein by Genbank Accession number, for example Genbank Accession Nos. shown in **Table I**.

In one embodiment, the invention features a method comprising: (a) generating a library of siNA constructs having a predetermined complexity; and (b) assaying the siNA constructs of (a) above, under conditions suitable to determine RNAi target sites within the target RNA sequence. In another embodiment, the siNA molecules of (a) have strands of a fixed length, for example, about 23 nucleotides in length. In yet another embodiment, the siNA molecules of (a) are of differing length, for example having strands of about 19 to about 25 (e.g., about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. In another embodiment, fragments of target RNA are analyzed for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target RNA sequence. The target RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by cellular expression in *in vivo* systems.

In one embodiment, the invention features a method comprising: (a) generating a randomized library of siNA constructs having a predetermined complexity, such as of 4^N , where N represents the number of base paired nucleotides in each of the siNA construct strands (eg. for a siNA construct having 21 nucleotide sense and antisense strands with 19 base pairs, the complexity would be 4^{19}); and (b) assaying the siNA constructs of (a) above, under conditions suitable to determine RNAi target sites within the target BACE RNA sequence. In another embodiment, the siNA molecules of (a) have strands of a fixed length, for example about 23 nucleotides in length. In yet another embodiment, the siNA molecules of (a) are of differing length, for example having strands of about 19 to about 25 (e.g., about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described in Example 7 herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. In another embodiment, fragments of BACE RNA are analyzed for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target BACE RNA sequence. The target BACE RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by cellular expression in *in vivo* systems.

In another embodiment, the invention features a method comprising: (a) analyzing the sequence of a RNA target encoded by a target gene; (b) synthesizing one or more sets of siNA molecules having sequence complementary to one or more regions of the RNA of (a); and (c) assaying the siNA molecules of (b) under conditions suitable to determine RNAi targets within the target RNA sequence. In one embodiment, the siNA molecules of (b) have strands of a fixed length, for example about 23 nucleotides in length. In another embodiment, the siNA molecules of (b) are of differing length, for example having strands of about 19 to about 25 (e.g., about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. Fragments of target RNA are analyzed for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target RNA sequence. The target RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by expression in *in vivo* systems.

By "target site" is meant a sequence within a target RNA that is "targeted" for cleavage mediated by a siNA construct which contains sequences within its antisense region that are complementary to the target sequence.

By "detectable level of cleavage" is meant cleavage of target RNA (and formation of cleaved product RNAs) to an extent sufficient to discern cleavage products above the background of RNAs produced by random degradation of the target RNA. Production of cleavage products from 1-5% of the target RNA is sufficient to detect above the background for most methods of detection.

In one embodiment, the invention features a composition comprising a siNA molecule of the invention, which can be chemically-modified, in a pharmaceutically acceptable carrier or diluent. In another embodiment, the invention features a pharmaceutical composition comprising siNA molecules of the invention, which can be chemically-modified, targeting one or more genes in a pharmaceutically acceptable carrier or diluent. In another embodiment, the invention features a method for treating or preventing a disease or condition in a subject, comprising administering to the subject

a composition of the invention under conditions suitable for the treatment or prevention of the disease or condition in the subject, alone or in conjunction with one or more other therapeutic compounds. In yet another embodiment, the invention features a method for reducing or preventing tissue rejection in a subject comprising administering to the
5 subject a composition of the invention under conditions suitable for the reduction or prevention of tissue rejection in the subject.

In another embodiment, the invention features a method for validating a BACE gene target, comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence
10 complementary to RNA of a BACE target gene; (b) introducing the siNA molecule into a cell, tissue, or organism under conditions suitable for modulating expression of the BACE target gene in the cell, tissue, or organism; and (c) determining the function of the gene by assaying for any phenotypic change in the cell, tissue, or organism.

In another embodiment, the invention features a method for validating a BACE
15 target comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of a BACE target gene; (b) introducing the siNA molecule into a biological system under conditions suitable for modulating expression of the BACE target gene in the biological system; and (c) determining the function of the gene by
20 assaying for any phenotypic change in the biological system.

By "biological system" is meant, material, in a purified or unpurified form, from biological sources, including but not limited to human, animal, plant, insect, bacterial, viral or other sources, wherein the system comprises the components required for RNAi activity. The term "biological system" includes, for example, a cell, tissue, or organism,
25 or extract thereof. The term biological system also includes reconstituted RNAi systems that can be used in an *in vitro* setting.

By "phenotypic change" is meant any detectable change to a cell that occurs in response to contact or treatment with a nucleic acid molecule of the invention (e.g., siNA). Such detectable changes include, but are not limited to, changes in shape, size,
30 proliferation, motility, protein expression or RNA expression or other physical or chemical changes as can be assayed by methods known in the art. The detectable change

can also include expression of reporter genes/molecules such as Green Florescent Protein (GFP) or various tags that are used to identify an expressed protein or any other cellular component that can be assayed.

5 In one embodiment, the invention features a kit containing a siNA molecule of the invention, which can be chemically-modified, that can be used to modulate the expression of a BACE target gene in a cell, tissue, or organism. In another embodiment, the invention features a kit containing more than one siNA molecule of the invention, which can be chemically-modified, that can be used to modulate the expression of more than one BACE target gene in a cell, tissue, or organism.

10 In one embodiment, the invention features a cell containing one or more siNA molecules of the invention, which can be chemically-modified. In another embodiment, the cell containing a siNA molecule of the invention is a mammalian cell. In yet another embodiment, the cell containing a siNA molecule of the invention is a human cell.

In one embodiment, the synthesis of a siNA molecule of the invention, which can
15 be chemically-modified, comprises: (a) synthesis of two complementary strands of the siNA molecule; (b) annealing the two complementary strands together under conditions suitable to obtain a double-stranded siNA molecule. In another embodiment, synthesis of the two complementary strands of the siNA molecule is by solid phase oligonucleotide synthesis. In yet another embodiment, synthesis of the two complementary strands of the
20 siNA molecule is by solid phase tandem oligonucleotide synthesis.

In one embodiment, the invention features a method for synthesizing a siNA duplex molecule comprising: (a) synthesizing a first oligonucleotide sequence strand of the siNA molecule, wherein the first oligonucleotide sequence strand comprises a
25 cleavable linker molecule that can be used as a scaffold for the synthesis of the second oligonucleotide sequence strand of the siNA; (b) synthesizing the second oligonucleotide sequence strand of siNA on the scaffold of the first oligonucleotide sequence strand, wherein the second oligonucleotide sequence strand further comprises a chemical moiety that can be used to purify the siNA duplex; (c) cleaving the linker molecule of (a) under conditions suitable for the two siNA oligonucleotide strands to hybridize and form a
30 stable duplex; and (d) purifying the siNA duplex utilizing the chemical moiety of the second oligonucleotide sequence strand. In one embodiment, cleavage of the linker

molecule in (c) above takes place during deprotection of the oligonucleotide, for example under hydrolysis conditions using an alkylamine base such as methylamine. In one embodiment, the method of synthesis comprises solid phase synthesis on a solid support such as controlled pore glass (CPG) or polystyrene, wherein the first sequence of (a) is
5 synthesized on a cleavable linker, such as a succinyl linker, using the solid support as a scaffold. The cleavable linker in (a) used as a scaffold for synthesizing the second strand can comprise similar reactivity as the solid support derivatized linker, such that cleavage of the solid support derivatized linker and the cleavable linker of (a) takes place concomitantly. In another embodiment, the chemical moiety of (b) that can be used to
10 isolate the attached oligonucleotide sequence comprises a trityl group, for example a dimethoxytrityl group, which can be employed in a trityl-on synthesis strategy as described herein. In yet another embodiment, the chemical moiety, such as a dimethoxytrityl group, is removed during purification, for example, using acidic conditions.

15 In a further embodiment, the method for siNA synthesis is a solution phase synthesis or hybrid phase synthesis wherein both strands of the siNA duplex are synthesized in tandem using a cleavable linker attached to the first sequence which acts a scaffold for synthesis of the second sequence. Cleavage of the linker under conditions suitable for hybridization of the separate siNA sequence strands results in formation of
20 the double-stranded siNA molecule.

In another embodiment, the invention features a method for synthesizing a siNA duplex molecule comprising: (a) synthesizing one oligonucleotide sequence strand of the siNA molecule, wherein the sequence comprises a cleavable linker molecule that can be used as a scaffold for the synthesis of another oligonucleotide sequence; (b)
25 synthesizing a second oligonucleotide sequence having complementarity to the first sequence strand on the scaffold of (a), wherein the second sequence comprises the other strand of the double-stranded siNA molecule and wherein the second sequence further comprises a chemical moiety than can be used to isolate the attached oligonucleotide sequence; (c) purifying the product of (b) utilizing the chemical moiety of the second
30 oligonucleotide sequence strand under conditions suitable for isolating the full-length sequence comprising both siNA oligonucleotide strands connected by the cleavable linker and under conditions suitable for the two siNA oligonucleotide strands to

hybridize and form a stable duplex. In one embodiment, cleavage of the linker molecule in (c) above takes place during deprotection of the oligonucleotide, for example under hydrolysis conditions. In another embodiment, cleavage of the linker molecule in (c) above takes place after deprotection of the oligonucleotide. In another embodiment, the method of synthesis comprises solid phase synthesis on a solid support such as controlled pore glass (CPG) or polystyrene, wherein the first sequence of (a) is synthesized on a cleavable linker, such as a succinyl linker, using the solid support as a scaffold. The cleavable linker in (a) used as a scaffold for synthesizing the second strand can comprise similar reactivity or differing reactivity as the solid support derivatized linker, such that cleavage of the solid support derivatized linker and the cleavable linker of (a) takes place either concomitantly or sequentially. In one embodiment, the chemical moiety of (b) that can be used to isolate the attached oligonucleotide sequence comprises a trityl group, for example a dimethoxytrityl group.

In another embodiment, the invention features a method for making a double-stranded siNA molecule in a single synthetic process comprising: (a) synthesizing an oligonucleotide having a first and a second sequence, wherein the first sequence is complementary to the second sequence, and the first oligonucleotide sequence is linked to the second sequence via a cleavable linker, and wherein a terminal 5'-protecting group, for example, a 5'-O-dimethoxytrityl group (5'-O-DMT) remains on the oligonucleotide having the second sequence; (b) deprotecting the oligonucleotide whereby the deprotection results in the cleavage of the linker joining the two oligonucleotide sequences; and (c) purifying the product of (b) under conditions suitable for isolating the double-stranded siNA molecule, for example using a trityl-on synthesis strategy as described herein.

In another embodiment, the method of synthesis of siNA molecules of the invention comprises the teachings of Scaringe *et al.*, US Patent Nos. 5,889,136; 6,008,400; and 6,111,086, incorporated by reference herein in their entirety.

In one embodiment, the invention features siNA constructs that mediate RNAi against a BACE, wherein the siNA construct comprises one or more chemical modifications, for example, one or more chemical modifications having any of Formulae

I-VII or any combination thereof that increases the nuclease resistance of the siNA construct.

5 In another embodiment, the invention features a method for generating siNA molecules with increased nuclease resistance comprising (a) introducing nucleotides having any of Formulae I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased nuclease resistance.

10 In one embodiment, the invention features siNA constructs that mediate RNAi against a BACE, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the sense and antisense strands of the siNA construct.

15 In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the sense and antisense strands of the siNA molecule comprising (a) introducing nucleotides having any of Formulae I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the sense and antisense strands of the siNA molecule.

20 In one embodiment, the invention features siNA constructs that mediate RNAi against a BACE, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the antisense strand of the siNA construct and a complementary target RNA sequence within a cell.

25 In one embodiment, the invention features siNA constructs that mediate RNAi against a BACE, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the antisense strand of the siNA construct and a complementary target DNA sequence within a cell.

30 In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the antisense strand of the siNA molecule and a complementary target RNA sequence comprising (a) introducing nucleotides having any of Formulae I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for

isolating siNA molecules having increased binding affinity between the antisense strand of the siNA molecule and a complementary target RNA sequence.

5 In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the antisense strand of the siNA molecule and a complementary target DNA sequence comprising (a) introducing nucleotides having any of Formulae I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the antisense strand of the siNA molecule and a complementary target DNA sequence.

10 In one embodiment, the invention features siNA constructs that mediate RNAi against a BACE, wherein the siNA construct comprises one or more chemical modifications described herein that modulate the polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to the chemically-modified siNA construct.

15 In another embodiment, the invention features a method for generating siNA molecules capable of mediating increased polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to a chemically-modified siNA molecule comprising (a) introducing nucleotides having any of Formulae I-VII or any combination thereof into a siNA molecule, and (b)
20 assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules capable of mediating increased polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to the chemically-modified siNA molecule.

25 In one embodiment, the invention features chemically-modified siNA constructs that mediate RNAi against a BACE in a cell, wherein the chemical modifications do not significantly effect the interaction of siNA with a target RNA molecule, DNA molecule and/or proteins or other factors that are essential for RNAi in a manner that would decrease the efficacy of RNAi mediated by such siNA constructs.

30 In another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against BACE comprising (a) introducing

nucleotides having any of Formulae I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved RNAi activity.

5 In yet another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against a BACE target RNA comprising (a) introducing nucleotides having any of Formulae I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved RNAi activity against the target RNA.

10 In yet another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against a BACE target DNA comprising (a) introducing nucleotides having any of Formulae I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved RNAi activity against the target DNA.

15 In one embodiment, the invention features siNA constructs that mediate RNAi against a BACE, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the cellular uptake of the siNA construct.

20 In another embodiment, the invention features a method for generating siNA molecules against BACE with improved cellular uptake comprising (a) introducing nucleotides having any of Formulae I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved cellular uptake.

25 In one embodiment, the invention features siNA constructs that mediate RNAi against a BACE, wherein the siNA construct comprises one or more chemical modifications described herein that increases the bioavailability of the siNA construct, for example, by attaching polymeric conjugates such as polyethyleneglycol or equivalent conjugates that improve the pharmacokinetics of the siNA construct, or by attaching conjugates that target specific tissue types or cell types *in vivo*. Non-limiting examples of such conjugates are described in Vargeese *et al.*, U.S. Serial No. 10/201,394 incorporated by reference herein.

In one embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability, comprising (a) introducing a conjugate into the structure of a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved
5 bioavailability. Such conjugates can include ligands for cellular receptors, such as peptides derived from naturally occurring protein ligands; protein localization sequences, including cellular ZIP code sequences; antibodies; nucleic acid aptamers; vitamins and other co-factors, such as folate and N-acetylgalactosamine; polymers, such as polyethyleneglycol (PEG); phospholipids; polyamines, such as spermine or spermidine;
10 and others.

In another embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability comprising (a) introducing an excipient formulation to a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved bioavailability.
15 Such excipients include polymers such as cyclodextrins, lipids, cationic lipids, polyamines, phospholipids, and others.

In another embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability comprising (a) introducing nucleotides having any of Formulae I-VII or any combination thereof into a siNA
20 molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved bioavailability.

In another embodiment, polyethylene glycol (PEG) can be covalently attached to siNA compounds of the present invention. The attached PEG can be any molecular weight, preferably from about 2,000 to about 50,000 daltons (Da).

25 The present invention can be used alone or as a component of a kit having at least one of the reagents necessary to carry out the *in vitro* or *in vivo* introduction of RNA to test samples and/or subjects. For example, preferred components of the kit include the siNA and a vehicle that promotes introduction of the siNA. Such a kit can also include instructions to allow a user of the kit to practice the invention.

The term "short interfering nucleic acid", "siNA", "short interfering RNA", "siRNA", "short interfering nucleic acid molecule", "short interfering oligonucleotide molecule", or "chemically-modified short interfering nucleic acid molecule" as used herein refers to any nucleic acid molecule capable of mediating RNA interference

5 ("RNAi") or gene silencing in a sequence-specific manner; see for example Bass, 2001, *Nature*, 411, 428-429; Elbashir *et al.*, 2001, *Nature*, 411, 494-498; and Kreutzer *et al.*, International PCT Publication No. WO 00/44895; Zernicka-Goetz *et al.*, International PCT Publication No. WO 01/36646; Fire, International PCT Publication No. WO 99/32619; Plaetinck *et al.*, International PCT Publication No. WO 00/01846; Mello and

10 Fire, International PCT Publication No. WO 01/29058; Deschamps-Depaillette, International PCT Publication No. WO 99/07409; and Li *et al.*, International PCT Publication No. WO 00/44914; Allshire, 2002, *Science*, 297, 1818-1819; Volpe *et al.*, 2002, *Science*, 297, 1833-1837; Jenuwein, 2002, *Science*, 297, 2215-2218; and Hall *et al.*, 2002, *Science*, 297, 2232-2237; Hutvagner and Zamore, 2002, *Science*, 297, 2056-

15 60; McManus *et al.*, 2002, *RNA*, 8, 842-850; Reinhart *et al.*, 2002, *Gene & Dev.*, 16, 1616-1626; and Reinhart & Bartel, 2002, *Science*, 297, 1831). Non-limiting examples of siNA molecules of the invention are shown in **Figures 4-6**, and **Tables II and III** herein. For example the siNA can be a double-stranded polynucleotide molecule comprising self-complementary sense and antisense regions, wherein the antisense region comprises

20 nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The siNA can be assembled from two separate oligonucleotides, where one strand is the sense strand and the other is the antisense strand, wherein the antisense and sense strands are self-

25 complementary (i.e. each strand comprises nucleotide sequence that is complementary to nucleotide sequence in the other strand); the antisense strand comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense strand comprises nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. Alternatively, the siNA is

30 assembled from a single oligonucleotide, where the self-complementary sense and antisense regions of the siNA are linked by means of a nucleic acid based or non-nucleic acid-based linker(s). The siNA can be a polynucleotide with a hairpin secondary structure, having self-complementary sense and antisense regions, wherein the antisense

region comprises nucleotide sequence that is complementary to nucleotide sequence in a separate target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The siNA can be a circular single-stranded polynucleotide having two or more

5 loop structures and a stem comprising self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof, and wherein the circular polynucleotide can be processed either *in vivo*

10 or *in vitro* to generate an active siNA molecule capable of mediating RNAi. The siNA can also comprise a single stranded polynucleotide having nucleotide sequence complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof (for example, where such siNA molecule does not require the presence within the siNA molecule of nucleotide sequence corresponding to the target nucleic acid sequence

15 or a portion thereof), wherein the single stranded polynucleotide can further comprise a terminal phosphate group, such as a 5'-phosphate (see for example Martinez *et al.*, 2002, *Cell.*, 110, 563-574 and Schwarz *et al.*, 2002, *Molecular Cell*, 10, 537-568), or 5',3'-diphosphate. In certain embodiments, the siNA molecules of the invention comprise nucleotide sequence that is complementary to nucleotide sequence of a target gene. In

20 another embodiment, the siNA molecule of the invention interacts with nucleotide sequence of a target gene in a manner that causes inhibition of expression of the target gene. As used herein, siNA molecules need not be limited to those molecules containing only RNA, but further encompasses chemically-modified nucleotides and non-nucleotides. In certain embodiments, the short interfering nucleic acid molecules of the

25 invention lack 2'-hydroxy (2'-OH) containing nucleotides. Applicant describes in certain embodiments short interfering nucleic acids that do not require the presence of nucleotides having a 2'-hydroxy group for mediating RNAi and as such, short interfering nucleic acid molecules of the invention optionally do not include any ribonucleotides (e.g., nucleotides having a 2'-OH group). Such siNA molecules that do not require the

30 presence of ribonucleotides within the siNA molecule to support RNAi can however have an attached linker or linkers or other attached or associated groups, moieties, or chains containing one or more nucleotides with 2'-OH groups. Optionally, siNA molecules can comprise ribonucleotides at about 5, 10, 20, 30, 40, or 50% of the

nucleotide positions. The modified short interfering nucleic acid molecules of the invention can also be referred to as short interfering modified oligonucleotides "siMON." As used herein, the term siNA is meant to be equivalent to other terms used to describe nucleic acid molecules that are capable of mediating sequence specific RNAi, for example short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), short hairpin RNA (shRNA), short interfering oligonucleotide, short interfering nucleic acid, short interfering modified oligonucleotide, chemically-modified siRNA, post-transcriptional gene silencing RNA (ptgsRNA), and others. In addition, as used herein, the term RNAi is meant to be equivalent to other terms used to describe sequence specific RNA interference, such as post transcriptional gene silencing, or epigenetics. For example, siNA molecules of the invention can be used to epigenetically silence genes at both the post-transcriptional level or the pre-transcriptional level. In a non-limiting example, epigenetic regulation of gene expression by siNA molecules of the invention can result from siNA mediated modification of chromatin structure to alter gene expression (see, for example, Allshire, 2002, *Science*, 297, 1818-1819; Volpe *et al.*, 2002, *Science*, 297, 1833-1837; Jenuwein, 2002, *Science*, 297, 2215-2218; and Hall *et al.*, 2002, *Science*, 297, 2232-2237).

By "modulate" is meant that the expression of the gene, or level of RNA molecule or equivalent RNA molecules encoding one or more proteins or protein subunits, or activity of one or more proteins or protein subunits is up regulated or down regulated, such that expression, level, or activity is greater than or less than that observed in the absence of the modulator. For example, the term "modulate" can mean "inhibit," but the use of the word "modulate" is not limited to this definition.

By "inhibit" it is meant that the activity of a gene expression product or level of RNAs or equivalent RNAs encoding one or more gene products is reduced below that observed in the absence of the nucleic acid molecule of the invention. In one embodiment, inhibition with a siNA molecule preferably is below that level observed in the presence of an inactive or attenuated molecule that is unable to mediate an RNAi response. In another embodiment, inhibition of gene expression with the siNA molecule of the instant invention is greater in the presence of the siNA molecule than in its absence.

By "gene" or "target gene" is meant, a nucleic acid that encodes an RNA, for example, nucleic acid sequences including, but not limited to, structural genes encoding a polypeptide. The target gene can be a gene derived from a cell, an endogenous gene, a transgene, or exogenous genes such as genes of a pathogen, for example a virus, which is present in the cell after infection thereof. The cell containing the target gene can be derived from or contained in any organism, for example a plant, animal, protozoan, virus, bacterium, or fungus. Non-limiting examples of plants include monocots, dicots, or gymnosperms. Non-limiting examples of animals include vertebrates or invertebrates. Non-limiting examples of fungi include molds or yeasts.

10 By "BACE" or "beta secretase" as used herein is meant, any protein, peptide, or polypeptide, having beta-secretase activity, such as that involved in generating beta-amyloid. The term BACE also refers to nucleotide sequences that encode BACE protein.

By "APP" or "amyloid precursor protein" as used herein is meant, any protein, peptide, or polypeptide, that is processed to generate beta-amyloid. The term APP also refers to nucleotide sequences that encode amyloid precursor protein.

15 By "presenillin" or "PS", eg "PS-1" or "PS-2" as used herein is meant, any protein, peptide, or polypeptide having gamma-secretase activity, such as that involved in generating beta-amyloid. The term presenillin also refers to nucleotide sequences that encode presenillin protein, eg PS-1 or PS-2.

20 By "PIN-1" as used herein is meant, any protein, peptide, or polypeptide having peptidyl-prolyl cis/trans isomerase activity, such as that involved in the development of Neurofibrillary Tangles. The term PIN-1 also refers to nucleotide sequences that encode PIN-1 protein.

By "highly conserved sequence region" is meant, a nucleotide sequence of one or more regions in a target gene does not vary significantly from one generation to the other or from one biological system to the other.

By "sense region" is meant a nucleotide sequence of a siNA molecule having complementarity to an antisense region of the siNA molecule. In addition, the sense region of a siNA molecule can comprise a nucleic acid sequence having homology with a target nucleic acid sequence.

By "antisense region" is meant a nucleotide sequence of a siNA molecule having complementarity to a target nucleic acid sequence. In addition, the antisense region of a siNA molecule can optionally comprise a nucleic acid sequence having complementarity to a sense region of the siNA molecule.

5 By "target nucleic acid" is meant any nucleic acid sequence whose expression or activity is to be modulated. The target nucleic acid can be DNA or RNA.

By "complementarity" is meant that a nucleic acid can form hydrogen bond(s) with another nucleic acid sequence by either traditional Watson-Crick or other non-traditional types. In reference to the nucleic molecules of the present invention, the binding free
 10 energy for a nucleic acid molecule with its complementary sequence is sufficient to allow the relevant function of the nucleic acid to proceed, e.g., RNAi activity. Determination of binding free energies for nucleic acid molecules is well known in the art (see, e.g., Turner *et al.*, 1987, *CSH Symp. Quant. Biol.* LII pp.123-133; Frier *et al.*, 1986, *Proc. Nat. Acad. Sci. USA* 83:9373-9377; Turner *et al.*, 1987, *J. Am. Chem. Soc.*
 15 109:3783-3785). A percent complementarity indicates the percentage of contiguous residues in a nucleic acid molecule that can form hydrogen bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g., 5, 6, 7, 8, 9, 10 out of 10 being 50%, 60%, 70%, 80%, 90%, and 100% complementary). "Perfectly complementary" means that all the contiguous residues of a nucleic acid sequence will hydrogen bond
 20 with the same number of contiguous residues in a second nucleic acid sequence.

The siRNA molecules of the invention represent a novel therapeutic approach to treat a variety of pathologic neurodegenerative indications and conditions, including Alzheimer's disease, dementia, stroke (CVA), and any other diseases or conditions that are related to the levels of BACE in a cell or tissue, alone or in combination with other
 25 therapies. The reduction of BACE expression (specifically BACE RNA levels) and thus reduction in the level of the respective protein relieves, to some extent, the symptoms of the disease or condition.

In one embodiment of the present invention, each sequence of a siNA molecule of the invention is independently about 18 to about 24 nucleotides in length, in specific
 30 embodiments about 18, 19, 20, 21, 22, 23, or 24 nucleotides in length. In another embodiment, the siNA duplexes of the invention independently comprise about 17 to

about 23 base pairs (*e.g.*, about 17, 18, 19, 20, 21, 22 or 23). In yet another embodiment, siNA molecules of the invention comprising hairpin or circular structures are about 35 to about 55 (*e.g.*, about 35, 40, 45, 50 or 55) nucleotides in length, or about 38 to about 44 (*e.g.*, 38, 39, 40, 41, 42, 43 or 44) nucleotides in length and comprising about 16 to about 22 (*e.g.*, about 16, 17, 18, 19, 20, 21 or 22) base pairs. Exemplary siNA molecules of the invention are shown in **Tables II and III** and **Figures 4 and 5**. Exemplary synthetic siNA molecules of the invention are shown in **Table III** and/or **Figures 4-5**.

As used herein "cell" is used in its usual biological sense, and does not refer to an entire multicellular organism, *e.g.*, specifically does not refer to a human. The cell can be present in an organism, *e.g.*, birds, plants and mammals such as humans, cows, sheep, apes, monkeys, swine, dogs, and cats. The cell can be prokaryotic (*e.g.*, bacterial cell) or eukaryotic (*e.g.*, mammalian or plant cell). The cell can be of somatic or germ line origin, totipotent or pluripotent, dividing or non-dividing. The cell can also be derived from or can comprise a gamete or embryo, a stem cell, or a fully differentiated cell.

The siNA molecules of the invention are added directly, or can be complexed with cationic lipids, packaged within liposomes, or otherwise delivered to target cells or tissues. The nucleic acid or nucleic acid complexes can be locally administered to relevant tissues *ex vivo*, or *in vivo* through injection, infusion pump or stent, with or without their incorporation in biopolymers. In particular embodiments, the nucleic acid molecules of the invention comprise sequences shown in **Tables II-III** and/or **Figures 4-5**. Examples of such nucleic acid molecules consist essentially of sequences defined in these tables and figures. Furthermore, the chemically modified constructs described in **Table IV** can be applied to any siNA sequence of the invention.

In another aspect, the invention provides mammalian cells containing one or more siNA molecules of this invention. The one or more siNA molecules can independently be targeted to the same or different sites.

By "RNA" is meant a molecule comprising at least one ribonucleotide residue. By "ribonucleotide" is meant a nucleotide with a hydroxyl group at the 2' position of a β -D-ribo-furanose moiety. The terms include double-stranded RNA, single-stranded RNA, isolated RNA such as partially purified RNA, essentially pure RNA, synthetic RNA, recombinantly produced RNA, as well as altered RNA that differs from naturally

occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides. Such alterations can include addition of non-nucleotide material, such as to the end(s) of the siNA or internally, for example at one or more nucleotides of the RNA. Nucleotides in the RNA molecules of the instant invention can also comprise non-
5 standard nucleotides, such as non-naturally occurring nucleotides or chemically synthesized nucleotides or deoxynucleotides. These altered RNAs can be referred to as analogs or analogs of naturally-occurring RNA.

By "subject" is meant an organism, which is a donor or recipient of explanted cells or the cells themselves. "Subject" also refers to an organism to which the nucleic acid
10 molecules of the invention can be administered. In one embodiment, a subject is a mammal or mammalian cells. In another embodiment, a subject is a human or human cells.

The term "phosphorothioate" as used herein refers to an internucleotide linkage having Formula I, wherein Z and/or W comprise a sulfur atom. Hence, the term
15 phosphorothioate refers to both phosphorothioate and phosphorodithioate internucleotide linkages.

The term "universal base" as used herein refers to nucleotide base analogs that form base pairs with each of the natural DNA/RNA bases with little discrimination between them. Non-limiting examples of universal bases include C-phenyl, C-naphthyl
20 and other aromatic derivatives, inosine, azole carboxamides, and nitroazole derivatives such as 3-nitropyrrole, 4-nitroindole, 5-nitroindole, and 6-nitroindole as known in the art (see for example Loakes, 2001, *Nucleic Acids Research*, 29, 2437-2447).

The term "acyclic nucleotide" as used herein refers to any nucleotide having an acyclic ribose sugar, for example where any of the ribose carbons (C1, C2, C3, C4, or
25 C5), are independently or in combination absent from the nucleotide.

The nucleic acid molecules of the instant invention, individually, or in combination or in conjunction with other drugs, can be used to treat diseases or conditions discussed herein (e.g., Alzheimer's disease and other neurodegenerative conditions). For example, to treat a particular disease or condition, the siNA molecules can be administered to a
30 subject or can be administered to other appropriate cells evident to those skilled in the

art, individually or in combination with one or more drugs under conditions suitable for the treatment.

In a further embodiment, the siNA molecules can be used in combination with other known treatments to treat conditions or diseases discussed above. For example, the described molecules could be used in combination with one or more known therapeutic agents to treat a disease or condition. Non-limiting examples of other therapeutic agents that can be readily combined with a siNA molecule of the invention are enzymatic nucleic acid molecules, allosteric nucleic acid molecules, antisense, decoy, or aptamer nucleic acid molecules, antibodies such as monoclonal antibodies, small molecules, and other organic and/or inorganic compounds including metals, salts and ions.

In one embodiment, the invention features an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the invention, in a manner which allows expression of the siNA molecule. For example, the vector can contain sequence(s) encoding both strands of a siNA molecule comprising a duplex. The vector can also contain sequence(s) encoding a single nucleic acid molecule that is self-complementary and thus forms a siNA molecule. Non-limiting examples of such expression vectors are described in Paul *et al.*, 2002, *Nature Biotechnology*, 19, 505; Miyagishi and Taira, 2002, *Nature Biotechnology*, 19, 497; Lee *et al.*, 2002, *Nature Biotechnology*, 19, 500; and Novina *et al.*, 2002, *Nature Medicine*, advance online publication doi:10.1038/nm725.

In another embodiment, the invention features a mammalian cell, for example, a human cell, including an expression vector of the invention.

In yet another embodiment, the expression vector of the invention comprises a sequence for a siNA molecule having complementarity to a RNA molecule referred to by a Genbank Accession numbers, for example Genbank Accession Nos. shown in **Table I**.

In one embodiment, an expression vector of the invention comprises a nucleic acid sequence encoding two or more siNA molecules, which can be the same or different.

In another aspect of the invention, siNA molecules that interact with target RNA molecules and down-regulate gene encoding target RNA molecules (for example target RNA molecules referred to by Genbank Accession numbers herein) are expressed from

transcription units inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. The recombinant vectors capable of expressing the siNA molecules can be delivered as described herein, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of siNA molecules. Such vectors can be repeatedly administered as necessary. Once expressed, the siNA molecules bind and down-regulate gene function or expression via RNA interference (RNAi). Delivery of siNA expressing vectors can be systemic, such as by intravenous or intramuscular administration, by administration to target cells ex-planted from a subject followed by reintroduction into the subject, or by any other means that would allow for introduction into the desired target cell.

By "vectors" is meant any nucleic acid- and/or viral-based technique used to deliver a desired nucleic acid.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a non-limiting example of a scheme for the synthesis of siNA molecules. The complementary siNA sequence strands, strand 1 and strand 2, are synthesized in tandem and are connected by a cleavable linkage, such as a nucleotide succinate or abasic succinate, which can be the same or different from the cleavable linker used for solid phase synthesis on a solid support. The synthesis can be either solid phase or solution phase, in the example shown, the synthesis is a solid phase synthesis. The synthesis is performed such that a protecting group, such as a dimethoxytrityl group, remains intact on the terminal nucleotide of the tandem oligonucleotide. Upon cleavage and deprotection of the oligonucleotide, the two siNA strands spontaneously hybridize to form a siNA duplex, which allows the purification of the duplex by utilizing the properties of the terminal protecting group, for example by applying a trityl on purification method wherein only duplexes/oligonucleotides with the terminal protecting group are isolated.

Figure 2 shows a MALDI-TOV mass spectrum of a purified siNA duplex synthesized by a method of the invention. The two peaks shown correspond to the predicted mass of the separate siNA sequence strands. This result demonstrates that the siNA duplex generated from tandem synthesis can be purified as a single entity using a simple trityl-on purification methodology.

Figure 3 shows a non-limiting proposed mechanistic representation of target RNA degradation involved in RNAi. Double-stranded RNA (dsRNA), which is generated by RNA-dependent RNA polymerase (RdRP) from foreign single-stranded RNA, for example viral, transposon, or other exogenous RNA, activates the DICER enzyme that in turn generates siNA duplexes. Alternately, synthetic or expressed siNA can be introduced directly into a cell by appropriate means. An active siNA complex forms which recognizes a target RNA, resulting in degradation of the target RNA by the RISC endonuclease complex or in the synthesis of additional RNA by RNA-dependent RNA polymerase (RdRP), which can activate DICER and result in additional siNA molecules, thereby amplifying the RNAi response.

Figure 4A-F shows non-limiting examples of chemically-modified siNA constructs of the present invention. In the figure, N stands for any nucleotide (adenosine, guanosine, cytosine, uridine, or optionally thymidine, for example thymidine can be substituted in the overhanging regions designated by parenthesis (N N)). Various modifications are shown for the sense and antisense strands of the siNA constructs.

Figure 4A: The sense strand comprises 21 nucleotides having four phosphorothioate 5'- and 3'-terminal internucleotide linkages, wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-O-methyl or 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and having one 3'-terminal phosphorothioate internucleotide linkage and four 5'-terminal phosphorothioate internucleotide linkages and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides,

which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein.

Figure 4B: The sense strand comprises 21 nucleotides wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-O-methyl or 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein.

Figure 4C: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-O-methyl or 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and having one 3'-terminal phosphorothioate internucleotide linkage and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein.

Figure 4D: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein and wherein and all purine nucleotides that may be present are 2'-deoxy nucleotides. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl

moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and having one 3'-terminal phosphorothioate internucleotide linkage and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein.

Figure 4E: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein.

Figure 4F: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and having one 3'-terminal phosphorothioate internucleotide linkage and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-deoxy nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand of constructs A-F comprise sequence complementary to any target nucleic acid sequence of the invention.

Figure 5A-F shows non-limiting examples of specific chemically-modified siNA sequences of the invention. **A-F** applies the chemical modifications described in **Figure 4A-F** to a BACE siNA sequence.

Figure 6 shows non-limiting examples of different siNA constructs of the invention. The examples shown (constructs 1, 2, and 3) have about 19 representative base pairs; however, different embodiments of the invention include any number of base pairs described herein. Bracketed regions represent nucleotide overhangs, for example comprising about 1, 2, 3, or 4 nucleotides in length, preferably about 2 nucleotides. Constructs 1 and 2 can be used independently for RNAi activity. Construct 2 can
 10 comprise a polynucleotide or non-nucleotide linker, which can optionally be designed as a biodegradable linker. In one embodiment, the loop structure shown in construct 2 can comprise a biodegradable linker that results in the formation of construct 1 *in vivo* and/or *in vitro*. In another example, construct 3 can be used to generate construct 2 under the same principle wherein a linker is used to generate the active siNA construct 2 *in vivo*
 15 and/or *in vitro*, which can optionally utilize another biodegradable linker to generate the active siNA construct 1 *in vivo* and/or *in vitro*. As such, the stability and/or activity of the siNA constructs can be modulated based on the design of the siNA construct for use *in vivo* or *in vitro* and/or *in vitro*.

Figure 7A-C is a diagrammatic representation of a scheme utilized in generating
 20 an expression cassette to generate siNA hairpin constructs.

Figure 7A: A DNA oligomer is synthesized with a 5'-restriction site (R1) sequence followed by a region having sequence identical (sense region of siNA) to a predetermined BACE target sequence, wherein the sense region comprises, for example, about 19, 20, 21, or 22 nucleotides (N) in length, which is followed by a loop sequence
 25 of defined sequence (X), comprising, for example, about 3 to about 10 nucleotides.

Figure 7B: The synthetic construct is then extended by DNA polymerase to generate a hairpin structure having self-complementary sequence that will result in a siNA transcript having specificity for a BACE target sequence and having self-complementary sense and antisense regions.

Figure 7C: The construct is heated (for example to about 95°C) to linearize the sequence, thus allowing extension of a complementary second DNA strand using a primer to the 3'-restriction sequence of the first strand. The double-stranded DNA is then inserted into an appropriate vector for expression in cells. The construct can be designed
 5 such that a 3'-terminal nucleotide overhang results from the transcription, for example by engineering restriction sites and/or utilizing a poly-U termination region as described in Paul *et al.*, 2002, *Nature Biotechnology*, 29, 505-508.

Figure 8A-C is a diagrammatic representation of a scheme utilized in generating an expression cassette to generate double-stranded siNA constructs.

10 **Figure 8A:** A DNA oligomer is synthesized with a 5'-restriction (R1) site sequence followed by a region having sequence identical (sense region of siNA) to a predetermined BACE target sequence, wherein the sense region comprises, for example, about 19, 20, 21, or 22 nucleotides (N) in length, and which is followed by a 3'-restriction site (R2) which is adjacent to a loop sequence of defined sequence (X).

15 **Figure 8B:** The synthetic construct is then extended by DNA polymerase to generate a hairpin structure having self-complementary sequence.

Figure 8C: The construct is processed by restriction enzymes specific to R1 and R2 to generate a double-stranded DNA which is then inserted into an appropriate vector for expression in cells. The transcription cassette is designed such that a U6 promoter
 20 region flanks each side of the dsDNA which generates the separate sense and antisense strands of the siNA. Poly T termination sequences can be added to the constructs to generate U overhangs in the resulting transcript.

Figure 9A-E is a diagrammatic representation of a method used to determine target sites for siNA mediated RNAi within a particular target nucleic acid sequence,
 25 such as messenger RNA.

Figure 9A: A pool of siNA oligonucleotides are synthesized wherein the antisense region of the siNA constructs has complementarity to target sites across the target nucleic acid sequence, and wherein the sense region comprises sequence complementary to the antisense region of the siNA.

Figure 9B&C: (Figure 9B) The sequences are pooled and are inserted into vectors such that (Figure 9C) transfection of a vector into cells results in the expression of the siNA.

Figure 9D: Cells are sorted based on phenotypic change that is associated with modulation of the target nucleic acid sequence.

Figure 9E: The siNA is isolated from the sorted cells and is sequenced to identify efficacious target sites within the target nucleic acid sequence.

Figure 10 shows non-limiting examples of different stabilization chemistries (1-10) that can be used, for example, to stabilize the 3'-end of siNA sequences of the invention, including (1) [3'-3']-inverted deoxyribose; (2) deoxyribonucleotide; (3) [5'-3']-3'-deoxyribonucleotide; (4) [5'-3']-ribonucleotide; (5) [5'-3']-3'-O-methyl ribonucleotide; (6) 3'-glyceryl; (7) [3'-5']-3'-deoxyribonucleotide; (8) [3'-3']-deoxyribonucleotide; (9) [5'-2']-deoxyribonucleotide; and (10) [5'-3']-dideoxyribonucleotide. In addition to modified and unmodified backbone chemistries indicated in the figure, these chemistries can be combined with different backbone modifications as described herein, for example, backbone modifications having Formula I. In addition, the 2'-deoxy nucleotide shown 5' to the terminal modifications shown can be another modified or unmodified nucleotide or non-nucleotide described herein, for example modifications having any of Formulae I-VII or any combination thereof.

Figure 11 shows a non-limiting example of a strategy used to identify chemically modified siNA constructs of the invention that are nuclease resistance while preserving the ability to mediate RNAi activity. Chemical modifications are introduced into the siNA construct based on educated design parameters (e.g. introducing 2'-modifications, base modifications, backbone modifications, terminal cap modifications etc). The modified construct is tested in an appropriate system (e.g. human serum for nuclease resistance, shown, or an animal model for PK/delivery parameters). In parallel, the siNA construct is tested for RNAi activity, for example in a cell culture system such as a luciferase reporter assay). Lead siNA constructs are then identified which possess a particular characteristic while maintaining RNAi activity, and can be further modified and assayed once again. This same approach can be used to identify siNA-conjugate molecules with improved pharmacokinetic profiles, delivery, and RNAi activity.

Figure 12 shows a non-limiting example of reduction of BACE mRNA in A549 cells mediated by siNAs that target BACE mRNA. A549 cells were transfected with 0.25 ug/well of lipid complexed with 25 nM siNA. A screen of siNA constructs comprising ribonucleotides and 3'-terminal dithymidine caps was compared to untreated cells, scrambled siNA control constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in the figure, all of the siNA constructs show significant reduction of BACE RNA expression.

DETAILED DESCRIPTION OF THE INVENTION

Mechanism of action of Nucleic Acid Molecules of the Invention

The discussion that follows discusses the proposed mechanism of RNA interference mediated by short interfering RNA as is presently known, and is not meant to be limiting and is not an admission of prior art. Applicant demonstrates herein that chemically-modified short interfering nucleic acids possess similar or improved capacity to mediate RNAi as do siRNA molecules and are expected to possess improved stability and activity *in vivo*; therefore, this discussion is not meant to be limiting only to siRNA and can be applied to siNA as a whole. By "improved capacity to mediate RNAi" or "improved RNAi activity" is meant to include RNAi activity measured *in vitro* and/or *in vivo* where the RNAi activity is a reflection of both the ability of the siNA to mediate RNAi and the stability of the siNAs of the invention. In this invention, the product of these activities can be increased *in vitro* and/or *in vivo* compared to an all RNA siRNA or a siNA containing a plurality of ribonucleotides. In some cases, the activity or stability of the siNA molecule can be decreased (i.e., less than ten-fold), but the overall activity of the siNA molecule is enhanced *in vitro* and/or *in vivo*.

RNA interference refers to the process of sequence specific post-transcriptional gene silencing in animals mediated by short interfering RNAs (siRNAs) (Fire *et al.*, 1998, *Nature*, 391, 806). The corresponding process in plants is commonly referred to as post-transcriptional gene silencing or RNA silencing and is also referred to as quelling in fungi. The process of post-transcriptional gene silencing is thought to be an evolutionarily-conserved cellular defense mechanism used to prevent the expression of foreign genes which is commonly shared by diverse flora and phyla (Fire *et al.*, 1999, *Trends Genet.*, 15, 358). Such protection from foreign gene expression may have

evolved in response to the production of double-stranded RNAs (dsRNAs) derived from viral infection or the random integration of transposon elements into a host genome via a cellular response that specifically destroys homologous single-stranded RNA or viral genomic RNA. The presence of dsRNA in cells triggers the RNAi response though a
5 mechanism that has yet to be fully characterized. This mechanism appears to be different from the interferon response that results from dsRNA-mediated activation of protein kinase PKR and 2', 5'-oligoadenylate synthetase resulting in non-specific cleavage of mRNA by ribonuclease L.

The presence of long dsRNAs in cells stimulates the activity of a ribonuclease III
10 enzyme referred to as Dicer. Dicer is involved in the processing of the dsRNA into short pieces of dsRNA known as short interfering RNAs (siRNAs) (Bernstein *et al.*, 2001, *Nature*, 409, 363). Short interfering RNAs derived from Dicer activity are typically about 21 to about 23 nucleotides in length and comprise about 19 base pair duplexes. Dicer has also been implicated in the excision of 21- and 22-nucleotide small temporal
15 RNAs (siRNAs) from precursor RNA of conserved structure that are implicated in translational control (Hutvagner *et al.*, 2001, *Science*, 293, 834). The RNAi response also features an endonuclease complex containing a siRNA, commonly referred to as an RNA-induced silencing complex (RISC), which mediates cleavage of single-stranded RNA having sequence homologous to the siRNA. Cleavage of the target RNA takes
20 place in the middle of the region complementary to the guide sequence of the siRNA duplex (Elbashir *et al.*, 2001, *Genes Dev.*, 15, 188). In addition, RNA interference can also involve small RNA (e.g., micro-RNA or miRNA) mediated gene silencing, presumably through cellular mechanisms that regulate chromatin structure and thereby prevent transcription of target gene sequences (see for example Allshire, 2002, *Science*,
25 297, 1818-1819; Volpe *et al.*, 2002, *Science*, 297, 1833-1837; Jenuwein, 2002, *Science*, 297, 2215-2218; and Hall *et al.*, 2002, *Science*, 297, 2232-2237). As such, siRNA molecules of the invention can be used to mediate gene silencing via interaction with RNA transcripts or alternately by interaction with particular gene sequences, wherein such interaction results in gene silencing either at the transcriptional level or post-
30 transcriptional level.

RNAi has been studied in a variety of systems. Fire *et al.*, 1998, *Nature*, 391, 806, were the first to observe RNAi in *C. elegans*. Wianny and Goetz, 1999, *Nature Cell*

Biol., 2, 70, describe RNAi mediated by dsRNA in mouse embryos. Hammond *et al.*, 2000, *Nature*, 404, 293, describe RNAi in *Drosophila* cells transfected with dsRNA. Elbashir *et al.*, 2001, *Nature*, 411, 494, describe RNAi induced by introduction of duplexes of synthetic 21-nucleotide RNAs in cultured mammalian cells including human embryonic kidney and HeLa cells. Recent work in *Drosophila* embryonic lysates (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877) has revealed certain requirements for siRNA length, structure, chemical composition, and sequence that are essential to mediate efficient RNAi activity. These studies have shown that 21-nucleotide siRNA duplexes are most active when containing 3'-terminal dinucleotide overhangs. Furthermore, complete substitution of one or both siRNA strands with 2'-deoxy (2'-H) or 2'-O-methyl nucleotides abolishes RNAi activity, whereas substitution of the 3'-terminal siRNA overhang nucleotides with 2'-deoxy nucleotides (2'-H) was shown to be tolerated. Single mismatch sequences in the center of the siRNA duplex were also shown to abolish RNAi activity. In addition, these studies also indicate that the position of the cleavage site in the target RNA is defined by the 5'-end of the siRNA guide sequence rather than the 3'-end of the guide sequence (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877). Other studies have indicated that a 5'-phosphate on the target-complementary strand of a siRNA duplex is required for siRNA activity and that ATP is utilized to maintain the 5'-phosphate moiety on the siRNA (Nykanen *et al.*, 2001, *Cell*, 107, 309).

20 Synthesis of Nucleic acid Molecules

Synthesis of nucleic acids greater than 100 nucleotides in length is difficult using automated methods, and the therapeutic cost of such molecules is prohibitive. In this invention, small nucleic acid motifs ("small" refers to nucleic acid motifs no more than 100 nucleotides in length, preferably no more than 80 nucleotides in length, and most preferably no more than 50 nucleotides in length; *e.g.*, individual siNA oligonucleotide sequences or siNA sequences synthesized in tandem) are preferably used for exogenous delivery. The simple structure of these molecules increases the ability of the nucleic acid to invade targeted regions of protein and/or RNA structure. Exemplary molecules of the instant invention are chemically synthesized, and others can similarly be synthesized.

30 Oligonucleotides (*e.g.*, certain modified oligonucleotides or portions of oligonucleotides lacking ribonucleotides) are synthesized using protocols known in the art, for example as described in Caruthers *et al.*, 1992, *Methods in Enzymology* 211, 3-

19, Thompson *et al.*, International PCT Publication No. WO 99/54459, Wincott *et al.*, 1995, *Nucleic Acids Res.* 23, 2677-2684, Wincott *et al.*, 1997, *Methods Mol. Bio.*, 74, 59, Brennan *et al.*, 1998, *Biotechnol Bioeng.*, 61, 33-45, and Brennan, U.S. Pat. No. 6,001,311. All of these references are incorporated herein by reference. The synthesis of

5 oligonucleotides makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 μ mol scale protocol with a 2.5 min coupling step for 2'-O-methylated nucleotides and a 45 sec coupling step for 2'-deoxy nucleotides or 2'-deoxy-

10 2'-fluoro nucleotides. **Table V** outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 μ mol scale can be performed on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal modification to the cycle. A 33-fold excess (60 μ L of 0.11 M = 6.6 μ mol) of 2'-O-methyl phosphoramidite and a 105-fold excess of S-ethyl

15 tetrazole (60 μ L of 0.25 M = 15 μ mol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'-hydroxyl. A 22-fold excess (40 μ L of 0.11 M = 4.4 μ mol) of deoxy phosphoramidite and a 70-fold excess of S-ethyl tetrazole (40 μ L of 0.25 M = 10 μ mol) can be used in each coupling cycle of deoxy residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems,

20 Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include the following: detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% *N*-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); and oxidation solution

25 is 16.9 mM I_2 , 49 mM pyridine, 9% water in THF (PERSEPTIVE™). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide,

30 0.05 M in acetonitrile) is used.

Deprotection of the DNA-based oligonucleotides is performed as follows: the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial

and suspended in a solution of 40% aq. methylamine (1 mL) at 65 °C for 10 min. After cooling to -20 °C, the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H₂O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants,
 5 containing the oligoribonucleotide, are dried to a white powder.

The method of synthesis used for RNA including certain siNA molecules of the invention follows the procedure as described in Usman *et al.*, 1987, *J. Am. Chem. Soc.*, 109, 7845; Scaringe *et al.*, 1990, *Nucleic Acids Res.*, 18, 5433; and Wincott *et al.*, 1995, *Nucleic Acids Res.* 23, 2677-2684 Wincott *et al.*, 1997, *Methods Mol. Bio.*, 74, 59, and
 10 makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 µmol scale protocol with a 7.5 min coupling step for alkylsilyl protected nucleotides and a 2.5 min coupling step for 2'-O-methylated nucleotides.
 15 **Table V** outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 µmol scale can be done on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal modification to the cycle. A 33-fold excess (60 µL of 0.11 M = 6.6 µmol) of 2'-O-methyl phosphoramidite and a 75-fold excess of S-ethyl tetrazole (60 µL of 0.25 M = 15
 20 µmol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'-hydroxyl. A 66-fold excess (120 µL of 0.11 M = 13.2 µmol) of alkylsilyl (ribo) protected phosphoramidite and a 150-fold excess of S-ethyl tetrazole (120 µL of 0.25 M = 30 µmol) can be used in each coupling cycle of ribo residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically
 25 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include the following: detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% *N*-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); oxidation solution is 16.9 mM I₂,
 30 49 mM pyridine, 9% water in THF (PERSEPTIVE™). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International

Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide 0.05 M in acetonitrile) is used.

Deprotection of the RNA is performed using either a two-pot or one-pot protocol. For the two-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aq. methylamine (1 mL) at 65 °C for 10 min. After cooling to -20 °C, the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H₂O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, are dried to a white powder. The base deprotected oligoribonucleotide is resuspended in anhydrous TEA/HF/NMP solution (300 µL of a solution of 1.5 mL N-methylpyrrolidinone, 750 µL TEA and 1 mL TEA•3HF to provide a 1.4 M HF concentration) and heated to 65 °C. After 1.5 h, the oligomer is quenched with 1.5 M NH₄HCO₃.

Alternatively, for the one-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 33% ethanolic methylamine/DMSO: 1/1 (0.8 mL) at 65 °C for 15 min. The vial is brought to rt. TEA•3HF (0.1 mL) is added and the vial is heated at 65 °C for 15 min. The sample is cooled at -20 °C and then quenched with 1.5 M NH₄HCO₃.

For purification of the trityl-on oligomers, the quenched NH₄HCO₃ solution is loaded onto a C-18 containing cartridge that had been pre-washed with acetonitrile followed by 50 mM TEAA. After washing the loaded cartridge with water, the RNA is detritylated with 0.5% TFA for 13 min. The cartridge is then washed again with water, salt exchanged with 1 M NaCl and washed with water again. The oligonucleotide is then eluted with 30% acetonitrile.

The average stepwise coupling yields are typically >98% (Wincott *et al.*, 1995 *Nucleic Acids Res.* 23, 2677-2684). Those of ordinary skill in the art will recognize that the scale of synthesis can be adapted to be larger or smaller than the example described above including but not limited to 96-well format.

Alternatively, the nucleic acid molecules of the present invention can be synthesized separately and joined together post-synthetically, for example, by ligation

(Moore *et al.*, 1992, *Science* 256, 9923; Draper *et al.*, International PCT publication No. WO 93/23569; Shabarova *et al.*, 1991, *Nucleic Acids Research* 19, 4247; Bellon *et al.*, 1997, *Nucleosides & Nucleotides*, 16, 951; Bellon *et al.*, 1997, *Bioconjugate Chem.* 8, 204), or by hybridization following synthesis and/or deprotection.

5 The siNA molecules of the invention can also be synthesized via a tandem synthesis methodology as described in Example 1 herein, wherein both siNA strands are synthesized as a single contiguous oligonucleotide fragment or strand separated by a cleavable linker which is subsequently cleaved to provide separate siNA fragments or strands that hybridize and permit purification of the siNA duplex. The linker can be a
10 polynucleotide linker or a non-nucleotide linker. The tandem synthesis of siNA as described herein can be readily adapted to both multiwell/multiplate synthesis platforms such as 96 well or similarly larger multi-well platforms. The tandem synthesis of siNA as described herein can also be readily adapted to large scale synthesis platforms employing batch reactors, synthesis columns and the like.

15 A siNA molecule can also be assembled from two distinct nucleic acid strands or fragments wherein one fragment comprises the sense region and the second fragment comprises the antisense region of the RNA molecule.

 The nucleic acid molecules of the present invention can be modified extensively to enhance stability by modification with nuclease resistant groups, for example, 2'-amino,
20 2'-C-allyl, 2'-fluoro, 2'-O-methyl, 2'-H (for a review see Usman and Cedergren, 1992, *TIBS* 17, 34; Usman *et al.*, 1994, *Nucleic Acids Symp. Ser.* 31, 163). siNA constructs can be purified by gel electrophoresis using general methods or can be purified by high pressure liquid chromatography (HPLC; see Wincott *et al.*, *supra*, the totality of which is hereby incorporated herein by reference) and re-suspended in water.

25 In another aspect of the invention, siNA molecules of the invention are expressed from transcription units inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. The recombinant vectors capable of expressing the siNA molecules can be delivered as
30 described herein, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of siNA molecules.

Optimizing Activity of the nucleic acid molecule of the invention.

Chemically synthesizing nucleic acid molecules with modifications (base, sugar and/or phosphate) can prevent their degradation by serum ribonucleases, which can increase their potency (see *e.g.*, Eckstein *et al.*, International Publication No. WO 92/07065; Perrault *et al.*, 1990 *Nature* 344, 565; Pieken *et al.*, 1991, *Science* 253, 314; Usman and Cedergren, 1992, *Trends in Biochem. Sci.* 17, 334; Usman *et al.*, International Publication No. WO 93/15187; and Rossi *et al.*, International Publication No. WO 91/03162; Sproat, U.S. Pat. No. 5,334,711; Gold *et al.*, U.S. Pat No. 6,300,074; and Burgin *et al.*, *supra*; all of which are incorporated by reference herein). All of the above
 5 references describe various chemical modifications that can be made to the base, phosphate and/or sugar moieties of the nucleic acid molecules described herein. Modifications that enhance their efficacy in cells, and removal of bases from nucleic acid molecules to shorten oligonucleotide synthesis times and reduce chemical requirements are desired.

There are several examples in the art describing sugar, base and phosphate
 15 modifications that can be introduced into nucleic acid molecules with significant enhancement in their nuclease stability and efficacy. For example, oligonucleotides are modified to enhance stability and/or enhance biological activity by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-fluoro, 2'-O-methyl, 2'-
 20 O-allyl, 2'-H, nucleotide base modifications (for a review see Usman and Cedergren, 1992, *TIBS* 17, 34; Usman *et al.*, 1994, *Nucleic Acids Symp. Ser.* 31, 163; Burgin *et al.*, 1996, *Biochemistry*, 35, 14090). Sugar modification of nucleic acid molecules have been extensively described in the art (see Eckstein *et al.*, International Publication PCT No. WO 92/07065; Perrault *et al.*, *Nature*, 1990, 344, 565-568; Pieken *et al.*, *Science*, 1991,
 25 254, 314-317; Usman and Cedergren, *Trends in Biochem. Sci.*, 1992, 17, 334-339; Usman *et al.*, International Publication PCT No. WO 93/15187; Sproat, U.S. Pat. No. 5,334,711 and Beigelman *et al.*, 1995, *J. Biol. Chem.*, 270, 25702; Beigelman *et al.*, International PCT Publication No. WO 97/26270; Beigelman *et al.*, U.S. Pat No. 5,716,824; Usman *et al.*, U.S. Pat No. 5,627,053; Woolf *et al.*, International PCT Publication No. WO
 30 98/13526; Thompson *et al.*, Karpeisky *et al.*, 1998, *Tetrahedron Lett.*, 39, 1131; Earnshaw and Gait, 1998, *Biopolymers (Nucleic Acid Sciences)*, 48, 39-55; Verma and Eckstein, 1998, *Annu.*

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Rev. Biochem., 67, 99-134; and Burlina *et al.*, 1997, *Bioorg. Med. Chem.*, 5, 1999-2010; all of the references are hereby incorporated in their totality by reference herein). Such publications describe general methods and strategies to determine the location of incorporation of sugar, base and/or phosphate modifications and the like into nucleic acid molecules without modulating catalysis, and are incorporated by reference herein. In view of such teachings, similar modifications can be used as described herein to modify the siNA nucleic acid molecules of the instant invention so long as the ability of siNA to promote RNAi in cells is not significantly inhibited.

While chemical modification of oligonucleotide internucleotide linkages with phosphorothioate, phosphorodithioate, and/or 5'-methylphosphonate linkages improves stability, excessive modifications can cause some toxicity or decreased activity. Therefore, when designing nucleic acid molecules, the amount of these internucleotide linkages should be minimized. The reduction in the concentration of these linkages should lower toxicity, resulting in increased efficacy and higher specificity of these molecules.

Short interfering nucleic acid (siNA) molecules having chemical modifications that maintain or enhance activity are provided. Such a nucleic acid is also generally more resistant to nucleases than an unmodified nucleic acid. Accordingly, the *in vitro* and/or *in vivo* activity should not be significantly lowered. In cases in which modulation is the goal, therapeutic nucleic acid molecules delivered exogenously should optimally be stable within cells until translation of the target RNA has been modulated long enough to reduce the levels of the undesirable protein. This period of time varies between hours to days depending upon the disease state. Improvements in the chemical synthesis of RNA and DNA (Wincott *et al.*, 1995, *Nucleic Acids Res.* 23, 2677; Caruthers *et al.*, 1992, *Methods in Enzymology* 211,3-19 (incorporated by reference herein)) have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability, as described above.

In one embodiment, nucleic acid molecules of the invention include one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) G-clamp nucleotides. A G-clamp nucleotide is a modified cytosine analog wherein the modifications confer the ability to hydrogen bond both Watson-Crick and Hoogsteen faces of a complementary guanine

within a duplex, see for example Lin and Matteucci, 1998, *J. Am. Chem. Soc.*, 120, 8531-8532. A single G-clamp analog substitution within an oligonucleotide can result in substantially enhanced helical thermal stability and mismatch discrimination when hybridized to complementary oligonucleotides. The inclusion of such nucleotides in
5 nucleic acid molecules of the invention results in both enhanced affinity and specificity to nucleic acid targets, complementary sequences, or template strands. In another embodiment, nucleic acid molecules of the invention include one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) LNA "locked nucleic acid" nucleotides such as a 2', 4'-C methylene bicyclo nucleotide (see for example Wengel *et al.*, International PCT
10 Publication No. WO 00/66604 and WO 99/14226).

In another embodiment, the invention features conjugates and/or complexes of siNA molecules of the invention. Such conjugates and/or complexes can be used to facilitate delivery of siNA molecules into a biological system, such as a cell. The conjugates and complexes provided by the instant invention can impart therapeutic
15 activity by transferring therapeutic compounds across cellular membranes, altering the pharmacokinetics, and/or modulating the localization of nucleic acid molecules of the invention. The present invention encompasses the design and synthesis of novel conjugates and complexes for the delivery of molecules, including, but not limited to, small molecules, lipids, phospholipids, nucleosides, nucleotides, nucleic acids,
20 antibodies, toxins, negatively charged polymers and other polymers, for example proteins, peptides, hormones, carbohydrates, polyethylene glycols, or polyamines, across cellular membranes. In general, the transporters described are designed to be used either individually or as part of a multi-component system, with or without degradable linkers. These compounds are expected to improve delivery and/or localization of nucleic acid
25 molecules of the invention into a number of cell types originating from different tissues, in the presence or absence of serum (see Sullenger and Cech, U.S. Pat. No. 5,854,038). Conjugates of the molecules described herein can be attached to biologically active molecules via linkers that are biodegradable, such as biodegradable nucleic acid linker molecules.

30 The term "biodegradable linker" as used herein, refers to a nucleic acid or non-nucleic acid linker molecule that is designed as a biodegradable linker to connect one molecule to another molecule, for example, a biologically active molecule to a siNA

molecule of the invention or the sense and antisense strands of a siNA molecule of the invention. The biodegradable linker is designed such that its stability can be modulated for a particular purpose, such as delivery to a particular tissue or cell type. The stability of a nucleic acid-based biodegradable linker molecule can be modulated by using various

5 chemistries, for example combinations of ribonucleotides, deoxyribonucleotides, and chemically-modified nucleotides, such as 2'-O-methyl, 2'-fluoro, 2'-amino, 2'-O-amino, 2'-C-allyl, 2'-O-allyl, and other 2'-modified or base modified nucleotides. The biodegradable nucleic acid linker molecule can be a dimer, trimer, tetramer or longer nucleic acid molecule, for example, an oligonucleotide of about 2, 3, 4, 5, 6, 7, 8, 9, 10,

10 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides in length, or can comprise a single nucleotide with a phosphorus-based linkage, for example, a phosphoramidate or phosphodiester linkage. The biodegradable nucleic acid linker molecule can also comprise nucleic acid backbone, nucleic acid sugar, or nucleic acid base modifications.

The term "biodegradable" as used herein, refers to degradation in a biological

15 system, for example enzymatic degradation or chemical degradation.

The term "biologically active molecule" as used herein, refers to compounds or molecules that are capable of eliciting or modifying a biological response in a system. Non-limiting examples of biologically active siNA molecules either alone or in combination with other molecules contemplated by the instant invention include

20 therapeutically active molecules such as antibodies, hormones, antivirals, peptides, proteins, chemotherapeutics, small molecules, vitamins, co-factors, nucleosides, nucleotides, oligonucleotides, enzymatic nucleic acids, antisense nucleic acids, triplex forming oligonucleotides, 2,5-A chimeras, siNA, dsRNA, allozymes, aptamers, decoys and analogs thereof. Biologically active molecules of the invention also include

25 molecules capable of modulating the pharmacokinetics and/or pharmacodynamics of other biologically active molecules, for example, lipids and polymers such as polyamines, polyamides, polyethylene glycol and other polyethers.

The term "phospholipid" as used herein, refers to a hydrophobic molecule comprising at least one phosphorus group. For example, a phospholipid can comprise a

30 phosphorus-containing group and saturated or unsaturated alkyl group, optionally substituted with OH, COOH, oxo, amine, or substituted or unsubstituted aryl groups.

Therapeutic nucleic acid molecules (*e.g.*, siNA molecules) delivered exogenously optimally are stable within cells until reverse transcription of the RNA has been modulated long enough to reduce the levels of the RNA transcript. The nucleic acid molecules are resistant to nucleases in order to function as effective intracellular
5 therapeutic agents. Improvements in the chemical synthesis of nucleic acid molecules described in the instant invention and in the art have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability as described above.

In yet another embodiment, siNA molecules having chemical modifications that
10 maintain or enhance enzymatic activity of proteins involved in RNAi are provided. Such nucleic acids are also generally more resistant to nucleases than unmodified nucleic acids. Thus, *in vitro* and/or *in vivo* the activity should not be significantly lowered.

Use of the nucleic acid-based molecules of the invention will lead to better treatment of the disease progression by affording the possibility of combination therapies
15 (*e.g.*, multiple siNA molecules targeted to different genes; nucleic acid molecules coupled with known small molecule modulators; or intermittent treatment with combinations of molecules, including different motifs and/or other chemical or biological molecules). The treatment of subjects with siNA molecules can also include combinations of different types of nucleic acid molecules, such as enzymatic nucleic acid
20 molecules (ribozymes), allozymes, antisense, 2,5-A oligoadenylate, decoys, and aptamers.

In another aspect a siNA molecule of the invention comprises one or more 5' and/or a 3'-cap structure, for example on only the sense siNA strand, the antisense siNA strand, or both siNA strands.

By "cap structure" is meant chemical modifications, which have been incorporated
25 at either terminus of the oligonucleotide (see, for example, Adamic *et al.*, U.S. Pat. No. 5,998,203, incorporated by reference herein). These terminal modifications protect the nucleic acid molecule from exonuclease degradation, and may help in delivery and/or localization within a cell. The cap may be present at the 5'-terminus (5'-cap) or at the 3'-
30 terminal (3'-cap) or may be present on both termini. In non-limiting examples, the 5'-cap is selected from the group consisting of glyceryl, inverted deoxy abasic residue (moiety);

4',5'-methylene nucleotide; 1-(beta-D-erythrofuransyl) nucleotide, 4'-thio nucleotide; carbocyclic nucleotide; 1,5-anhydrohexitol nucleotide; L-nucleotides; alpha-nucleotides; modified base nucleotide; phosphorodithioate linkage; *threo*-pentofuransyl nucleotide; acyclic 3',4'-seco nucleotide; acyclic 3,4-dihydroxybutyl nucleotide; acyclic 3,5-dihydroxypentyl nucleotide, 3'-3'-inverted nucleotide moiety; 3'-3'-inverted abasic moiety; 3'-2'-inverted nucleotide moiety; 3'-2'-inverted abasic moiety; 1,4-butanediol phosphate; 3'-phosphoramidate; hexylphosphate; aminohexyl phosphate; 3'-phosphate; 3'-phosphorothioate; phosphorodithioate; or bridging or non-bridging methylphosphonate moiety.

10 In non-limiting examples, the 3'-cap is selected from the group consisting of glyceryl, inverted deoxy abasic residue (moiety), 4',5'-methylene nucleotide; 1-(beta-D-erythrofuransyl) nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propyl phosphate; 3-aminopropyl phosphate; 6-aminohexyl phosphate; 1,2-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol
15 nucleotide; L-nucleotide; alpha-nucleotide; modified base nucleotide; phosphorodithioate; *threo*-pentofuransyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide, 5'-5'-inverted nucleotide moiety; 5'-5'-inverted abasic moiety; 5'-phosphoramidate; 5'-phosphorothioate; 1,4-butanediol phosphate; 5'-amino; bridging and/or non-bridging 5'-phosphoramidate,
20 phosphorothioate and/or phosphorodithioate, bridging or non bridging methylphosphonate and 5'-mercapto moieties (for more details see Beaucage and Iyer, 1993, *Tetrahedron* 49, 1925; incorporated by reference herein).

By the term "non-nucleotide" is meant any group or compound which can be incorporated into a nucleic acid chain in the place of one or more nucleotide units,
25 including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound is abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine and therefore lacks a base at the 1'-position.

An "alkyl" group refers to a saturated aliphatic hydrocarbon, including straight-chain, branched-chain, and cyclic alkyl groups. Preferably, the alkyl group has 1 to 12
30 carbons. More preferably, it is a lower alkyl of from 1 to 7 carbons, more preferably 1 to

4 carbons. The alkyl group can be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO₂ or N(CH₃)₂, amino, or SH. The term also includes alkenyl groups that are unsaturated hydrocarbon groups containing at least one carbon-carbon double bond, including straight-chain, 5 branched-chain, and cyclic groups. Preferably, the alkenyl group has 1 to 12 carbons. More preferably, it is a lower alkenyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkenyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO₂, halogen, N(CH₃)₂, amino, or SH. The term "alkyl" also includes alkynyl groups that have an 10 unsaturated hydrocarbon group containing at least one carbon-carbon triple bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkynyl group has 1 to 12 carbons. More preferably, it is a lower alkynyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkynyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, 15 -S, NO₂ or N(CH₃)₂, amino or SH.

Such alkyl groups can also include aryl, alkylaryl, carbocyclic aryl, heterocyclic aryl, amide and ester groups. An "aryl" group refers to an aromatic group that has at least one ring having a conjugated pi electron system and includes carbocyclic aryl, heterocyclic aryl and biaryl groups, all of which may be optionally substituted. The 20 preferred substituent(s) of aryl groups are halogen, trihalomethyl, hydroxyl, SH, OH, cyano, alkoxy, alkyl, alkenyl, alkynyl, and amino groups. An "alkylaryl" group refers to an alkyl group (as described above) covalently joined to an aryl group (as described above). Carbocyclic aryl groups are groups wherein the ring atoms on the aromatic ring are all carbon atoms. The carbon atoms are optionally substituted. Heterocyclic aryl 25 groups are groups having from 1 to 3 heteroatoms as ring atoms in the aromatic ring and the remainder of the ring atoms are carbon atoms. Suitable heteroatoms include oxygen, sulfur, and nitrogen, and include furanyl, thienyl, pyridyl, pyrrolyl, N-lower alkyl pyrrolo, pyrimidyl, pyrazinyl, imidazolyl and the like, all optionally substituted. An "amide" refers to an -C(O)-NH-R, where R is either alkyl, aryl, alkylaryl or hydrogen. 30 An "ester" refers to an -C(O)-OR', where R is either alkyl, aryl, alkylaryl or hydrogen.

By "nucleotide" as used herein is as recognized in the art to include natural bases (standard), and modified bases well known in the art. Such bases are generally located at

the 1' position of a nucleotide sugar moiety. Nucleotides generally comprise a base, sugar and a phosphate group. The nucleotides can be unmodified or modified at the sugar, phosphate and/or base moiety, (also referred to interchangeably as nucleotide analogs, modified nucleotides, non-natural nucleotides, non-standard nucleotides and
 5 other; see, for example, Usman and McSwiggen, *supra*; Eckstein *et al.*, International PCT Publication No. WO 92/07065; Usman *et al.*, International PCT Publication No. WO 93/15187; Uhlman & Peyman, *supra*, all are hereby incorporated by reference herein). There are several examples of modified nucleic acid bases known in the art as summarized by Limbach *et al.*, 1994, *Nucleic Acids Res.* 22, 2183. Some of the non-
 10 limiting examples of base modifications that can be introduced into nucleic acid molecules include, inosine, purine, pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2, 4, 6-trimethoxy benzene, 3-methyl uracil, dihydrouridine, naphthyl, aminophenyl, 5-alkylcytidines (*e.g.*, 5-methylcytidine), 5-alkyluridines (*e.g.*, ribothymidine), 5-halouridine (*e.g.*, 5-bromouridine) or 6-azapyrimidines or 6-alkylpyrimidines (*e.g.* 6-
 15 methyluridine), propyne, and others (Burgin *et al.*, 1996, *Biochemistry*, 35, 14090; Uhlman & Peyman, *supra*). By "modified bases" in this aspect is meant nucleotide bases other than adenine, guanine, cytosine and uracil at 1' position or their equivalents.

In one embodiment, the invention features modified siNA molecules, with phosphate backbone modifications comprising one or more phosphorothioate, phosphorodithioate, methylphosphonate, phosphotriester, morpholino, amidate
 20 carbamate, carboxymethyl, acetamidate, polyamide, sulfonate, sulfonamide, sulfamate, formacetal, thioformacetal, and/or alkylsilyl, substitutions. For a review of oligonucleotide backbone modifications, see Hunziker and Leumann, 1995, *Nucleic Acid Analogues: Synthesis and Properties*, in *Modern Synthetic Methods*, VCH, 331-417, and
 25 Mesmacker *et al.*, 1994, *Novel Backbone Replacements for Oligonucleotides*, in *Carbohydrate Modifications in Antisense Research*, ACS, 24-39.

By "abasic" is meant sugar moieties lacking a base or having other chemical groups in place of a base at the 1' position, see for example Adamic *et al.*, U.S. Pat. No. 5,998,203.

30 By "unmodified nucleoside" is meant one of the bases adenine, cytosine, guanine, thymine, or uracil joined to the 1' carbon of β -D-ribo-furanose.

By "modified nucleoside" is meant any nucleotide base which contains a modification in the chemical structure of an unmodified nucleotide base, sugar and/or phosphate. Non-limiting examples of modified nucleotides are shown by Formulae I-VII and/or other modifications described herein.

5 In connection with 2'-modified nucleotides as described for the present invention, by "amino" is meant 2'-NH₂ or 2'-O- NH₂, which can be modified or unmodified. Such modified groups are described, for example, in Eckstein *et al.*, U.S. Pat. No. 5,672,695 and Matulic-Adamic *et al.*, U.S. Pat. No. 6,248,878, which are both incorporated by reference in their entireties.

10 Various modifications to nucleic acid siNA structure can be made to enhance the utility of these molecules. Such modifications will enhance shelf-life, half-life *in vitro*, stability, and ease of introduction of such oligonucleotides to the target site, *e.g.*, to enhance penetration of cellular membranes, and confer the ability to recognize and bind to targeted cells.

15 Administration of Nucleic Acid Molecules

A siNA molecule of the invention can be adapted for use to treat a variety of neurodegenerative diseases, including Alzheimer's disease, dementia, stroke (CVA), and any other diseases or conditions that are related to the levels of BACE in a cell or tissue, alone or in combination with other therapies. For example, a siNA molecule can
20 comprise a delivery vehicle, including liposomes, for administration to a subject, carriers and diluents and their salts, and/or can be present in pharmaceutically acceptable formulations. Methods for the delivery of nucleic acid molecules are described in Akhtar *et al.*, 1992, *Trends Cell Bio.*, 2, 139; *Delivery Strategies for Antisense Oligonucleotide Therapeutics*, ed. Akhtar, 1995, Maurer *et al.*, 1999, *Mol. Membr. Biol.*,
25 16, 129-140; Hofland and Huang, 1999, *Handb. Exp. Pharmacol.*, 137, 165-192; and Lee *et al.*, 2000, *ACS Symp. Ser.*, 752, 184-192, all of which are incorporated herein by reference. Beigelman *et al.*, U.S. Pat. No. 6,395,713 and Sullivan *et al.*, PCT WO 94/02595 further describe the general methods for delivery of nucleic acid molecules. These protocols can be utilized for the delivery of virtually any nucleic acid molecule.
30 Nucleic acid molecules can be administered to cells by a variety of methods known to those of skill in the art, including, but not restricted to, encapsulation in liposomes, by

iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins (see for example Gonzalez *et al.*, 1999, *Bioconjugate Chem.*, 10, 1068-1074), biodegradable nanocapsules, and bioadhesive microspheres, or by proteinaceous vectors (O'Hare and Normand, International PCT Publication No. WO 00/53722). Alternatively, 5 the nucleic acid/vehicle combination is locally delivered by direct injection or by use of an infusion pump. Direct injection of the nucleic acid molecules of the invention, whether subcutaneous, intramuscular, or intradermal, can take place using standard needle and syringe methodologies, or by needle-free technologies such as those described in Conry *et al.*, 1999, *Clin. Cancer Res.*, 5, 2330-2337 and Barry *et al.*, 10 International PCT Publication No. WO 99/31262. The molecules of the instant invention can be used as pharmaceutical agents. Pharmaceutical agents prevent, modulate the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state in a subject.

Thus, the invention features a pharmaceutical composition comprising one or more 15 nucleic acid(s) of the invention in an acceptable carrier, such as a stabilizer, buffer, and the like. The polynucleotides of the invention can be administered (*e.g.*, RNA, DNA or protein) and introduced into a subject by any standard means, with or without stabilizers, buffers, and the like, to form a pharmaceutical composition. When it is desired to use a liposome delivery mechanism, standard protocols for formation of liposomes can be 20 followed. The compositions of the present invention can also be formulated and used as tablets, capsules or elixirs for oral administration, suppositories for rectal administration, sterile solutions, suspensions for injectable administration, and the other compositions known in the art.

The present invention also includes pharmaceutically acceptable formulations of 25 the compounds described. These formulations include salts of the above compounds, *e.g.*, acid addition salts, for example, salts of hydrochloric, hydrobromic, acetic acid, and benzene sulfonic acid.

A pharmacological composition or formulation refers to a composition or formulation in a form suitable for administration, *e.g.*, systemic administration, into a 30 cell or subject, including for example a human. Suitable forms, in part, depend upon the use or the route of entry, for example oral, transdermal, or by injection. Such forms

should not prevent the composition or formulation from reaching a target cell (*i.e.*, a cell to which the negatively charged nucleic acid is desirable for delivery). For example, pharmacological compositions injected into the blood stream should be soluble. Other factors are known in the art, and include considerations such as toxicity and forms that prevent the composition or formulation from exerting its effect.

By "systemic administration" is meant *in vivo* systemic absorption or accumulation of drugs in the blood stream followed by distribution throughout the entire body. Administration routes that lead to systemic absorption include, without limitation: intravenous, subcutaneous, intraperitoneal, inhalation, oral, intrapulmonary and intramuscular. Each of these administration routes exposes the siNA molecules of the invention to an accessible diseased tissue. The rate of entry of a drug into the circulation has been shown to be a function of molecular weight or size. The use of a liposome or other drug carrier comprising the compounds of the instant invention can potentially localize the drug, for example, in certain tissue types, such as the tissues of the reticular endothelial system (RES). A liposome formulation that can facilitate the association of drug with the surface of cells, such as, lymphocytes and macrophages is also useful. This approach can provide enhanced delivery of the drug to target cells by taking advantage of the specificity of macrophage and lymphocyte immune recognition of abnormal cells, such as cells producing excess BACE.

By "pharmaceutically acceptable formulation" is meant, a composition or formulation that allows for the effective distribution of the nucleic acid molecules of the instant invention in the physical location most suitable for their desired activity. Non-limiting examples of agents suitable for formulation with the nucleic acid molecules of the instant invention include: P-glycoprotein inhibitors (such as Pluronic P85), which can enhance entry of drugs into the CNS (Joliet-Riant and Tillement, 1999, *Fundam. Clin. Pharmacol.*, 13, 16-26); biodegradable polymers, such as poly (DL-lactide-coglycolide) microspheres for sustained release delivery after intracerebral implantation (Emerich, DF *et al*, 1999, *Cell Transplant*, 8, 47-58) (Alkermes, Inc. Cambridge, MA); and loaded nanoparticles, such as those made of polybutylcyanoacrylate, which can deliver drugs across the blood brain barrier and can alter neuronal uptake mechanisms (*Prog Neuropsychopharmacol Biol Psychiatry*, 23, 941-949, 1999). Other non-limiting examples of delivery strategies for the nucleic acid molecules of the instant invention

include material described in Boado *et al.*, 1998, *J. Pharm. Sci.*, 87, 1308-1315; Tyler *et al.*, 1999, *FEBS Lett.*, 421, 280-284; Pardridge *et al.*, 1995, *PNAS USA.*, 92, 5592-5596; Boado, 1995, *Adv. Drug Delivery Rev.*, 15, 73-107; Aldrian-Herrada *et al.*, 1998, *Nucleic Acids Res.*, 26, 4910-4916; and Tyler *et al.*, 1999, *PNAS USA.*, 96, 7053-7058.

5 The invention also features the use of the composition comprising surface-modified liposomes containing poly (ethylene glycol) lipids (PEG-modified, or long-circulating liposomes or stealth liposomes). These formulations offer a method for increasing the accumulation of drugs in target tissues. This class of drug carriers resists opsonization and elimination by the mononuclear phagocytic system (MPS or RES),
10 thereby enabling longer blood circulation times and enhanced tissue exposure for the encapsulated drug (Lasic *et al. Chem. Rev.* 1995, 95, 2601-2627; Ishiwata *et al., Chem. Pharm. Bull.* 1995, 43, 1005-1011). Such liposomes have been shown to accumulate selectively in tumors, presumably by extravasation and capture in the neovascularized target tissues (Lasic *et al., Science* 1995, 267, 1275-1276; Oku *et al.*, 1995, *Biochim.*
15 *Biophys. Acta*, 1238, 86-90). The long-circulating liposomes enhance the pharmacokinetics and pharmacodynamics of DNA and RNA, particularly compared to conventional cationic liposomes which are known to accumulate in tissues of the MPS (Liu *et al., J. Biol. Chem.* 1995, 42, 24864-24870; Choi *et al.*, International PCT Publication No. WO 96/10391; Ansell *et al.*, International PCT Publication No. WO
20 96/10390; Holland *et al.*, International PCT Publication No. WO 96/10392). Long-circulating liposomes are also likely to protect drugs from nuclease degradation to a greater extent compared to cationic liposomes, based on their ability to avoid accumulation in metabolically aggressive MPS tissues such as the liver and spleen.

 The present invention also includes compositions prepared for storage or
25 administration that include a pharmaceutically effective amount of the desired compounds in a pharmaceutically acceptable carrier or diluent. Acceptable carriers or diluents for therapeutic use are well known in the pharmaceutical art, and are described, for example, in *Remington's Pharmaceutical Sciences*, Mack Publishing Co. (A.R. Gennaro edit. 1985), hereby incorporated by reference herein. For example,
30 preservatives, stabilizers, dyes and flavoring agents can be provided. These include sodium benzoate, sorbic acid and esters of *p*-hydroxybenzoic acid. In addition, antioxidants and suspending agents can be used.

A pharmaceutically effective dose is that dose required to prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state. The pharmaceutically effective dose depends on the type of disease, the composition used, the route of administration, the type of mammal being treated, the physical characteristics of the specific mammal under consideration, concurrent medication, and other factors that those skilled in the medical arts will recognize. Generally, an amount from about 0.1 mg/kg to about 100 mg/kg body weight/day of active ingredients is administered dependent upon potency of the negatively charged polymer.

The nucleic acid molecules of the invention and formulations thereof can be administered orally, topically, parenterally, by inhalation or spray, or rectally in dosage unit formulations containing conventional non-toxic pharmaceutically acceptable carriers, adjuvants and/or vehicles. The term parenteral as used herein includes percutaneous, subcutaneous, intravascular (e.g., intravenous), intramuscular, or intrathecal injection or infusion techniques and the like. In addition, there is provided a pharmaceutical formulation comprising a nucleic acid molecule of the invention and a pharmaceutically acceptable carrier. One or more nucleic acid molecules of the invention can be present in association with one or more non-toxic pharmaceutically acceptable carriers and/or diluents and/or adjuvants, and if desired other active ingredients. The pharmaceutical compositions containing nucleic acid molecules of the invention can be in a form suitable for oral use, for example, as tablets, troches, lozenges, aqueous or oily suspensions, dispersible powders or granules, emulsion, hard or soft capsules, or syrups or elixirs.

Compositions intended for oral use can be prepared according to any method known to the art for the manufacture of pharmaceutical compositions and such compositions can contain one or more such sweetening agents, flavoring agents, coloring agents or preservative agents in order to provide pharmaceutically elegant and palatable preparations. Tablets contain the active ingredient in admixture with non-toxic pharmaceutically acceptable excipients that are suitable for the manufacture of tablets. These excipients can be, for example, inert diluents; such as calcium carbonate, sodium carbonate, lactose, calcium phosphate or sodium phosphate; granulating and disintegrating agents, for example, corn starch, or alginic acid; binding agents, for

example starch, gelatin or acacia; and lubricating agents, for example magnesium stearate, stearic acid or talc. The tablets can be uncoated or they can be coated by known techniques. In some cases such coatings can be prepared by known techniques to delay disintegration and absorption in the gastrointestinal tract and thereby provide a sustained
5 action over a longer period. For example, a time delay material such as glyceryl monostearate or glyceryl distearate can be employed.

Formulations for oral use can also be presented as hard gelatin capsules wherein the active ingredient is mixed with an inert solid diluent, for example, calcium carbonate, calcium phosphate or kaolin, or as soft gelatin capsules wherein the active ingredient is
10 mixed with water or an oil medium, for example peanut oil, liquid paraffin or olive oil.

Aqueous suspensions contain the active materials in a mixture with excipients suitable for the manufacture of aqueous suspensions. Such excipients are suspending agents, for example sodium carboxymethylcellulose, methylcellulose, hydropropyl-methylcellulose, sodium alginate, polyvinylpyrrolidone, gum tragacanth and gum acacia;
15 dispersing or wetting agents can be a naturally-occurring phosphatide, for example, lecithin, or condensation products of an alkylene oxide with fatty acids, for example polyoxyethylene stearate, or condensation products of ethylene oxide with long chain aliphatic alcohols, for example heptadecaethyleneoxycetanol, or condensation products of ethylene oxide with partial esters derived from fatty acids and a hexitol such as
20 polyoxyethylene sorbitol monooleate, or condensation products of ethylene oxide with partial esters derived from fatty acids and hexitol anhydrides, for example polyethylene sorbitan monooleate. The aqueous suspensions can also contain one or more preservatives, for example ethyl, or n-propyl p-hydroxybenzoate, one or more coloring agents, one or more flavoring agents, and one or more sweetening agents, such as
25 sucrose or saccharin.

Oily suspensions can be formulated by suspending the active ingredients in a vegetable oil, for example arachis oil, olive oil, sesame oil or coconut oil, or in a mineral oil such as liquid paraffin. The oily suspensions can contain a thickening agent, for example beeswax, hard paraffin or cetyl alcohol. Sweetening agents and flavoring
30 agents can be added to provide palatable oral preparations. These compositions can be preserved by the addition of an anti-oxidant such as ascorbic acid

Dispersible powders and granules suitable for preparation of an aqueous suspension by the addition of water provide the active ingredient in admixture with a dispersing or wetting agent, suspending agent and one or more preservatives. Suitable dispersing or wetting agents or suspending agents are exemplified by those already
5 mentioned above. Additional excipients, for example sweetening, flavoring and coloring agents, can also be present.

Pharmaceutical compositions of the invention can also be in the form of oil-in-water emulsions. The oily phase can be a vegetable oil or a mineral oil or mixtures of these. Suitable emulsifying agents can be naturally-occurring gums, for example gum
10 acacia or gum tragacanth, naturally-occurring phosphatides, for example soy bean, lecithin, and esters or partial esters derived from fatty acids and hexitol, anhydrides, for example sorbitan monooleate, and condensation products of the said partial esters with ethylene oxide, for example polyoxyethylene sorbitan monooleate. The emulsions can also contain sweetening and flavoring agents.

Syrups and elixirs can be formulated with sweetening agents, for example glycerol,
15 propylene glycol, sorbitol, glucose or sucrose. Such formulations can also contain a demulcent, a preservative and flavoring and coloring agents. The pharmaceutical compositions can be in the form of a sterile injectable aqueous or oleaginous suspension. This suspension can be formulated according to the known art using those suitable
20 dispersing or wetting agents and suspending agents that have been mentioned above. The sterile injectable preparation can also be a sterile injectable solution or suspension in a non-toxic parentally acceptable diluent or solvent, for example as a solution in 1,3-butanediol. Among the acceptable vehicles and solvents that can be employed are water, Ringer's solution and isotonic sodium chloride solution. In addition, sterile, fixed oils
25 are conventionally employed as a solvent or suspending medium. For this purpose, any bland fixed oil can be employed including synthetic mono-or diglycerides. In addition, fatty acids such as oleic acid find use in the preparation of injectables.

The nucleic acid molecules of the invention can also be administered in the form of suppositories, *e.g.*, for rectal administration of the drug. These compositions can be
30 prepared by mixing the drug with a suitable non-irritating excipient that is solid at ordinary temperatures but liquid at the rectal temperature and will therefore melt in the

rectum to release the drug. Such materials include cocoa butter and polyethylene glycols.

Nucleic acid molecules of the invention can be administered parenterally in a sterile medium. The drug, depending on the vehicle and concentration used, can either
5 be suspended or dissolved in the vehicle. Advantageously, adjuvants such as local anesthetics, preservatives and buffering agents can be dissolved in the vehicle.

Dosage levels of the order of from about 0.1 mg to about 140 mg per kilogram of body weight per day are useful in the treatment of the above-indicated conditions (about 0.5 mg to about 7 g per subject per day). The amount of active ingredient that can be
10 combined with the carrier materials to produce a single dosage form varies depending upon the host treated and the particular mode of administration. Dosage unit forms generally contain about 1 mg to about 500 mg of an active ingredient.

It is understood that the specific dose level for any particular subject depends upon a variety of factors including the activity of the specific compound employed, the age,
15 body weight, general health, sex, diet, time of administration, route of administration, and rate of excretion, drug combination and the severity of the particular disease undergoing therapy.

For administration to non-human animals, the composition can also be added to the animal feed or drinking water. It can be convenient to formulate the animal feed and
20 drinking water compositions so that the animal takes in a therapeutically appropriate quantity of the composition along with its diet. It can also be convenient to present the composition as a premix for addition to the feed or drinking water.

The nucleic acid molecules of the present invention can also be administered to a subject in combination with other therapeutic compounds to increase the overall
25 therapeutic effect. The use of multiple compounds to treat an indication can increase the beneficial effects while reducing the presence of side effects.

In one embodiment, the invention provides compositions suitable for administering nucleic acid molecules of the invention to specific cell types. For example, the asialoglycoprotein receptor (ASGPr) (Wu and Wu, 1987, *J. Biol. Chem.* 262, 4429-4432)
30 is unique to hepatocytes and binds branched galactose-terminal glycoproteins, such as

asialoorosomucoid (ASOR). In another example, the folate receptor is overexpressed in many cancer cells. Binding of such glycoproteins, synthetic glycoconjugates, or folates to the receptor takes place with an affinity that strongly depends on the degree of branching of the oligosaccharide chain, for example, triantennary structures are bound with greater affinity than biantennary or monoantennary chains (Baenziger and Fiete, 1980, *Cell*, 22, 611-620; Connolly *et al.*, 1982, *J. Biol. Chem.*, 257, 939-945). Lee and Lee, 1987, *Glycoconjugate J.*, 4, 317-328, obtained this high specificity through the use of N-acetyl-D-galactosamine as the carbohydrate moiety, which has higher affinity for the receptor, compared to galactose. This "clustering effect" has also been described for the binding and uptake of mannosyl-terminating glycoproteins or glycoconjugates (Ponpipom *et al.*, 1981, *J. Med. Chem.*, 24, 1388-1395). The use of galactose, galactosamine, or folate based conjugates to transport exogenous compounds across cell membranes can provide a targeted delivery approach to, for example, the treatment of liver disease, cancers of the liver, or other cancers. The use of bioconjugates can also provide a reduction in the required dose of therapeutic compounds required for treatment. Furthermore, therapeutic bioavailability, pharmacodynamics, and pharmacokinetic parameters can be modulated through the use of nucleic acid bioconjugates of the invention. Non-limiting examples of such bioconjugates are described in Vargeese *et al.*, USSN 10/201,394, filed August 13, 2001; and Matulic-Adamic *et al.*, USSN 60/362,016, filed March 6, 2002.

Alternatively, certain siNA molecules of the instant invention can be expressed within cells from eukaryotic promoters (e.g., Izant and Weintraub, 1985, *Science*, 229, 345; McGarry and Lindquist, 1986, *Proc. Natl. Acad. Sci.*, USA 83, 399; Scanlon *et al.*, 1991, *Proc. Natl. Acad. Sci. USA*, 88, 10591-5; Kashani-Sabet *et al.*, 1992, *Antisense Res. Dev.*, 2, 3-15; Dropulic *et al.*, 1992, *J. Virol.*, 66, 1432-41; Weerasinghe *et al.*, 1991, *J. Virol.*, 65, 5531-4; Ojwang *et al.*, 1992, *Proc. Natl. Acad. Sci. USA*, 89, 10802-6; Chen *et al.*, 1992, *Nucleic Acids Res.*, 20, 4581-9; Sarver *et al.*, 1990 *Science*, 247, 1222-1225; Thompson *et al.*, 1995, *Nucleic Acids Res.*, 23, 2259; Good *et al.*, 1997, *Gene Therapy*, 4, 45. Those skilled in the art realize that any nucleic acid can be expressed in eukaryotic cells from the appropriate DNA/RNA vector. The activity of such nucleic acids can be augmented by their release from the primary transcript by an enzymatic nucleic acid (Draper *et al.*, PCT WO 93/23569, and Sullivan *et al.*, PCT WO 94/02595; Ohkawa *et al.*, 1992, *Nucleic Acids Symp. Ser.*, 27, 15-6; Taira *et al.*, 1991,

Nucleic Acids Res., 19, 5125-30; Ventura *et al.*, 1993, *Nucleic Acids Res.*, 21, 3249-55; Chowrira *et al.*, 1994, *J. Biol. Chem.*, 269, 25856.

In another aspect of the invention, RNA molecules of the present invention can be expressed from transcription units (see for example Couture *et al.*, 1996, *TIG.*, 12, 510) inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. In another embodiment, pol III based constructs are used to express nucleic acid molecules of the invention (see for example Thompson, U.S. Pats. Nos. 5,902,880 and 6,146,886). The recombinant vectors capable of expressing the siNA molecules can be delivered as described above, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of nucleic acid molecules. Such vectors can be repeatedly administered as necessary. Once expressed, the siNA molecule interacts with the target mRNA and generates an RNAi response. Delivery of siNA molecule expressing vectors can be systemic, such as by intravenous or intra-muscular administration, by administration to target cells ex-planted from a subject followed by reintroduction into the subject, or by any other means that would allow for introduction into the desired target cell (for a review see Couture *et al.*, 1996, *TIG.*, 12, 510).

In one aspect the invention features an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the instant invention. The expression vector can encode one or both strands of a siNA duplex, or a single self-complementary strand that self hybridizes into a siNA duplex. The nucleic acid sequences encoding the siNA molecules of the instant invention can be operably linked in a manner that allows expression of the siNA molecule (see for example Paul *et al.*, 2002, *Nature Biotechnology*, 19, 505; Miyagishi and Taira, 2002, *Nature Biotechnology*, 19, 497; Lee *et al.*, 2002, *Nature Biotechnology*, 19, 500; and Novina *et al.*, 2002, *Nature Medicine*, advance online publication doi:10.1038/nm725).

In another aspect, the invention features an expression vector comprising: a) a transcription initiation region (*e.g.*, eukaryotic pol I, II or III initiation region); b) a transcription termination region (*e.g.*, eukaryotic pol I, II or III termination region); and c) a nucleic acid sequence encoding at least one of the siNA molecules of the instant

invention wherein said sequence is operably linked to said initiation region and said termination region in a manner that allows expression and/or delivery of the siNA molecule. The vector can optionally include an open reading frame (ORF) for a protein operably linked on the 5' side or the 3'-side of the sequence encoding the siNA of the invention, and/or an intron (intervening sequences).

Transcription of the siNA molecule sequences can be driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters are expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type depends on the nature of the gene regulatory sequences (enhancers, silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters are also used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and Moss, 1990, *Proc. Natl. Acad. Sci. U S A*, 87, 6743-7; Gao and Huang 1993, *Nucleic Acids Res.*, 21, 2867-72; Lieber *et al.*, 1993, *Methods Enzymol.*, 217, 47-66; Zhou *et al.*, 1990, *Mol. Cell. Biol.*, 10, 4529-37). Several investigators have demonstrated that nucleic acid molecules expressed from such promoters can function in mammalian cells (e.g. Kashani-Sabet *et al.*, 1992, *Antisense Res. Dev.*, 2, 3-15; Ojwang *et al.*, 1992, *Proc. Natl. Acad. Sci. U S A*, 89, 10802-6; Chen *et al.*, 1992, *Nucleic Acids Res.*, 20, 4581-9; Yu *et al.*, 1993, *Proc. Natl. Acad. Sci. U S A*, 90, 6340-4; L'Huillier *et al.*, 1992, *EMBO J.*, 11, 4411-8; Lisiewicz *et al.*, 1993, *Proc. Natl. Acad. Sci. U. S. A*, 90, 8000-4; Thompson *et al.*, 1995, *Nucleic Acids Res.*, 23, 2259; Sullenger & Cech, 1993, *Science*, 262, 1566). More specifically, transcription units such as the ones derived from genes encoding U6 small nuclear (snRNA), transfer RNA (tRNA) and adenovirus VA RNA are useful in generating high concentrations of desired RNA molecules such as siNA in cells (Thompson *et al.*, *supra*; Couture and Stinchcomb, 1996, *supra*; Noonberg *et al.*, 1994, *Nucleic Acid Res.*, 22, 2830; Noonberg *et al.*, U.S. Pat. No. 5,624,803; Good *et al.*, 1997, *Gene Ther.*, 4, 45; Beigelman *et al.*, International PCT Publication No. WO 96/18736. The above siNA transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated virus vectors), or viral RNA vectors (such as retroviral or alphavirus vectors) (for a review see Couture and Stinchcomb, 1996, *supra*).

In another aspect the invention features an expression vector comprising a nucleic acid sequence encoding at least one of the siNA molecules of the invention in a manner that allows expression of that siNA molecule. The expression vector comprises in one embodiment; a) a transcription initiation region; b) a transcription termination region; and c) a nucleic acid sequence encoding at least one strand of the siNA molecule, wherein the sequence is operably linked to the initiation region and the termination region in a manner that allows expression and/or delivery of the siNA molecule.

In another embodiment the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an open reading frame; and d) a nucleic acid sequence encoding at least one strand of a siNA molecule, wherein the sequence is operably linked to the 3'-end of the open reading frame and wherein the sequence is operably linked to the initiation region, the open reading frame and the termination region in a manner that allows expression and/or delivery of the siNA molecule. In yet another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; and d) a nucleic acid sequence encoding at least one siNA molecule, wherein the sequence is operably linked to the initiation region, the intron and the termination region in a manner which allows expression and/or delivery of the nucleic acid molecule.

In another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; d) an open reading frame; and e) a nucleic acid sequence encoding at least one strand of a siNA molecule, wherein the sequence is operably linked to the 3'-end of the open reading frame and wherein the sequence is operably linked to the initiation region, the intron, the open reading frame and the termination region in a manner which allows expression and/or delivery of the siNA molecule.

BACE biology and biochemistry

Alzheimer's disease is characterized by the progressive formation of insoluble plaques and vascular deposits in the brain consisting of the 4 kD amyloid β peptide ($A\beta$). These plaques are characterized by dystrophic neurites that show profound synaptic loss, neurofibrillary tangle formation, and gliosis. $A\beta$ arises from the proteolytic cleavage of the large type I transmembrane protein, β -amyloid precursor protein (APP) (Kang *et al.*,

1987, *Nature*, 325, 733). Processing of APP to generate A β requires two sites of cleavage by a β -secretase and a γ -secretase. β -secretase cleavage of APP results in the cytoplasmic release of a 100 kD soluble amino-terminal fragment, APPs β , leaving behind a 12 kD transmembrane carboxy-terminal fragment, C99. Alternately, APP can
 5 be cleaved by a α -secretase to generate cytoplasmic APPs α and transmembrane C83 fragments. Both remaining transmembrane fragments, C99 and C83, can be further cleaved by a γ -secretase, leading to the release and secretion of Alzheimer's related A β and a non-pathogenic peptide, p3, respectively (Vassar *et al.*, 1999, *Science*, 286, 735-741). Early onset familial Alzheimer's disease is characterized by mutant APP protein
 10 with a Met to Leu substitution at position P1, characterized as the "Swedish" familial mutation (Mullan *et al.*, 1992, *Nature Genet.*, 1, 345). This APP mutation is characterized by a dramatic enhancement in β -secretase cleavage (Citron *et al.*, 1992, *Nature*, 360, 672).

The identification of β -secretase and γ -secretase constituents involved in the
 15 release of β -amyloid protein is of primary importance in the development of treatment strategies for Alzheimer's disease. Characterization of α -secretase is also important in this regard since α -secretase cleavage may compete with β -secretase cleavage resulting in changes in the relative amounts of non-pathogenic and pathogenic protein production. Involvement of the two metalloproteases, ADAM 10 and TACE, has been demonstrated
 20 in α -cleavage of AAP (Buxbaum *et al.*, 1999, *J. Biol. Chem.*, 273, 27765, and Lammich *et al.*, 1999, *Proc. Natl. Acad. Sci. U.S.A.*, 96, 3922). Studies of γ -secretase activity have demonstrated presenilin dependence (De Strooper *et al.*, 1998, *Nature*, 391, 387, and De Strooper *et al.*, 1999, *Nature*, 398, 518), and as such, presenilins have been proposed as γ -secretase even though presenilin does not present proteolytic activity (Wolfe *et al.*, 1999,
 25 *Nature*, 398, 513).

Studies have shown β -secretase cleavage of AAP by the transmembrane aspartic protease beta site APP cleaving enzyme, BACE (Vassar *et al.*, *supra*). While other potential candidates for β -secretase have been proposed (for review see Evin *et al.*, 1999, *Proc. Natl. Acad. Sci. U.S.A.*, 96, 3922), none have demonstrated the full range of
 30 characteristics expected from this enzyme. Studies have shown that BACE expression and localization are as expected for β -secretase, that BACE overexpression in cells

results in increased β -secretase cleavage of APP and Swedish APP, that isolated BACE demonstrates site specific proteolytic activity on APP derived peptide substrates, and that antisense mediated endogenous BACE inhibition results in dramatically reduced β -secretase activity (Vassar *et al.*, supra).

- 5 Current treatment strategies for Alzheimer's disease rely on either the prevention or the alleviation of symptoms and/or the slowing down of disease progression. Two drugs approved in the treatment of Alzheimer's, donepezil (Aricept®) and tacrine (Cognex®), both cholinomimetics, attempt to slow the loss of cognitive ability by increasing the amount of acetylcholine available to the brain. Antioxidant therapy
10 through the use of antioxidant compounds such as alpha-tocopherol (vitamin E), melatonin, and selegiline (Eldepryl®) attempt to slow disease progression by minimizing free radical damage. Estrogen replacement therapy is thought to incur a possible preventative benefit in the development of Alzheimer's disease based on limited data. The use of anti-inflammatory drugs may be associated with a reduced risk of
15 Alzheimer's as well. Calcium channel blockers such as Nimodipine® are considered to have a potential benefit in treating Alzheimer's disease due to protection of nerve cells from calcium overload, thereby prolonging nerve cell survival. Nootropic compounds, such as acetyl-L-carnitine (Alcar®) and insulin, have been proposed to have some benefit in treating Alzheimer's due to enhancement of cognitive and memory function
20 based on cellular metabolism.

- Whereby the above treatment strategies can all improve quality of life in Alzheimer's patients, there exists an unmet need in the comprehensive treatment and prevention of this disease. As such, there exists the need for therapeutics effective in reversing the physiological changes associated with Alzheimer's disease, specifically,
25 therapeutics that can eliminate and/or reverse the deposition of amyloid β peptide. The use of compounds, such as small nucleic acid molecules (e.g., short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules capable of mediating RNA interference (RNAi)), to modulate the expression of proteases that are instrumental in the
30 release of amyloid β peptide, namely β -secretase (BACE), γ -secretase (presenilin), and the amyloid precursor protein (APP), is of therapeutic significance.

Examples:

The following are non-limiting examples showing the selection, isolation, synthesis and activity of nucleic acids of the instant invention.

Example 1: Tandem synthesis of siNA constructs

5 Exemplary siNA molecules of the invention are synthesized in tandem using a cleavable linker, for example, a succinyl-based linker. Tandem synthesis as described herein is followed by a one-step purification process that provides RNAi molecules in high yield. This approach is highly amenable to siNA synthesis in support of high throughput RNAi screening, and can be readily adapted to multi-column or multi-well
10 synthesis platforms.

After completing a tandem synthesis of a siNA oligo and its complement in which the 5'-terminal dimethoxytrityl (5'-O-DMT) group remains intact (trityl on synthesis), the oligonucleotides are deprotected as described above. Following deprotection, the siNA sequence strands are allowed to spontaneously hybridize. This hybridization yields a
15 duplex in which one strand has retained the 5'-O-DMT group while the complementary strand comprises a terminal 5'-hydroxyl. The newly formed duplex behaves as a single molecule during routine solid-phase extraction purification (Trityl-On purification) even though only one molecule has a dimethoxytrityl group. Because the strands form a stable duplex, this dimethoxytrityl group (or an equivalent group, such as other trityl
20 groups or other hydrophobic moieties) is all that is required to purify the pair of oligos, for example, by using a C18 cartridge.

Standard phosphoramidite synthesis chemistry is used up to the point of introducing a tandem linker, such as an inverted deoxy abasic succinate or glyceryl succinate linker (see **Figure 1**) or an equivalent cleavable linker. A non-limiting
25 example of linker coupling conditions that can be used includes a hindered base such as diisopropylethylamine (DIPA) and/or DMAP in the presence of an activator reagent such as Bromotripyrrolidinophosphoniumhexafluorophosphate (PyBrOP). After the linker is coupled, standard synthesis chemistry is utilized to complete synthesis of the second sequence leaving the terminal the 5'-O-DMT intact. Following synthesis, the resulting

oligonucleotide is deprotected according to the procedures described herein and quenched with a suitable buffer, for example with 50mM NaOAc or 1.5M $\text{NH}_4\text{H}_2\text{CO}_3$.

Purification of the siNA duplex can be readily accomplished using solid phase extraction, for example using a Waters C18 SepPak 1g cartridge conditioned with 1 column volume (CV) of acetonitrile, 2 CV H_2O , and 2 CV 50mM NaOAc. The sample is loaded and then washed with 1 CV H_2O or 50mM NaOAc. Failure sequences are eluted with 1 CV 14% ACN (Aqueous with 50mM NaOAc and 50mM NaCl). The column is then washed, for example with 1 CV H_2O followed by on-column detritylation, for example by passing 1 CV of 1% aqueous trifluoroacetic acid (TFA) over the column, then adding a second CV of 1% aqueous TFA to the column and allowing to stand for approximately 10 minutes. The remaining TFA solution is removed and the column washed with H_2O followed by 1 CV 1M NaCl and additional H_2O . The siNA duplex product is then eluted, for example, using 1 CV 20% aqueous CAN.

Figure 2 provides an example of MALDI-TOV mass spectrometry analysis of a purified siNA construct in which each peak corresponds to the calculated mass of an individual siNA strand of the siNA duplex. The same purified siNA provides three peaks when analyzed by capillary gel electrophoresis (CGE), one peak presumably corresponding to the duplex siNA, and two peaks presumably corresponding to the separate siNA sequence strands. Ion exchange HPLC analysis of the same siNA construct only shows a single peak. Testing of the purified siNA construct using a luciferase reporter assay described below demonstrated the same RNAi activity compared to siNA constructs generated from separately synthesized oligonucleotide sequence strands.

Example 2: Identification of potential siNA target sites in any RNA sequence

The sequence of an RNA target of interest, such as a viral or human mRNA transcript, is screened for target sites, for example by using a computer folding algorithm. In a non-limiting example, the sequence of a gene or RNA gene transcript derived from a database, such as Genbank, is used to generate siNA targets having complementarity to the target. Such sequences can be obtained from a database, or can be determined experimentally as known in the art. Target sites that are known, for example, those target sites determined to be effective target sites based on studies with

other nucleic acid molecules, for example ribozymes or antisense, or those targets known to be associated with a disease or condition such as those sites containing mutations or deletions, can be used to design siNA molecules targeting those sites. Various parameters can be used to determine which sites are the most suitable target sites within the target RNA sequence. These parameters include but are not limited to secondary or tertiary RNA structure, the nucleotide base composition of the target sequence, the degree of homology between various regions of the target sequence, or the relative position of the target sequence within the RNA transcript. Based on these determinations, any number of target sites within the RNA transcript can be chosen to screen siNA molecules for efficacy, for example by using *in vitro* RNA cleavage assays, cell culture, or animal models. In a non-limiting example, anywhere from 1 to 1000 target sites are chosen within the transcript based on the size of the siNA construct to be used. High throughput screening assays can be developed for screening siNA molecules using methods known in the art, such as with multi-well or multi-plate assays to determine efficient reduction in target gene expression.

Example 3: Selection of siNA molecule target sites in a RNA

The following non-limiting steps can be used to carry out the selection of siNAs targeting a given gene sequence or transcript.

1. The target sequence is parsed *in silico* into a list of all fragments or subsequences of a particular length, for example 23 nucleotide fragments, contained within the target sequence. This step is typically carried out using a custom Perl script, but commercial sequence analysis programs such as Oligo, MacVector, or the GCG Wisconsin Package can be employed as well.
2. In some instances the siNAs correspond to more than one target sequence; such would be the case for example in targeting different transcripts of the same gene, targeting different transcripts of more than one gene, or for targeting both the human gene and an animal homolog. In this case, a subsequence list of a particular length is generated for each of the targets, and then the lists are compared to find matching sequences in each list. The subsequences are then ranked according to the number of target sequences that contain the given subsequence; the goal is to find subsequences that are present in most or all of the target sequences. Alternately, the ranking can

identify subsequences that are unique to a target sequence, such as a mutant target sequence. Such an approach would enable the use of siNA to target specifically the mutant sequence and not effect the expression of the normal sequence.

3. In some instances the siNA subsequences are absent in one or more sequences while
5 present in the desired target sequence; such would be the case if the siNA targets a gene with a paralogous family member that is to remain untargeted. As in case 2 above, a subsequence list of a particular length is generated for each of the targets, and then the lists are compared to find sequences that are present in the target gene but are absent in the untargeted paralog.
- 10 4. The ranked siNA subsequences can be further analyzed and ranked according to GC content. A preference can be given to sites containing 30-70% GC, with a further preference to sites containing 40-60% GC.
5. The ranked siNA subsequences can be further analyzed and ranked according to self-folding and internal hairpins. Weaker internal folds are preferred; strong hairpin
15 structures are to be avoided.
6. The ranked siNA subsequences can be further analyzed and ranked according to whether they have runs of GGG or CCC in the sequence. GGG (or even more Gs) in either strand can make oligonucleotide synthesis problematic and can potentially interfere with RNAi activity, so it is avoided whenever better sequences are
20 available. CCC is searched in the target strand because that will place GGG in the antisense strand.
7. The ranked siNA subsequences can be further analyzed and ranked according to whether they have the dinucleotide UU (uridine dinucleotide) on the 3'-end of the sequence, and/or AA on the 5'-end of the sequence (to yield 3' UU on the antisense
25 sequence). These sequences allow one to design siNA molecules with terminal TT thymidine dinucleotides.
8. Four or five target sites are chosen from the ranked list of subsequences as described above. For example, in subsequences having 23 nucleotides, the right 21 nucleotides of each chosen 23-mer subsequence are then designed and synthesized for the upper
30 (sense) strand of the siNA duplex, while the reverse complement of the left 21

nucleotides of each chosen 23-mer subsequence are then designed and synthesized for the lower (antisense) strand of the siNA duplex (see **Tables II and III**). If terminal TT residues are desired for the sequence (as described in paragraph 7), then the two 3' terminal nucleotides of both the sense and antisense strands are replaced by TT prior to synthesizing the oligos.

9. The siNA molecules are screened in an *in vitro*, cell culture or animal model system to identify the most active siNA molecule or the most preferred target site within the target RNA sequence.

In an alternate approach, a pool of siNA constructs specific to a BACE target sequence is used to screen for target sites in cells expressing BACE RNA, such A549 cells, 7PA2 Chinese hamster ovary (CHO) cells or APPsw (Swedish type amyloid precursor protein expressing) cells. The general strategy used in this approach is shown in **Figure 9**. A non-limiting example of such a pool is a pool comprising sequences having sense sequences comprising SEQ ID NOs. 1-325, 651-658, 663-666, and 671-674, and antisense sequences comprising SEQ ID NOs. 326-650, 659-662, 667-670, and 675-678, respectively. Cells expressing BACE (e.g., A549 cells) are transfected with the pool of siNA constructs, and cells that demonstrate a phenotype associated with BACE inhibition are sorted. The pool of siNA constructs can be expressed from transcription cassettes inserted into appropriate vectors (see for example **Figure 7** and **Figure 8**). The siNA from cells demonstrating a positive phenotypic change (e.g., decreased proliferation, decreased BACE mRNA levels or decreased BACE protein expression), are sequenced to determine the most suitable target site(s) within the target BACE RNA sequence.

Example 4: BACE targeted siNA design

siNA target sites were chosen by analyzing sequences of the BACE RNA target and optionally prioritizing the target sites on the basis of folding (structure of any given sequence analyzed to determine siNA accessibility to the target), by using a library of siNA molecules as described in Example 3, or alternately by using an *in vitro* siNA system as described in Example 6 herein. siNA molecules were designed that could bind each target and are optionally individually analyzed by computer folding to assess whether the siNA molecule can interact with the target sequence. Varying the length of

the siNA molecules can be chosen to optimize activity. Generally, a sufficient number of complementary nucleotide bases are chosen to bind to, or otherwise interact with, the target RNA, but the degree of complementarity can be modulated to accommodate siNA duplexes or varying length or base composition. By using such methodologies, siNA molecules can be designed to target sites within any known RNA sequence, for example those RNA sequences corresponding to the any gene transcript.

Chemically modified siNA constructs are designed to provide nuclease stability for systemic administration in vivo and/or improved pharmacokinetic, localization, and delivery properties while preserving the ability to mediate RNAi activity. Chemical modifications as described herein are introduced synthetically using synthetic methods described herein and those generally known in the art. The synthetic siNA constructs are then assayed for nuclease stability in serum and/or cellular/tissue extracts (e.g. liver extracts). The synthetic siNA constructs are also tested in parallel for RNAi activity using an appropriate assay, such as a luciferase reporter assay as described herein or another suitable assay that can quantify RNAi activity. Synthetic siNA constructs that possess both nuclease stability and RNAi activity can be further modified and re-evaluated in stability and activity assays. The chemical modifications of the stabilized active siNA constructs can then be applied to any siNA sequence targeting any chosen RNA and used, for example, in target screening assays to pick lead siNA compounds for therapeutic development (see for example **Figure 11**).

Example 5: Chemical Synthesis and Purification of siNA

siNA molecules can be designed to interact with various sites in the RNA message, for example, target sequences within the RNA sequences described herein. The sequence of one strand of the siNA molecule(s) is complementary to the target site sequences described above. The siNA molecules can be chemically synthesized using methods described herein. Inactive siNA molecules that are used as control sequences can be synthesized by scrambling the sequence of the siNA molecules such that it is not complementary to the target sequence. Generally, siNA constructs can be synthesized using solid phase oligonucleotide synthesis methods as described herein (see for example Usman *et al.*, US Patent Nos. 5,804,683; 5,831,071; 5,998,203; 6,117,657; 6,353,098; 6,362,323; 6,437,117; 6,469,158; Scaringe *et al.*, US Patent Nos. 6,111,086; 6,008,400; 6,111,086 all incorporated by reference herein in their entirety).

In a non-limiting example, RNA oligonucleotides are synthesized in a stepwise fashion using the phosphoramidite chemistry as is known in the art. Standard phosphoramidite chemistry involves the use of nucleosides comprising any of 5'-O-dimethoxytrityl, 2'-O-tert-butyldimethylsilyl, 3'-O-2-Cyanoethyl N,N-diisopropylphosphoroamidite groups, and exocyclic amine protecting groups (e.g. N6-benzoyl adenosine, N4 acetyl cytidine, and N2-isobutyryl guanosine). Alternately, 2'-O-Silyl Ethers can be used in conjunction with acid-labile 2'-O-orthoester protecting groups in the synthesis of RNA as described by Scaringe *supra*. Differing 2' chemistries can require different protecting groups, for example 2'-deoxy-2'-amino nucleosides can utilize N-phthaloyl protection as described by Usman *et al.*, US Patent 5,631,360, incorporated by reference herein in its entirety).

During solid phase synthesis, each nucleotide is added sequentially (3'- to 5'-direction) to the solid support-bound oligonucleotide. The first nucleoside at the 3'-end of the chain is covalently attached to a solid support (e.g., controlled pore glass or polystyrene) using various linkers. The nucleotide precursor, a ribonucleoside phosphoramidite, and activator are combined resulting in the coupling of the second nucleoside phosphoramidite onto the 5'-end of the first nucleoside. The support is then washed and any unreacted 5'-hydroxyl groups are capped with a capping reagent such as acetic anhydride to yield inactive 5'-acetyl moieties. The trivalent phosphorus linkage is then oxidized to a more stable phosphate linkage. At the end of the nucleotide addition cycle, the 5'-O-protecting group is cleaved under suitable conditions (e.g., acidic conditions for trityl-based groups and Fluoride for silyl-based groups). The cycle is repeated for each subsequent nucleotide.

Modification of synthesis conditions can be used to optimize coupling efficiency, for example, by using differing coupling times, differing reagent/phosphoramidite concentrations, differing contact times, differing solid supports and solid support linker chemistries depending on the particular chemical composition of the siNA to be synthesized. Deprotection and purification of the siNA can be performed as is generally described in Scaringe *supra*, Usman *et al.*, US 5,831,071, US 6,353,098, US 6,437,117, and Bellon *et al.*, US 6,054,576, US 6,162,909, US 6,303,773, all of which are incorporated by reference herein in their entireties.

Additionally, deprotection conditions can be modified to provide the best possible yield and purity of siNA constructs. For example, applicant has observed that oligonucleotides comprising 2'-deoxy-2'-fluoro nucleotides can degrade under inappropriate deprotection conditions. Such oligonucleotides are deprotected using aqueous methylamine at about 35°C for 30 minutes. If the 2'-deoxy-2'-fluoro containing oligonucleotide also comprises ribonucleotides, after deprotection with aqueous methylamine at about 35°C for 30 minutes, TEA-HF is added and the reaction maintained at about 65°C for an additional 15 minutes.

Example 6: RNAi *in vitro* assay to assess siNA activity

10 An *in vitro* assay that recapitulates RNAi in a cell-free system is used to evaluate siNA constructs targeting BACE RNA targets. The assay comprises the system described by Tuschl *et al.*, 1999, *Genes and Development*, 13, 3191-3197 and Zamore *et al.*, 2000, *Cell*, 101, 25-33 adapted for use with BACE target RNA. A *Drosophila* extract derived from syncytial blastoderm is used to reconstitute RNAi activity *in vitro*.

15 Target RNA is generated via *in vitro* transcription from an appropriate BACE expressing plasmid using T7 RNA polymerase or via chemical synthesis as described herein. Sense and antisense siNA strands (for example 20 uM each) are annealed by incubation in buffer (such as 100 mM potassium acetate, 30 mM HEPES-KOH, pH 7.4, 2 mM magnesium acetate) for 1 min. at 90°C followed by 1 hour at 37°C, then diluted in lysis

20 buffer (for example 100 mM potassium acetate, 30 mM HEPES-KOH at pH 7.4, 2mM magnesium acetate). Annealing can be monitored by gel electrophoresis on an agarose gel in TBE buffer and stained with ethidium bromide. The *Drosophila* lysate is prepared using zero to two-hour-old embryos from Oregon R flies collected on yeasted molasses agar that are dechorionated and lysed. The lysate is centrifuged and the supernatant

25 isolated. The assay comprises a reaction mixture containing 50% lysate [vol/vol], RNA (10-50 pM final concentration), and 10% [vol/vol] lysis buffer containing siNA (10 nM final concentration). The reaction mixture also contains 10 mM creatine phosphate, 10 ug/ml creatine phosphokinase, 100 uM GTP, 100 uM UTP, 100 uM CTP, 500 uM ATP, 5 mM DTT, 0.1 U/uL RNasin (Promega), and 100 uM of each amino acid. The final

30 concentration of potassium acetate is adjusted to 100 mM. The reactions are pre-assembled on ice and preincubated at 25° C for 10 minutes before adding RNA, then incubated at 25° C for an additional 60 minutes. Reactions are quenched with 4 volumes

of 1.25 x Passive Lysis Buffer (Promega). Target RNA cleavage is assayed by RT-PCR analysis or other methods known in the art and are compared to control reactions in which siNA is omitted from the reaction.

Alternately, internally-labeled target RNA for the assay is prepared by *in vitro* transcription in the presence of [α - 32 P] CTP, passed over a G 50 Sephadex column by spin chromatography and used as target RNA without further purification. Optionally, target RNA is 5'- 32 P-end labeled using T4 polynucleotide kinase enzyme. Assays are performed as described above and target RNA and the specific RNA cleavage products generated by RNAi are visualized on an autoradiograph of a gel. The percentage of cleavage is determined by Phosphor Imager[®] quantitation of bands representing intact control RNA or RNA from control reactions without siNA and the cleavage products generated by the assay.

In one embodiment, this assay is used to determine target sites the BACE RNA target for siNA mediated RNAi cleavage, wherein a plurality of siNA constructs are screened for RNAi mediated cleavage of the BACE RNA target, for example, by analyzing the assay reaction by electrophoresis of labeled target RNA, or by northern blotting, as well as by other methodology well known in the art.

Example 7: Nucleic acid inhibition of BACE target RNA *in vivo*

siNA molecules targeted to the human BACE RNA are designed and synthesized as described above. These nucleic acid molecules can be tested for cleavage activity *in vivo*, for example, using the following procedure. The target sequences and the nucleotide location within the BACE RNA are given in **Tables II and III**.

Two formats are used to test the efficacy of siNAs targeting BACE. First, the reagents are tested in cell culture using, for example, A549 cells, 7PA2 Chinese hamster ovary (CHO) cells or APPsw (Swedish type amyloid precursor protein expressing) cells to determine the extent of RNA and protein inhibition. siNA reagents (*e.g.*, see **Tables II and III**) are selected against the BACE target as described herein. RNA inhibition is measured after delivery of these reagents by a suitable transfection agent to, for example, A549 cells, 7PA2 Chinese hamster ovary (CHO) cells or APPsw (Swedish type amyloid precursor protein expressing) cells. Relative amounts of target RNA are measured

versus actin using real-time PCR monitoring of amplification (eg., ABI 7700 Taqman®). A comparison is made to a mixture of oligonucleotide sequences made to unrelated targets or to a randomized siNA control with the same overall length and chemistry, but randomly substituted at each position. Primary and secondary lead reagents are chosen for the target and optimization performed. After an optimal transfection agent concentration is chosen, a RNA time-course of inhibition is performed with the lead siNA molecule. In addition, a cell-plating format can be used to determine RNA inhibition.

Delivery of siNA to Cells

Cells (e.g., A549 cells, 7PA2, CHO, or APPsw cells) are seeded, for example, at 1×10^5 cells per well of a six-well dish in EGM-2 (BioWhittaker) the day before transfection. siNA (final concentration, for example 20nM) and cationic lipid (e.g., final concentration 2 μ g/ml) are complexed in EGM basal media (Biowhittaker) at 37°C for 30 mins in polystyrene tubes. Following vortexing, the complexed siNA is added to each well and incubated for the times indicated. For initial optimization experiments, cells are seeded, for example, at 1×10^3 in 96 well plates and siNA complex added as described. Efficiency of delivery of siNA to cells is determined using a fluorescent siNA complexed with lipid. Cells in 6-well dishes are incubated with siNA for 24 hours, rinsed with PBS and fixed in 2% paraformaldehyde for 15 minutes at room temperature. Uptake of siNA is visualized using a fluorescent microscope.

Taqman and Lightcycler quantification of mRNA

Total RNA is prepared from cells following siNA delivery, for example, using Qiagen RNA purification kits for 6-well or Rneasy extraction kits for 96-well assays. For Taqman analysis, dual-labeled probes are synthesized with the reporter dye, FAM or JOE, covalently linked at the 5'-end and the quencher dye TAMRA conjugated to the 3'-end. One-step RT-PCR amplifications are performed on, for example, an ABI PRISM 7700 Sequence Detector using 50 μ l reactions consisting of 10 μ l total RNA, 100 nM forward primer, 900 nM reverse primer, 100 nM probe, 1X TaqMan PCR reaction buffer (PE-Applied Biosystems), 5.5 mM MgCl₂, 300 μ M each dATP, dCTP, dGTP, and dTTP, 10U RNase Inhibitor (Promega), 1.25U AmpliTaq Gold (PE-Applied Biosystems) and

10U M-MLV Reverse Transcriptase (Promega). The thermal cycling conditions can consist of 30 min at 48°C, 10 min at 95°C, followed by 40 cycles of 15 sec at 95°C and 1 min at 60°C. Quantitation of mRNA levels is determined relative to standards generated from serially diluted total cellular RNA (300, 100, 33, 11 ng/txn) and normalizing to β -actin or GAPDH mRNA in parallel TaqMan reactions. For each gene of interest an upper and lower primer and a fluorescently labeled probe are designed. Real time incorporation of SYBR Green I dye into a specific PCR product can be measured in glass capillary tubes using a lightcycler. A standard curve is generated for each primer pair using control cRNA. Values are represented as relative expression to GAPDH in each sample.

Western blotting

Nuclear extracts can be prepared using a standard micro preparation technique (see for example Andrews and Faller, 1991, *Nucleic Acids Research*, 19, 2499). Protein extracts from supernatants are prepared, for example using TCA precipitation. An equal volume of 20% TCA is added to the cell supernatant, incubated on ice for 1 hour and pelleted by centrifugation for 5 minutes. Pellets are washed in acetone, dried and resuspended in water. Cellular protein extracts are run on a 10% Bis-Tris NuPage (nuclear extracts) or 4-12% Tris-Glycine (supernatant extracts) polyacrylamide gel and transferred onto nitro-cellulose membranes. Non-specific binding can be blocked by incubation, for example, with 5% non-fat milk for 1 hour followed by primary antibody for 16 hour at 4°C. Following washes, the secondary antibody is applied, for example (1:10,000 dilution) for 1 hour at room temperature and the signal detected with SuperSignal reagent (Pierce).

Example 8: Models useful to evaluate the down-regulation of BACE gene expression

25 *Cell Culture*

Vassar *et al.*, 1999, *Science*, 286, 735-741, describe a cell culture model for studying BACE inhibition. Specific antisense nucleic acid molecules targeting BACE mRNA were used for inhibition studies of endogenous BACE expression in 101 cells and APPsw (Swedish type amyloid precursor protein expressing) cells via lipid mediated transfection. Antisense treatment resulted in dramatic reduction of both BACE mRNA

by Northern blot analysis, and APPs β sw ("Swedish" type β -secretase cleavage product) by ELISA, with maximum inhibition of both parameters at 75-80%. This model was also used to study the effect of BACE inhibition on amyloid β -peptide production in APPsw cells. Similarly, such a model can be used to screen siRNA molecules of the
 5 instant invention for efficacy and potency.

In several cell culture systems, cationic lipids have been shown to enhance the bioavailability of oligonucleotides to cells in culture (Bennet, *et al.*, 1992, *Mol. Pharmacology*, 41, 1023-1033). In one embodiment, siNA molecules of the invention are complexed with cationic lipids for cell culture experiments. siNA and cationic lipid
 10 mixtures are prepared in serum-free DMEM immediately prior to addition to the cells. DMEM plus additives are warmed to room temperature (about 20-25°C) and cationic lipid is added to the final desired concentration and the solution is vortexed briefly. siNA molecules are added to the final desired concentration and the solution is again vortexed briefly and incubated for 10 minutes at room temperature. In dose response
 15 experiments, the RNA/lipid complex is serially diluted into DMEM following the 10 minute incubation.

Animal Models

Evaluating the efficacy of anti-BACE agents in animal models is an important prerequisite to human clinical trials. Games *et al.*, 1995, *Nature*, 373, 523-527, describe
 20 a transgenic mouse model in which mutant human familial type APP (Phe 717 instead of Val) is overexpressed. This model results in mice that progressively develop many of the pathological hallmarks of Alzheimer's disease, and as such, provides a model for testing therapeutic drugs, including siNA constructs of the instant invention.

Example 9: RNAi mediated inhibition of BACE RNA expression

25 siNA constructs (**Tables II and III**) are tested for efficacy in reducing BACE RNA expression in, for example in A549 cells. Cells are plated approximately 24h before transfection in 96-well plates at 5,000-7,500 cells/well, 100 μ l/well, such that at the time of transfection cells are 70-90% confluent. For transfection, annealed siNAs are mixed with the transfection reagent (Lipofectamine 2000, Invitrogen) in a volume of 50 μ l/well and
 30 incubated for 20 min. at room temperature. The siNA transfection mixtures are added to

cells to give a final siNA concentration of 25 nM in a volume of 150 μ l. Each siNA transfection mixture is added to 3 wells for triplicate siNA treatments. Cells are incubated at 37° for 24h in the continued presence of the siNA transfection mixture. At 24h, RNA is prepared from each well of treated cells. The supernatants with the transfection mixtures are first removed and discarded, then the cells are lysed and RNA prepared from each well. Target gene expression following treatment is evaluated by RT-PCR for the target gene and for a control gene (36B4, an RNA polymerase subunit) for normalization. The triplicate data is averaged and the standard deviations determined for each treatment. Normalized data are graphed and the percent reduction of target mRNA by active siNAs in comparison to their respective inverted control siNAs was determined.

In a non-limiting example, siNA constructs were screened for activity (see **Figure 12**) and compared to untreated cells, scrambled siNA control constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in **Figure 12**, the siNA constructs show significant reduction of BACE RNA expression. Leads generated from such a screen are then further assayed. In a non-limiting example, siNA constructs comprising ribonucleotides and 3'-terminal dithymidine caps are assayed along with a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine nucleotides and purine ribonucleotides, in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and the antisense strand comprises a 3'-terminal phosphorothioate internucleotide linkage. Additional stabilization chemistries as described in **Table IV** are similarly assayed for activity. These siNA constructs are compared to appropriate matched chemistry inverted controls. In addition, the siNA constructs are also compared to untreated cells, cells transfected with lipid and scrambled siNA constructs, and cells transfected with lipid alone (transfection control).

Example 10: Indications

Particular degenerative and disease states that can be associated with BACE expression modulation include but are not limited to: Alzheimer's disease, dementia, stroke (CVA) and any other diseases or conditions that are related to the levels of BACE in a cell or tissue, alone or in combination with other therapies. The reduction of BACE

expression (specifically BACE RNA levels) and thus reduction in the level of the respective protein relieves, to some extent, the symptoms of the disease or condition.

Those skilled in the art will recognize that other drug compounds and therapies may be readily combined with or used in conjunction with the nucleic acid molecules of the instant invention (e.g., siNA molecules) are hence within the scope of the instant invention.

Example 11: Diagnostic uses

The siNA molecules of the invention can be used in a variety of diagnostic applications, such as in the identification of molecular targets (e.g., RNA) in a variety of applications, for example, in clinical, industrial, environmental, agricultural and/or research settings. Such diagnostic use of siNA molecules involves utilizing reconstituted RNAi systems, for example, using cellular lysates or partially purified cellular lysates. siNA molecules of this invention can be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of endogenous or exogenous, for example viral, RNA in a cell. The close relationship between siNA activity and the structure of the target RNA allows the detection of mutations in any region of the molecule, which alters the base-pairing and three-dimensional structure of the target RNA. By using multiple siNA molecules described in this invention, one can map nucleotide changes, which are important to RNA structure and function *in vitro*, as well as in cells and tissues. Cleavage of target RNAs with siNA molecules can be used to inhibit gene expression and define the role of specified gene products in the progression of disease or infection. In this manner, other genetic targets can be defined as important mediators of the disease. These experiments will lead to better treatment of the disease progression by affording the possibility of combination therapies (e.g., multiple siNA molecules targeted to different genes, siNA molecules coupled with known small molecule inhibitors, or intermittent treatment with combinations siNA molecules and/or other chemical or biological molecules). Other *in vitro* uses of siNA molecules of this invention are well known in the art, and include detection of the presence of mRNAs associated with a disease, infection, or related condition. Such RNA is detected by determining the presence of a cleavage product after treatment with a

siNA using standard methodologies, for example, fluorescence resonance emission transfer (FRET).

In a specific example, siNA molecules that cleave only wild-type or mutant forms of the target RNA are used for the assay. The first siNA molecules (*i.e.*, those that
5 cleave only wild-type forms of target RNA) are used to identify wild-type RNA present in the sample and the second siNA molecules (*i.e.*, those that cleave only mutant forms of target RNA) are used to identify mutant RNA in the sample. As reaction controls, synthetic substrates of both wild-type and mutant RNA are cleaved by both siNA molecules to demonstrate the relative siNA efficiencies in the reactions and the absence
10 of cleavage of the "non-targeted" RNA species. The cleavage products from the synthetic substrates also serve to generate size markers for the analysis of wild-type and mutant RNAs in the sample population. Thus, each analysis requires two siNA molecules, two substrates and one unknown sample, which is combined into six reactions. The presence of cleavage products is determined using an RNase protection
15 assay so that full-length and cleavage fragments of each RNA can be analyzed in one lane of a polyacrylamide gel. It is not absolutely required to quantify the results to gain insight into the expression of mutant RNAs and putative risk of the desired phenotypic changes in target cells. The expression of mRNA whose protein product is implicated in the development of the phenotype (*i.e.*, disease related or infection related) is adequate to
20 establish risk. If probes of comparable specific activity are used for both transcripts, then a qualitative comparison of RNA levels is adequate and decreases the cost of the initial diagnosis. Higher mutant form to wild-type ratios are correlated with higher risk whether RNA levels are compared qualitatively or quantitatively.

All patents and publications mentioned in the specification are indicative of the
25 levels of skill of those skilled in the art to which the invention pertains. All references cited in this disclosure are incorporated by reference to the same extent as if each reference had been incorporated by reference in its entirety individually.

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as
30 those inherent therein. The methods and compositions described herein as presently representative of preferred embodiments are exemplary and are not intended as

limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art, which are encompassed within the spirit of the invention, are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and
5 modifications can be made to the invention disclosed herein without departing from the scope and spirit of the invention. Thus, such additional embodiments are within the scope of the present invention and the following claims. The present invention teaches one skilled in the art to test various combinations and/or substitutions of chemical
10 modifications described herein toward generating nucleic acid constructs with improved activity for mediating RNAi activity. Such improved activity can comprise improved stability, improved bioavailability, and/or improved activation of cellular responses mediating RNAi. Therefore, the specific embodiments described herein are not limiting and one skilled in the art can readily appreciate that specific combinations of the
15 modifications described herein can be tested without undue experimentation toward identifying siNA molecules with improved RNAi activity.

The invention illustratively described herein suitably can be practiced in the absence of any element or elements, limitation or limitations that are not specifically disclosed herein. Thus, for example, in each instance herein any of the terms
20 "comprising", "consisting essentially of", and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although
25 the present invention has been specifically disclosed by preferred embodiments, optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the description and the appended claims.

In addition, where features or aspects of the invention are described in terms of
30 Markush groups or other grouping of alternatives, those skilled in the art will recognize

that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.

Table I: BACE Accession Numbers

5	NM_012104 Homo sapiens beta-site APP-cleaving enzyme (BACE), transcript variant a, mRNA gi 21040369 ref NM_012104.2 [21040369]
10	NM_006222 Homo sapiens protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1-like (PIN1L), mRNA gi 5453899 ref NM_006222.1 [5453899]
15	L76517 Homo sapiens (clone cc44) senilin 1 (PS1; S182) mRNA, complete cds
20	gi 1479973 gb L76517.1 HUMPS1MRNA [1479973]
25	L43964 Homo sapiens (clone F-T03796) STM-2 mRNA, complete cds gi 951202 gb L43964.1 HUMSTM2R [951202]
30	NM_138973 Homo sapiens beta-site APP-cleaving enzyme (BACE), transcript variant d, mRNA gi 21040367 ref NM_138973.1 [21040367]
35	NM_138972 Homo sapiens beta-site APP-cleaving enzyme (BACE), transcript variant b, mRNA gi 21040365 ref NM_138972.1 [21040365]
40	NM_138971 Homo sapiens beta-site APP-cleaving enzyme (BACE), transcript variant c, mRNA gi 21040363 ref NM_138971.1 [21040363]
45	AK075049 Homo sapiens cDNA FLJ90568 fis, clone OVARC1001570, highly similar to Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA
50	gi 22760888 dbj AK075049.1 [22760888]

5 AF527782
Homo sapiens beta-site APP-cleaving enzyme (BACE)
mRNA, partial cds,
alternatively spliced
gi|22094870|gb|AF527782.1| [22094870]

10 AF324837
Homo sapiens beta-site APP cleaving enzyme mRNA,
partial cds, alternatively
spliced
gi|21449275|gb|AF324837.1| [21449275]

15 AF338817
Homo sapiens beta-site APP cleaving enzyme type C
mRNA, complete cds
gi|13699247|gb|AF338817.1| [13699247]

20 AF338816
Homo sapiens beta-site APP cleaving enzyme type B
mRNA, complete cds
gi|13699245|gb|AF338816.1| [13699245]

30 AB050438
Homo sapiens BACE mRNA for beta-site APP cleaving
enzyme I-432, complete cds
gi|13568410|dbj|AB050438.1| [13568410]

35 AB050437
Homo sapiens BACE mRNA for beta-site APP cleaving
enzyme I-457, complete cds
gi|13568408|dbj|AB050437.1| [13568408]

40 AB050436
Homo sapiens BACE mRNA for beta-site APP cleaving
enzyme I-476, complete cds
gi|13568406|dbj|AB050436.1| [13568406]

45 AF190725
Homo sapiens beta-site APP cleaving enzyme (BACE)
mRNA, complete cds
gi|6118538|gb|AF190725.1|AF190725 [6118538]

50

NM_007319
Homo sapiens presenilin 1 (Alzheimer disease 3)
(PSEN1), transcript variant
I-374., mRNA
5 gi|7549814|ref|NM_007319.1|[7549814]

NM_138992
Homo sapiens beta-site APP-cleaving enzyme 2 (BACE2),
transcript variant b, mRNA
10 gi|21040361|ref|NM_138992.1|[21040361]

NM_138991
Homo sapiens beta-site APP-cleaving enzyme 2 (BACE2),
transcript variant c, mRNA
15 gi|21040359|ref|NM_138991.1|[21040359]

NM_012105
Homo sapiens beta-site APP-cleaving enzyme 2 (BACE2),
transcript variant a, mRNA
20 gi|21040358|ref|NM_012105.3|[21040358]

AB066441
Homo sapiens APP mRNA for amyloid precursor protein,
partial cds, D678N mutant
25 gi|16904654|dbj|AB066441.1|[16904654]

AB050438
Homo sapiens BACE mRNA for beta-site APP cleaving
enzyme I-432, complete cds
30 gi|13568410|dbj|AB050438.1|[13568410]

AB050437
Homo sapiens BACE mRNA for beta-site APP cleaving
enzyme I-457, complete cds
35 gi|13568408|dbj|AB050437.1|[13568408]

AB050436
Homo sapiens BACE mRNA for beta-site APP cleaving
enzyme I-476, complete cds
40 gi|13568406|dbj|AB050436.1|[13568406]

NM_012486

- 5 Homo sapiens presenilin 2 (Alzheimer disease 4)
(PSEN2), transcript variant 2,
mRNA
gi|7108359|ref|NM_012486.1|[7108359]
- 10 NM_000447
Homo sapiens presenilin 2 (Alzheimer disease 4)
(PSEN2), transcript variant 1,
mRNA
gi|4506164|ref|NM_000447.1|[4506164]
- 15 AF188277
Homo sapiens aspartyl protease (BACE2) mRNA, complete
cds, alternatively spliced
gi|7025334|gb|AF188277.1|AF188277[7025334]
- 20 AF188276
Homo sapiens aspartyl protease (BACE2) mRNA, complete
cds, alternatively spliced
gi|7025332|gb|AF188276.1|AF188276[7025332]
- 25 AF178532
Homo sapiens aspartyl protease (BACE2) mRNA, complete
cds
gi|6851265|gb|AF178532.1|AF178532[6851265]
- 30 D87675
Homo sapiens DNA for amyloid precursor protein,
complete cds
gi|2429080|dbj|D87675.1|[2429080]
- 40 AF201468
Homo sapiens APP beta-secretase mRNA, complete cds
gi|6601444|gb|AF201468.1|AF201468[6601444]
- 45 AF190725
Homo sapiens beta-site APP cleaving enzyme (BACE)
mRNA, complete cds
gi|6118538|gb|AF190725.1|AF190725[6118538]
- 50 E14707
DNA encoding a mutated amyloid precursor protein

gi|5709390|dbj|E14707.1|pat|JP|1998001499|1[5709390]

5 AF168956
Homo sapiens amyloid precursor protein homolog HSD-2
mRNA, complete cds
gi|5702387|gb|AF168956.1|AF168956[5702387]

10 S60099
APPH=amyloid precursor protein homolog [human,
placenta, mRNA, 3727 nt]
gi|300168|bbm|300685|bbs|131198|gb|S60099.1|S60099[300
168]

15

U50939
Human amyloid precursor protein-binding protein 1
mRNA, complete cds
20 gi|1314559|gb|U50939.1|HSU50939[1314559]

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Table II: BACE siNA and Target Sequences

NM_012104 BACE									
Pos	Target Sequence	Seq ID	UPos	Upper seq	Seq ID	LPos	Lower seq	Seq ID	
1	CGCACUCUGUCCCGAGCCCG	1	1	CGCACUCUGUCCCGAGCCCG	1	23	CGGCGUGGGGACGAGUGCG	326	
19	GCCCGGAGCUGCGAGCCG	2	19	GCCCGGAGCUGCGAGCCG	2	41	CGGCGUGGGGACGAGUGCG	327	
37	GCAGCUGGAGUUAUGGUGG	3	37	GCAGCUGGAGUUAUGGUGG	3	59	CCACCAUAAUCCAGCUCGC	328	
55	GCUGAGCAGCCACGCGAG	4	55	GCUGAGCAGCCACGCGAG	4	77	CUGCGUUGGCGUCUACGCG	329	
73	GCCGAGGAGCCCGGAGCC	5	73	GCCGAGGAGCCCGGAGCC	5	95	GGUCCCGGGCUCUUGCGGC	330	
91	CCUUGCCCGUGCCCGCGCC	6	91	CCUUGCCCGUGCCCGCGCC	6	113	GGCGCGGCGAGGGGCAAGG	331	
109	CGCGCGCGCGCGGGGAGC	7	109	CGCGCGCGCGCGGGGAGC	7	131	GUCCCGCGGGCGGGCGCG	332	
127	CCAGGGAAGCCGCCACCGG	8	127	CCAGGGAAGCCGCCACCGG	8	149	CCGUGGCGGGCUUCCCGUG	333	
145	GCCCGCAUCCCGCCCGCCU	9	145	GCCCGCAUCCCGCCCGCCU	9	167	AGGGCGGGCAUUGCGCGGC	334	
163	UCCAGCCCGCGCGGGAGC	10	163	UCCAGCCCGCGCGGGAGC	10	185	GUCCCGCGGGCGUGGGA	335	
181	CCGCGCCCGUGCCCGAGG	11	181	CCGCGCCCGUGCCCGAGG	11	203	CCUGGCGAGCGGGCGCGGG	336	
199	GUUGGCGCGCGCGGUGCCG	12	199	GUUGGCGCGCGCGGUGCCG	12	221	CGGCACGCGCGCGCGCGGC	337	
217	GAUGAGCGGCGUCGGAU	13	217	GAUGAGCGGCGUCGGAU	13	239	AUCGGAGCGCGCUACAUC	338	
235	UCCAGCCUCUCCCGUGCU	14	235	UCCAGCCUCUCCCGUGCU	14	257	AGCAGGGAGAGCGCUGGGA	339	
253	UCCGUGGCGUGCGGAGCU	15	253	UCCGUGGCGUGCGGAGCU	15	275	AGAUCCGAGAGCACCGGA	340	
271	UCCGUGGCGUGCGGAGCU	16	271	UCCGUGGCGUGCGGAGCU	16	293	GUAGAGCGGCGUACGGGA	341	
289	CAGCCCGGAGCCCGGGGCGU	17	289	CAGCCCGGAGCCCGGGGCGU	17	311	AGCCCGCGGGUCCCGGCGUG	342	
307	UGGCCAGGCGCCUGCAGG	18	307	UGGCCAGGCGCCUGCAGG	18	329	CCUGCAGGGCGCGUGGCGCA	343	
325	GCCUGGCGUCCUGAUGCC	19	325	GCCUGGCGUCCUGAUGCC	19	347	GGCAUCAGGAGCGCCAGGGC	344	
343	CCCAAGCGCCCGUCCUGG	20	343	CCCAAGCGCCCGUCCUGG	20	365	CAGGAGAGGGAGCUGUGGGG	345	
361	GAGAAGCCAGCAGCACAC	21	361	GAGAAGCCAGCAGCACAC	21	383	GUGGUGUGGUGGCUUCUC	346	
379	CCAGACUUGGGGCGAGGC	22	379	CCAGACUUGGGGCGAGGC	22	401	CCUGCCCCCAAGUUCUGG	347	
397	CGCCAGGAGCGGAGCGUGG	23	397	CGCCAGGAGCGGAGCGUGG	23	419	CCACGUGCCGUCUCCUGCG	348	
415	GCCAGUCGAGCCAGAGG	24	415	GCCAGUCGAGCCAGAGG	24	437	CCUGGCGUCGACACUGGC	349	
433	GCCCGAAGCGCGGGGCC	25	433	GCCCGAAGCGCGGGGCC	25	455	GGGCCCGGGCUCUCCGGCC	350	
451	CACCAUGGCCCAAGCCUG	26	451	CACCAUGGCCCAAGCCUG	26	473	CAGGGCUUGGGCAUUGGUG	351	
469	GCCUGGCGUCCUGUGG	27	469	GCCUGGCGUCCUGUGG	27	491	CCACAGGAGGAGCCAGGGC	352	
487	GAUGGCGCGGGAGUGCUG	28	487	GAUGGCGCGGGAGUGCUG	28	509	CAGCACUCCCGCGCCCAUC	353	
505	GCUGGCCAGCGACCCAG	29	505	GCUGGCCAGCGACCCAG	29	527	CUGGUGCCGUGGGGAGGC	354	
523	GCAGGCAUCGGGUGGCC	30	523	GCAGGCAUCGGGUGGCC	30	545	GGGCGCGCGGAGUGCGUGC	355	
541	CCUGGCGAGCGCGGUGGG	31	541	CCUGGCGAGCGCGGUGGG	31	563	CCCGAGCGCGGCGCGGAGG	356	
559	GCGCGCGCCCGUGGGGCG	32	559	GCGCGCGCCCGUGGGGCG	32	581	CAGCCCCAGGGGCGCGCC	357	

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577	GCGGCGUGCCCGGGAGACC	33	577	GCGGCGUGCCCGGGAGACC	33	599	GGUUCUCCCGGGGACGCCG	358
595	CGACGAAGCCCGGAGAG	34	595	CGACGAAGCCCGGAGAG	34	617	GUCCUGGGGCUUUCGUG	359
613	GCCGGCGGAGGGGACG	35	613	GCCGGCGGAGGGGACG	35	635	GGUCCUCCCGCGCGGCG	360
631	CUUUGUGAGAUUGUGAC	36	631	CUUUGUGAGAUUGUGAC	36	653	GUCCACCAUCCACAAAG	361
649	CAACUGAGGGGCAAGUUG	37	649	CAACUGAGGGGCAAGUUG	37	671	CGACUUGCCCGUCCAGGUG	362
667	GGGCGAGGCUACUACUG	38	667	GGGCGAGGCUACUACUG	38	689	CACGUAGUAGCCUUGCCCG	363
685	GGAGAUACCGUGGGGACG	39	685	GGAGAUACCGUGGGGACG	39	707	GCUGCCACGGUACUCC	364
703	CCCCCGGAGAGCUCAAC	40	703	CCCCCGGAGAGCUCAAC	40	725	GUUGAGCGUUGGGGGGG	365
721	CAUCCUGUGGUAACAGGC	41	721	CAUCCUGUGGUAACAGGC	41	743	GCUGUAUCCACAGGAUG	366
739	CAGCAGUAACUUGCAGUG	42	739	CAGCAGUAACUUGCAGUG	42	761	CACUGCAAGUUAUCUGUG	367
757	GGUGUGUGCCCGACCCG	43	757	GGUGUGUGCCCGACCCG	43	779	GGGGUGGGGGGACGACCC	368
775	CUUCUGCAUCGUACUAC	44	775	CUUCUGCAUCGUACUAC	44	797	GUAGUAGCGAUUGCAGGAAG	369
793	CCAGAGGCGUUCUACG	45	793	CCAGAGGCGUUCUACG	45	815	GCUGGACAGUCCUUGUG	370
811	CACAUACCGGACUCCGG	46	811	CACAUACCGGACUCCGG	46	833	CCGGAGUCCCGGUUUG	371
829	GAAGGUGUGUUGUGGCC	47	829	GAAGGUGUGUUGUGGCC	47	851	GGGCACAUACACACCCUUC	372
847	CUACACCGGGGCAAGUGG	48	847	CUACACCGGGGCAAGUGG	48	869	CCACUUGCCUUGGUGUAG	373
865	GGAGGGGAGGUGGGACCC	49	865	GGAGGGGAGGUGGGACCC	49	887	GGUGCCCGAGUCCCUUCC	374
883	CGACUUGUAAGCAUCCCG	50	883	CGACUUGUAAGCAUCCCG	50	905	GGGGAUGCUUACAGGUG	375
901	CCAUUGCCCGACGUCACU	51	901	CCAUUGCCCGACGUCACU	51	923	AGUGACGUGGGGCGUUG	376
919	UGUGGUGGCAACAUUGCU	52	919	UGUGGUGGCAACAUUGCU	52	941	AGCAUUGUUGGCGCACAC	377
937	UGCCAUCACUGAAUCAGAC	53	937	UGCCAUCACUGAAUCAGAC	53	959	GUUGAUUCAGUAGGCA	378
955	CAAGUUCUUCUACACGGG	54	955	CAAGUUCUUCUACACGGG	54	977	GCCUUGAUAGAAACUUG	379
973	CUCCAACUGGGAAGGAUC	55	973	CUCCAACUGGGAAGGAUC	55	995	GAUGCUUCCAGUUGGAG	380
991	CUUGGGGUGGCUUAGCU	56	991	CUUGGGGUGGCUUAGCU	56	1013	AGCAUAGGCCAGCCCGAG	381
1009	UGAGAUUGCCAGGCCUGAC	57	1009	UGAGAUUGCCAGGCCUGAC	57	1031	GUACGGCCUGGCAUUCUAC	382
1027	CGACUCCUGGAGCCUUC	58	1027	CGACUCCUGGAGCCUUC	58	1049	GAAGGCUCCAGGGAGUCC	383
1045	CUUUGACUUCUGGUAAAG	59	1045	CUUUGACUUCUGGUAAAG	59	1067	CUUACCGAGAGUCAAAG	384
1063	GCAGACCCACGUUCCCAAC	60	1063	GCAGACCCACGUUCCCAAC	60	1085	GUUGGGAACGUGGGUUGC	385
1081	CCUUCUUCUCCUGCAGCUU	61	1081	CCUUCUUCUCCUGCAGCUU	61	1103	AAGCUAGCAGGAGAGAGG	386
1099	UUGUGGUGUGGCUUCCCG	62	1099	UUGUGGUGUGGCUUCCCG	62	1121	GGGGAAGCCACACACAA	387
1117	CCUACACGAGUCUGAAGUG	63	1117	CCUACACGAGUCUGAAGUG	63	1139	CACUUCAGACUUGGUUGAG	388
1135	GUUGGCCUUGUGGAGGG	64	1135	GUUGGCCUUGUGGAGGG	64	1157	CCUCCGACAGAGGCCAGC	389
1153	GAGCAUGAUUUGGAGGU	65	1153	GAGCAUGAUUUGGAGGU	65	1175	ACCUCCAAUGAUCAUGCUC	390
1171	UAUCAGCACUCGCUUAC	66	1171	UAUCAGCACUCGCUUAC	66	1193	GUACGCGAGUGGUGUA	391
1189	CACAGGCGUUCUGGUU	67	1189	CACAGGCGUUCUGGUU	67	1211	AUACAGAGACUGCCUUG	392
1207	UACACCAUCCCGGGGAG	68	1207	UACACCAUCCCGGGGAG	68	1229	CUCCCGCGGAGUGGUGUA	393

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1225	GUGGUUUAUUGAGGUCAUC	69	1225	GUGGUUUAUUGAGGUCAUC	69	1247	GAUGACCUCAUUAUACCAAC	394
1243	CAUUGUGGGGUGGGAUC	70	1243	CAUUGUGGGGUGGGAUC	70	1265	GAUUCACCCCGCAAAUG	395
1261	CAUUGGACAGGAUCUGAAA	71	1261	CAUUGGACAGGAUCUGAAA	71	1283	UUUCAGAUCCUGUCCAUUG	396
1279	AAUGGACUGCAAGGAGUAC	72	1279	AAUGGACUGCAAGGAGUAC	72	1301	GUACUCUUUGGAGUCCAUU	397
1297	CAACUUAUACAAGAGCAU	73	1297	CAACUUAUACAAGAGCAU	73	1319	AAUGCUUUGUCAUAGUUG	398
1315	UGUGGACAGUGGCACACAC	74	1315	UGUGGACAGUGGCACACAC	74	1337	GGUGGUGCCACUGUCCACA	399
1333	CAACCUUGUUUGCCCAAG	75	1333	CAACCUUGUUUGCCCAAG	75	1355	CUUGGGCAACGAAAGGUUG	400
1351	GAAAGUGUUUGAAGCUGCA	76	1351	GAAAGUGUUUGAAGCUGCA	76	1373	UGCAGCUUCAAACACUUIUC	401
1369	AGUCAAUCCAUCAAGGCA	77	1369	AGUCAAUCCAUCAAGGCA	77	1391	UGCCUUGAUGGAUUUGACU	402
1387	AGCCUCCUCCAGGAGAA	78	1387	AGCCUCCUCCAGGAGAA	78	1409	CUUCUCCUGUGGAGGAGGU	403
1405	GUUCUUUGUUGUUCUGG	79	1405	GUUCUUUGUUGUUCUGG	79	1427	CCAGAAACCAUACAGGGAAC	404
1423	GUAGGAGAGCAGCUGGUG	80	1423	GUAGGAGAGCAGCUGGUG	80	1445	CACGAGCUGCUCUCCUAGC	405
1441	GUUGUGGCAAGCAGGCACC	81	1441	GUUGUGGCAAGCAGGCACC	81	1463	GGUGCGUGUUGCCAGCAC	406
1459	CACCCUUGGAACAUUIUC	82	1459	CACCCUUGGAACAUUIUC	82	1481	GAAAUGUUCCAAGGGGUG	407
1477	CCCAGUACUCACUCUAC	83	1477	CCCAGUACUCACUCUAC	83	1499	GUAGAGUGAGAUACUCUGG	408
1495	CCUAAUUGGUGAGGUUACC	84	1495	CCUAAUUGGUGAGGUUACC	84	1517	GGUAAUCCUACCCAUUAGG	409
1513	CAACGAGUCCUUCGCGAUC	85	1513	CAACGAGUCCUUCGCGAUC	85	1535	GAUGCGGAAGGACUGGUUG	410
1531	CACCAUCCUUCGCGACAA	86	1531	CACCAUCCUUCGCGACAA	86	1553	UUUCUGCGGAAAGGAGUGUG	411
1549	AUACUGCGGCGAGUGGAA	87	1549	AUACUGCGGCGAGUGGAA	87	1571	UUCCACUGGCGCGAGGUU	412
1567	AGAUGUGGCCACGUCGCCAA	88	1567	AGAUGUGGCCACGUCGCCAA	88	1589	UUUGGAGCUGGCGCCACAUUCU	413
1585	AGAGACUGUUAACAAGUUU	89	1585	AGAGACUGUUAACAAGUUU	89	1607	AAACUUGUAACAGUCUGUCU	414
1603	UGCCAUUCACAGUACUCC	90	1603	UGCCAUUCACAGUACUCC	90	1625	GGAUAGACUGUGAGAUAGCA	415
1621	CACGGGACUGUUUAUGGGA	91	1621	CACGGGACUGUUUAUGGGA	91	1643	UCCCAUAAACAGUGCCCGUG	416
1639	AGCUGUUAUUGGAGGGC	92	1639	AGCUGUUAUUGGAGGGC	92	1661	GCCUCCAUAGUAAACAGCU	417
1657	CUUCUACGUUGUUCUUGAU	93	1657	CUUCUACGUUGUUCUUGAU	93	1679	AUCAAAGACAAACGUAAG	418
1675	UCGGGCGGCAAAACGAAUU	94	1675	UCGGGCGGCAAAACGAAUU	94	1697	AAUUCGUUUUGGGCCCGGA	419
1693	UGGCUUUGUGUGCAGCGCU	95	1693	UGGCUUUGUGUGCAGCGCU	95	1715	AGCGUUGACAGCAAAAGCA	420
1711	UUGCCAUUGCAGCAGUAG	96	1711	UUGCCAUUGCAGCAGUAG	96	1733	CUCAUCGUGCACAUGGCAA	421
1729	GUUCAGGAGCGGACGGGUG	97	1729	GUUCAGGAGCGGACGGGUG	97	1751	CACCGCUGCCGUCUUGAAC	422
1747	GGAGGCGCCUUUUGUCACC	98	1747	GGAGGCGCCUUUUGUCACC	98	1769	GGUGACAAAAGGGCCUUC	423
1765	CUUGGACAUUGGAGACUGU	99	1765	CUUGGACAUUGGAGACUGU	99	1787	ACAGCUUCCAUUGUCCAAAG	424
1783	UGGCUAACAAUUCACAG	100	1783	UGGCUAACAAUUCACAG	100	1805	CUUGGGAUUGUUGAGCCA	425
1801	GACCAUAGUACAACCCUC	101	1801	GACCAUAGUACAACCCUC	101	1823	GAGGGUUGACUCAUCUGUC	426
1819	CAUGACCAUAGCCUUAUGUC	102	1819	CAUGACCAUAGCCUUAUGUC	102	1841	GACAUAGGCUUAUGGUCAUG	427
1837	CAUGGCGUCCAUUGCGCC	103	1837	CAUGGCGUCCAUUGCGCC	103	1859	GGCGCAGAUUGGCGCAUG	428
1855	CCUCUUAUUGCUGCCACUC	104	1855	CCUCUUAUUGCUGCCACUC	104	1877	GAGUGGCGAGCAUGAAGAGG	429

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1873	CUGCCUACAUGGUGUGUACAG	105	1873	CUGCCUACAUGGUGUGUACAG	105	1895	CUGACACACAUAGAGGAG	430
1891	GUUGGCGUCCUCCGUGC	106	1891	GUUGGCGUCCUCCGUGC	106	1913	GCAGCGGAGGACGCGCCAC	431
1909	CCUGCGCCAGCAGCAUGAU	107	1909	CCUGCGCCAGCAGCAUGAU	107	1931	AUCAUGUCUGUGCGCGAGG	432
1927	UGACUUUGCUGAUAGACAU	108	1927	UGACUUUGCUGAUAGACAU	108	1949	GAUGUCAUCAGCAAAAGUCA	433
1945	CUCGUGUGUAGAGGAGGA	109	1945	CUCGUGUGUAGAGGAGGA	109	1967	UCCUCACUUCAGCAGGAGG	434
1963	AGGCCAUUGGCGCAGAGAU	110	1963	AGGCCAUUGGCGCAGAGAU	110	1985	AUCUUCUGCCCAUGGGCCU	435
1981	UAGAGAUUCCUUGGACCA	111	1981	UAGAGAUUCCUUGGACCA	111	2003	UGGUCACAGGGGAUUCUUA	436
1999	ACACUCCUGUGUACAU	112	1999	ACACUCCUGUGUACAU	112	2021	AAGUGAACCCAGGAGUGU	437
2017	UUGUICACAAGUAGGAGAC	113	2017	UUGUICACAAGUAGGAGAC	113	2039	GUCUCCUACUUGUACCAA	438
2035	CACAGAUCCACUUGUGGC	114	2035	CACAGAUCCACUUGUGGC	114	2057	GCCACAGGUGCCAUUCUGUG	439
2053	CCAGAGCACUCCAGGACCC	115	2053	CCAGAGCACUCCAGGACCC	115	2075	GGGUCUGAGGUGUCUUGG	440
2071	CUCCCAACCCACAAUUGC	116	2071	CUCCCAACCCACAAUUGC	116	2093	GCAUUGGUGGUGGGGAG	441
2089	CCUCUGCCUUGAUUGGAGAA	117	2089	CCUCUGCCUUGAUUGGAGAA	117	2111	UUCUCCCAUCAAGGCAGAGG	442
2107	AGGAAAGGCUUGGCAAGGU	118	2107	AGGAAAGGCUUGGCAAGGU	118	2129	ACCUUGCCAGCCUUIUCU	443
2125	UGGUGUCCAGGGACUUGAC	119	2125	UGGUGUCCAGGGACUUGAC	119	2147	GUACAGUCCUGGAACCA	444
2143	CCUGUAGGAAACAGAAAAG	120	2143	CCUGUAGGAAACAGAAAAG	120	2165	CUUUUCUGUUUCUACAGG	445
2161	GAGAAAGAAAGACACUCU	121	2161	GAGAAAGAAAGACACUCU	121	2183	AGAGUGUUCUUCUUCUC	446
2179	UGUGGCGGGAAUACUCUU	122	2179	UGUGGCGGGAAUACUCUU	122	2201	AAGAGUAUUCGCGCCAGCA	447
2197	UGGUCACCUCAAAUUAAG	123	2197	UGGUCACCUCAAAUUAAG	123	2219	CUUAAAUUUGAGGUGACCA	448
2215	GUCCGGAUUUCUGUGCU	124	2215	GUCCGGAUUUCUGUGCU	124	2237	AGCAGCAGAAUUCGCGAC	449
2233	UUGAAACUUCAGCCUGAA	125	2233	UUGAAACUUCAGCCUGAA	125	2255	UUCAGGGCUGAAUUCAA	450
2251	ACCUUUGCCACCAUUCU	126	2251	ACCUUUGCCACCAUUCU	126	2273	AGGAAUGGUGGACAAAGGU	451
2269	UUUAAAUUCUCCAAACCAA	127	2269	UUUAAAUUCUCCAAACCAA	127	2291	UUGGUGGAGAAUUAUA	452
2287	AAGUUAUCUUCUUUUA	128	2287	AAGUUAUCUUCUUUUA	128	2309	UAAAGAAAGAAUUAUUA	453
2305	AGUUCAGAAUACUGGCA	129	2305	AGUUCAGAAUACUGGCA	129	2327	UGCCAGUACUUCUGAAACU	454
2323	AUCACACGAGGUUACCU	130	2323	AUCACACGAGGUUACCU	130	2345	AAGGUAACCCUGCGUGUAU	455
2341	UGGCGUGUGUCCUGUGGU	131	2341	UGGCGUGUGUCCUGUGGU	131	2363	ACCACAGGGACACCGCA	456
2359	UACCUUGCCAGAGAGAGA	132	2359	UACCUUGCCAGAGAGAGA	132	2381	UCUUCUUCUGCCAGGGUA	457
2377	ACCAAGCUUUGUUUCCUGC	133	2377	ACCAAGCUUUGUUUCCUGC	133	2399	GCAGGGAACAAAGCUUGGU	458
2395	CUGGCAAGUUCAGUAGGA	134	2395	CUGGCAAGUUCAGUAGGA	134	2417	UCCUACUGACUUGGCCAG	459
2413	AGAGAUCCACAGUUUGCU	135	2413	AGAGAUCCACAGUUUGCU	135	2435	AGCAACUUGGCAUUCUCU	460
2431	UAUUUGCUUUAGAGACAGG	136	2431	UAUUUGCUUUAGAGACAGG	136	2453	CCUGUCUCUAAAAGCAUA	461
2449	GGACUGUAUAAACAGCCU	137	2449	GGACUGUAUAAACAGCCU	137	2471	AGGCUUGUUUAUACAGUCC	462
2467	UAACAUUGGUGCAAGAUU	138	2467	UAACAUUGGUGCAAGAUU	138	2489	AALUUGGACCAAGUUA	463
2485	UGCCUCUUGAAUUAUAAAA	139	2485	UGCCUCUUGAAUUAUAAAA	139	2507	UUUUUAUUUCAAAGAGCA	464
2503	AAAAACUAGAUUGACUUAU	140	2503	AAAAACUAGAUUGACUUAU	140	2525	AUAGUCAAUUCUAGUUUUU	465

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2521	UUUAUACAAUUGGGGGGGG	141	2521	UUUAUACAAUUGGGGGGGG	141	2543	CCGCCCCCAUUGUAUAAA	486
2539	GCUGGAAAGAGGAGAGGA	142	2539	GCUGGAAAGAGGAGAGGA	142	2561	UCCUUCUUCUUCUUCUUCG	487
2557	AGAGGGAGUACAAAGACAG	143	2557	AGAGGGAGUACAAAGACAG	143	2579	CUGUCUUCUUCUUCUUCG	488
2575	GGGAUAGUGGGAUCAAAG	144	2575	GGGAUAGUGGGAUCAAAG	144	2597	CUUUGAUCCCAUUAUCCG	489
2593	GCUAGGAAAGGCAGAAACA	145	2593	GCUAGGAAAGGCAGAAACA	145	2615	UGUUUCUGCCUUCUUCUAGC	490
2611	ACAACACUACACAGUCU	146	2611	ACAACACUACACAGUCU	146	2633	AGGACUGGUGAGUGGUGU	491
2629	UAGUUUAGACCUCAUCUC	147	2629	UAGUUUAGACCUCAUCUC	147	2651	GAGAUGAGGUCUAAACUA	492
2647	CCAAGAAGCAUCCCAUCU	148	2647	CCAAGAAGCAUCCCAUCU	148	2669	AGAUGGAUGCUUUCUUGG	493
2665	UCAGAAGUGGUGUUGU	149	2665	UCAGAAGUGGUGUUGU	149	2687	AACAACCCCAUUCUUGA	494
2683	UUUCAUUGUUUUUUUUU	150	2683	UUUCAUUGUUUUUUUUU	150	2705	AGAAAAGAAACAUUGAAA	495
2701	UGUGGUUGCAGCCUGAGCA	151	2701	UGUGGUUGCAGCCUGAGCA	151	2723	UGGUCAGGCUAGCAACACA	496
2719	AAAAGUGAGUGGGAAGG	152	2719	AAAAGUGAGUGGGAAGG	152	2741	CCCUUCCCAUCUCACU	497
2737	GCUUUUCUAGCCAAAGAGC	153	2737	GCUUUUCUAGCCAAAGAGC	153	2759	GCUUUUGGCUAGAUAGC	498
2755	CUCUUUUUAGCUCUCUUA	154	2755	CUCUUUUUAGCUCUCUUA	154	2777	UAGAGAGCUAAAAAGAG	499
2773	AAUAGAUGCCCAUAAAG	155	2773	AAUAGAUGCCCAUAAAG	155	2795	CUUAGUGGACAUUCAUUU	500
2791	GAAUUUCCCAUUAACAU	156	2791	GAAUUUCCCAUUAACAU	156	2813	AUGUGUUUAGUGGAACUUC	501
2809	UGAAUUCUGCCAUUAUA	157	2809	UGAAUUCUGCCAUUAUA	157	2831	UUAUUAUGGCAAAUUA	502
2827	UUUCAUUGUCUUAUCUG	158	2827	UUUCAUUGUCUUAUCUG	158	2849	CAGAUAGAGACAUGAAAU	503
2845	GAACCAUUCUUAUUCUAC	159	2845	GAACCAUUCUUAUUCUAC	159	2867	GUAGAAUAAAGGGUGUUC	504
2863	CAUUAUAGGACGACUUG	160	2863	CAUUAUAGGACGACUUG	160	2885	CAGUGCUGCCUUAUUAUG	505
2881	GAAUAUCCUAAACCCCUA	161	2881	GAAUAUCCUAAACCCCUA	161	2903	UAGGGGUUAGGAUUAUUC	506
2899	AAGCUCCAGGUGCCUUG	162	2899	AAGCUCCAGGUGCCUUG	162	2921	CACAGGACCCUUGGACUUC	507
2917	GGGAGAGCAACUGGACUUA	163	2917	GGGAGAGCAACUGGACUUA	163	2939	AUAGUCCAGUUGCUCUCC	508
2935	UAGCAGGGCUGGGCUCUGU	164	2935	UAGCAGGGCUGGGCUCUGU	164	2957	ACAGAGCCAGCCUUGCUA	509
2953	UCUUCUGGUAUAGGCUC	165	2953	UCUUCUGGUAUAGGCUC	165	2975	GAGCCUUAUAGCAGGAAGA	510
2971	CACUCUUCUCCCAUUAUCU	166	2971	CACUCUUCUCCCAUUAUCU	166	2993	AGAUUUGGGGGAAGAGUG	511
2989	UUCUCUGGAGCUUUGCAG	167	2989	UUCUCUGGAGCUUUGCAG	167	3011	CUGCAAAGCUCAGAGGAA	512
3007	GCCAAGGUGCUAAAGGAA	168	3007	GCCAAGGUGCUAAAGGAA	168	3029	UUCUUUUAAGCAGCUGGC	513
3025	AUAGGUAGGAGACCUUUC	169	3025	AUAGGUAGGAGACCUUUC	169	3047	GAAGAGGUCUCCUACCUAU	514
3043	CUAUCUAAUCCUAAAGC	170	3043	CUAUCUAAUCCUAAAGC	170	3065	GCUUUUAAGGAUUAUAUG	515
3061	CAUUAUUGUAACAUUCAU	171	3061	CAUUAUUGUAACAUUCAU	171	3083	AUGAAUUGUACAAUUAUG	516
3079	UUAACAGCUGAUGCCCUA	172	3079	UUAACAGCUGAUGCCCUA	172	3101	UAGGGCAUACGCUUGUAA	517
3097	AUAACCCUUGCUGGAUUU	173	3097	AUAACCCUUGCUGGAUUU	173	3119	AAUCCAGGAGGGGUAU	518
3115	UCUUCUUAUAGGCUAUA	174	3115	UCUUCUUAUAGGCUAUA	174	3137	UUUAAGCUUAUAGGAAGA	519
3133	AGAAGUAGCAAGAUUUUA	175	3133	AGAAGUAGCAAGAUUUUA	175	3155	UAAAGAUUCUUGCUACUUCU	520
3151	ACAUAAUUCAGAGUGGUU	176	3151	ACAUAAUUCAGAGUGGUU	176	3173	AAACCACUCUGAAUUUAUG	521

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3169	UCALUGCCUUCGUACCCUC	177	3169	UCALUGCCUUCGUACCCUC	177	3191	GAGGGUAGGAAGGCAUUA	502
3187	CUUUAUUGGCCCUCCAUU	178	3187	CUUUAUUGGCCCUCCAUU	178	3209	AAUGGAGGGCCCAUUAAG	503
3205	UUUUUUGACUAAAGCAUCA	179	3205	UUUUUUGACUAAAGCAUCA	179	3227	UGAUUGCUUUUAGUCUAAUAA	504
3223	ACACAGUGGCACUAGCAUU	180	3223	ACACAGUGGCACUAGCAUU	180	3245	AAUGCUUAGGCCACUGUGU	505
3241	UAUACCAAGAGUAAGAA	181	3241	UAUACCAAGAGUAAGAA	181	3263	UUCUCUACUCUUGGUUAU	506
3259	AAUACAGUGCUUUUUGGCU	182	3259	AAUACAGUGCUUUUUGGCU	182	3281	AGCCAUAAAGACUUAUU	507
3277	UCUAAACUUAUUGCCUUA	183	3277	UCUAAACUUAUUGCCUUA	183	3299	UGAAGGCAGUAUUGUUA	508
3295	AGUAUCAAGGCUUGCCUGGA	184	3295	AGUAUCAAGGCUUGCCUGGA	184	3317	UCCAGGCAGCCUUGAUACU	509
3313	AGAAAGGAUGGCAGCCUCA	185	3313	AGAAAGGAUGGCAGCCUCA	185	3335	UGAGGCGUCCAUUCUUAU	510
3331	AGGGCUUCCUUAUUGCCUC	186	3331	AGGGCUUCCUUAUUGCCUC	186	3353	GAGGACUAAGGAAGCCCU	511
3349	CCACCACAGAGCCUCCUG	187	3349	CCACCACAGAGCCUCCUG	187	3371	CAAGGAGCCUUGUGUGG	512
3367	GAUGAAGGUCAUCUUAUUC	188	3367	GAUGAAGGUCAUCUUAUUC	188	3389	GAAAAAGAUAGCCUUAUC	513
3385	CCCCUACUGCUUUCUCCC	189	3385	CCCCUACUGCUUUCUCCC	189	3407	GGGAAGACAGGAUAGGGG	514
3403	CCUCCCGCCUUAUUGGU	190	3403	CCUCCCGCCUUAUUGGU	190	3425	ACCAUUAAGGCGGGGAGG	515
3421	UACGUGGUAUCCAGGCUG	191	3421	UACGUGGUAUCCAGGCUG	191	3443	CAGCCUGGUAUCCAGGCUG	516
3439	GGUUCUUGGGCUAGGUAGU	192	3439	GGUUCUUGGGCUAGGUAGU	192	3461	ACUACCUAGCCCAAGAAC	517
3457	UGGGACCAAGUUAUUAU	193	3457	UGGGACCAAGUUAUUAU	193	3479	GUAAUGAACUUGGUCUCCA	518
3475	CUUCCUUAUAGUUAUAGC	194	3475	CUUCCUUAUAGUUAUAGC	194	3497	GUUAGAACUUAUAGGAGG	519
3493	CAUAGUAAACUAGGUUACC	195	3493	CAUAGUAAACUAGGUUACC	195	3515	GGUACCGUAGUUUAUUAUG	520
3511	CAGUGUUAUUGGGAAGAGC	196	3511	CAGUGUUAUUGGGAAGAGC	196	3533	GCUCUCCACUUAACUUG	521
3529	CUUGGUUUUCCUAGUAUAC	197	3529	CUUGGUUUUCCUAGUAUAC	197	3551	GUUUAUAGGAAAAACCCAG	522
3547	CCACUGCAUCCUACUCCU	198	3547	CCACUGCAUCCUACUCCU	198	3569	AGGAGUAGGAUGCAGUGGG	523
3565	UACGUGUACACCCGUGC	199	3565	UACGUGUACACCCGUGC	199	3587	GCAGCGGUUUGACCCAGGUA	524
3583	CUUCCAGUUAUGGACCCUG	200	3583	CUUCCAGUUAUGGACCCUG	200	3605	CAGGUCCAUUACCUUGGAG	525
3601	GCUAAGUGUGGAUUUAUCCU	201	3601	GCUAAGUGUGGAUUUAUCCU	201	3623	AGGUAAUCCACACUUAUAGC	526
3619	UGUAAGGGAGAGGGAU	202	3619	UGUAAGGGAGAGGGAU	202	3641	AUUUCCUCCUCCUUAUUA	527
3637	UACAGAGGGCCUUGGU	203	3637	UACAGAGGGCCUUGGU	203	3659	ACCAGAGGCCUCCUUAUUA	528
3655	UGUUCUUGGCCUUGCCAG	204	3655	UGUUCUUGGCCUUGCCAG	204	3677	CUUGGCUUGAGGCCAGGAACA	529
3673	GCUGCCCAAGCCAUAAA	205	3673	GCUGCCCAAGCCAUAAA	205	3695	UUUAUGGUUUGUGGGCAGC	530
3691	ACCAUUAACAAAGAAUAC	206	3691	ACCAUUAACAAAGAAUAC	206	3713	GUUUUUUUUUUUUUUUUGGU	531
3709	CUGAGUCAGUUUUUAUUCU	207	3709	CUGAGUCAGUUUUUAUUCU	207	3731	AGAUAAAAACUAGACUCCAG	532
3727	UGGUUUCUUAUUAUCCCA	208	3727	UGGUUUCUUAUUAUCCCA	208	3749	UGGGAUUAAGAGAACCCA	533
3745	ACUGACUUGGUGGUGCUU	209	3745	ACUGACUUGGUGGUGCUU	209	3767	AAGGACACCAAGUGGACAGU	534
3763	UUGGUGACUGGGAACACC	210	3763	UUGGUGACUGGGAACACC	210	3785	GGUUCUCCACAGUAGCCAA	535
3781	CCCAUUAUACAGAGUUG	211	3781	CCCAUUAUACAGAGUUG	211	3803	CAGACUCUGUAGUUAUUGG	536
3799	GACAGGAAGAGUGGAGACU	212	3799	GACAGGAAGAGUGGAGACU	212	3821	AGUCCACAGUUCUCCUGUC	537

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3817	UGUCCACUUCUAGGUCGGA	213	3817	UGUCCACUUCUAGGUCGGA	213	3839	UCCGAGCUAGAAUGGACA	538
3835	AACUUAACUGUAAUAAA	214	3835	AACUUAACUGUAAUAAA	214	3857	UUUAUUUACACAGUAAGUU	539
3853	ACUUUCAGAACUGCUACCA	215	3853	ACUUUCAGAACUGCUACCA	215	3875	UGGUAGCAGUUCUGCAAGU	540
3871	AUGAAGUGAAAUGCCACA	216	3871	AUGAAGUGAAAUGCCACA	216	3893	UGUGCAUUUUUCACUUCAU	541
3889	AUUUUGCUUUAUAAUUCU	217	3889	AUUUUGCUUUAUAAUUCU	217	3911	AGAAAUUUAUAAAGCAAAU	542
3907	UACCCAGUUGGGAAAAAC	218	3907	UACCCAGUUGGGAAAAAC	218	3929	GUUUUCCCAACAUGGGUA	543
3925	CUGGCUUUUCCAGCCCU	219	3925	CUGGCUUUUCCAGCCCU	219	3947	AGGCGUGGAAAAAGCCAG	544
3943	UUUCCAGGCAUAAACUC	220	3943	UUUCCAGGCAUAAACUC	220	3965	GAGUUUAUAGCCCGUGGAA	545
3961	CAACCCUUCGUAAGCAAG	221	3961	CAACCCUUCGUAAGCAAG	221	3983	CUUGCUUUCGAAAGGGGUG	546
3979	GUCCCAUCAGCUAUUAU	222	3979	GUCCCAUCAGCUAUUAU	222	4001	AUUAAUAGGCGUGAUGGAC	547
3997	UUUUUAAAGAAACUUGC	223	3997	UUUUUAAAGAAACUUGC	223	4019	GCAAGUUUUCUUUAAAAA	548
4015	CACUUGUUUUUUUUUUA	224	4015	CACUUGUUUUUUUUUUA	224	4037	GUAAAAAGAAAAACAAGU	549
4033	CAGUUAUUUUUUUUUUA	225	4033	CAGUUAUUUUUUUUUUA	225	4055	GGCAGGAAAGAAUAACUG	550
4051	CCCAAAAUUAAACUCUA	226	4051	CCCAAAAUUAAACUCUA	226	4073	UAGAGUUUAUUUUUUGGG	551
4069	AAGUGUAAAAAAAGUCUU	227	4069	AAGUGUAAAAAAAGUCUU	227	4091	AAGACUUUUUUUUUACACU	552
4087	UAACACAGCUUCUUGCUU	228	4087	UAACACAGCUUCUUGCUU	228	4109	AAGCAAGAGCGUUGUUA	553
4105	UGUAAAAAUUGUAUUUAU	229	4105	UGUAAAAAUUGUAUUUAU	229	4127	UAUAUAACAUUUUUUACA	554
4123	ACAUUCGUUUUUUUAAUU	230	4123	ACAUUCGUUUUUUUAAUU	230	4145	AUUUUAAAAUACAGAGU	555
4141	UCUGUCCUGAAAAUGAC	231	4141	UCUGUCCUGAAAAUGAC	231	4163	GUCAUUUUUCAGGAGCAGA	556
4159	UGUCCCAUUUCCCAUCUA	232	4159	UGUCCCAUUUCCCAUCUA	232	4181	UGAGUGGAGAUUGGGACAG	557
4177	ACUGCAUUUGGGCGUUUC	233	4177	ACUGCAUUUGGGCGUUUC	233	4199	GAAAGGCCCAAUUGCAGU	558
4195	CCCAUUGGUCUGCAUGUCU	234	4195	CCCAUUGGUCUGCAUGUCU	234	4217	AGACAUUGCAGACCAUUGGG	559
4213	UUUUUAUUGCAGGCCAG	235	4213	UUUUUAUUGCAGGCCAG	235	4235	CUUGGCUUGCAUUGAUAAA	560
4231	GUUGACAGAGGAGAGGG	236	4231	GUUGACAGAGGAGAGGG	236	4253	CCCUUCUCCUCUGUCCAC	561
4249	GAGAACAGGGGUGGCCAAC	237	4249	GAGAACAGGGGUGGCCAAC	237	4271	GUUGGCGACCCUGUUCUC	562
4267	CACUUGUGUUCUUUCUGA	238	4267	CACUUGUGUUCUUUCUGA	238	4289	UCAGAAAGCAACACAGUG	563
4285	ACUGAUCCUGAACAAAGAA	239	4285	ACUGAUCCUGAACAAAGAA	239	4307	UUUCUUGUUCAGGAUCAGU	564
4303	AGAGUAAACUGAGGCGCU	240	4303	AGAGUAAACUGAGGCGCU	240	4325	AGGCCUUCAGUGUUUACUCU	565
4321	UCGUCUCCAUGCACACUC	241	4321	UCGUCUCCAUGCACACUC	241	4343	GAGUUGUGAUGGAGGAGGCA	566
4339	CUCCAAACACUUAUCCUC	242	4339	CUCCAAACACUUAUCCUC	242	4361	GAGGAUAAAGUUIUUGGAG	567
4357	CCUGCAAGAGUGGGCUUUC	243	4357	CCUGCAAGAGUGGGCUUUC	243	4379	GAAAGCCACUCUUGCAGG	568
4375	CCAGGGUUAUUAUUGGAA	244	4375	CCAGGGUUAUUAUUGGAA	244	4397	UUCCCAAGAAAGACCCUGG	569
4393	AGCAGUUAAGCCCCUCCU	245	4393	AGCAGUUAAGCCCCUCCU	245	4415	AGGAGGGGCUUAACUUGCU	570
4411	UCACCCUUCUCCUUUUUCU	246	4411	UCACCCUUCUCCUUUUUCU	246	4433	AGAAAAAGGAAGGGGUGA	571
4429	UUUCUUUACUCCUUGGCU	247	4429	UUUCUUUACUCCUUGGCU	247	4451	AGCCAAAGAGUAAAGAA	572
4447	UUCAAAGGAUUUUGGAAA	248	4447	UUCAAAGGAUUUUGGAAA	248	4469	UUUCCAAAAUCCUUAUGAA	573

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4485	AGAAACAUAUUGCUUUA	249	4485	AGAAACAUAUUGCUUUA	249	4487	UGUAAGCAUAUUGUUUCU	574
4483	ACUCAUUAUUAUUAUA	250	4483	ACUCAUUAUUAUUAUA	250	4505	UUAAGAAUUGAAAUAGU	575
4501	AUUUGCAGGGGUAUUA	251	4501	AUUUGCAGGGGUAUUA	251	4523	UCAGUAUCCCCUUGCAAUU	576
4519	AAAAUACGGGAGGUGGC	252	4519	AAAAUACGGGAGGUGGC	252	4541	GGCCACUUGCGGUUAUUU	577
4537	CUAAGGUGUGUAUAUA	253	4537	CUAAGGUGUGUAUAUA	253	4559	AACUUAACAGCAGCUCUAG	578
4555	UGAGGGGAGGAAUUAU	254	4555	UGAGGGGAGGAAUUAU	254	4577	AGAAUUCUUCUCCCUUA	579
4573	UAAGAUUAACAUAUAAA	255	4573	UAAGAUUAACAUAUAAA	255	4595	UUUUUAUUGUAUAUUA	580
4591	AACGAUCCCUAAACAAA	256	4591	AACGAUCCCUAAACAAA	256	4613	UUUUUAUUGUAUAUUA	581
4609	AAAGAACAUAAGACUGU	257	4609	AAAGAACAUAAGACUGU	257	4631	ACCAGUUAUUAUUGUUAU	582
4627	UCUUCUUAUUGCCACUU	258	4627	UCUUCUUAUUGCCACUU	258	4649	AAGUGGCAAAUUGGAAGA	583
4645	UUCUGUUAUAGACAGUA	259	4645	UUCUGUUAUAGACAGUA	259	4667	UAGCUGUAUUAAGACAGAA	584
4663	ACUAAACUUGGAGACAGUA	260	4663	ACUAAACUUGGAGACAGUA	260	4685	UUAUUGUCCAGGUUAUAGU	585
4681	ACAUUAUAUAACCAAGA	261	4681	ACAUUAUAUAACCAAGA	261	4703	UGUUUGUUAUUAAGAAUUGU	586
4699	AMGUGGUGUACCUUAUA	262	4699	AAAGUGGUGUACCUUAUA	262	4721	AGGUCAGGUGACCCACUUU	587
4717	UCUAAAGAGCUGUAUAUC	263	4717	UCUAAAGAGCUGUAUAUC	263	4739	GAGUACUACGUCUUAUUA	588
4735	CAGGCACUCCAAUACCC	264	4735	CAGGCACUCCAAUACCC	264	4757	GGGUUAUUGGAGUGGCCUG	589
4753	CUACAAGAUUGCAAGGAG	265	4753	CUACAAGAUUGCAAGGAG	265	4775	CCUCCUUGGCAUUAUUAU	590
4771	GUCCAGGAGUCCAGCUC	266	4771	GUCCAGGAGUCCAGCUC	266	4793	GAGCUGGAGUCCUGGGAC	591
4789	CCUUAACUUGACGUAGUC	267	4789	CCUUAACUUGACGUAGUC	267	4811	GACUAGCUGCAGUUAAGG	592
4807	CAUAUAACUUGGCAAGUG	268	4807	CAUAUAACUUGGCAAGUG	268	4829	CACUUGCCAGGUUAUUAU	593
4825	GAGCAAGAGAAUUAAGGA	269	4825	GAGCAAGAGAAUUAAGGA	269	4847	UCCUUAUUAUUAUUAUUAU	594
4843	AAGAUCCAUUCUGAGGU	270	4843	AAGAUCCAUUCUGAGGU	270	4865	ACCUACAGAUUGAUUAUUA	595
4861	UGACAGGCAAGGAUUAAG	271	4861	UGACAGGCAAGGAUUAAG	271	4883	CUUUAUCCUUGCCUUAUA	596
4879	GACAAAGAGGAAUUAAGU	272	4879	GACAAAGAGGAAUUAAGU	272	4901	AGUCUUUUCUUAUUAUUAU	597
4897	UAUCAAAGGCAAGAGGAG	273	4897	UAUCAAAGGCAAGAGGAG	273	4919	CUCCUUUUGCCUUUAUAUA	598
4915	GAUCAUUAUUGGUGUCUG	274	4915	GAUCAUUAUUGGUGUCUG	274	4937	CAGACCCAAUAUUAUUAU	599
4933	GAAAGGAAAGUUAUUAU	275	4933	GAAAGGAAAGUUAUUAU	275	4955	AGCAAGAGUUAUUAUUAU	600
4951	UAUCCGACAUUAUUAUUA	276	4951	UAUCCGACAUUAUUAUUA	276	4973	UAGCAGUUAUUAUUAUUAU	601
4969	AGUACCUUGUAAGAUUAUA	277	4969	AGUACCUUGUAAGAUUAUA	277	4991	UAAAUUGCUUAUUAUUAU	602
4987	AGUCCAGAUUAUUAUUA	278	4987	AGUCCAGAUUAUUAUUA	278	5009	UUUUUCCAUUAUUAUUAU	603
5005	AAAAUACGUAUUAUUAU	279	5005	AAAAUACGUAUUAUUAU	279	5027	UUACCAUUAUUAUUAUUAU	604
5023	AUAUAUAUUAUUAUUAU	280	5023	AUAUAUAUUAUUAUUAU	280	5045	GGAAAGGACAUUAUUAUUAU	605
5041	CCUGGAGUUAUUAUUAU	281	5041	CCUGGAGUUAUUAUUAU	281	5063	UAAAAACUUAUUAUUAUUAU	606
5059	AAAAUUAUUAUUAUUAU	282	5059	AAAAUUAUUAUUAUUAU	282	5081	AACUUAAGAGUUAUUAUUAU	607
5077	UUUAUUAUUAUUAUUAU	283	5077	UUUAUUAUUAUUAUUAU	283	5099	UAGAUUAUUAUUAUUAUUAU	608
5095	AAAAGAGAGGAGGUGAG	284	5095	AAAAGAGAGGAGGUGAG	284	5117	CUACAGUCCCUUAUUAUUAU	609

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5113	GGCAUUCUCCUUGUAGGAGU	285	5113	GGCAUUCUCCUUGUAGGAGU	285	5185	ACUCCUACACGGGAUUGGCC	610
5131	UAAAGAUAAAAGGAGUAGGA	286	5131	UAAAGAUAAAAGGAGUAGGA	286	5185	UCCUUAUCCUUAUUAUUAUUA	611
5149	AAAAGAUCAAAGCUCUAA	287	5149	AAAAGAUCAAAGCUCUAA	287	5171	UUAGAGCULUUGAAUUAUUAU	612
5167	AUAGAGUCACGCUUCC	288	5167	AUAGAGUCACGCUUCC	288	5189	GGGAAAGCUGUGACUUAU	613
5185	CAGGUAAACACUAAAU	289	5185	CAGGUAAACACUAAAU	289	5207	AUUUAGGUUUUAUUAUUAU	614
5203	UUAGAAGUACAAUAGCA	290	5203	UUAGAAGUACAAUAGCA	290	5225	UCCUUAUUGUACUUAUUA	615
5221	AGAGGUGGAAAUUAUUA	291	5221	AGAGGUGGAAAUUAUUA	291	5243	UAGAUAUUUUAUUAUUAUUA	616
5239	AGUUCUUAUAGCUACCA	292	5239	AGUUCUUAUAGCUACCA	292	5261	UGGUAGCUUAUUAUUAUUA	617
5257	ACAGAGCAAGUUAUUAU	293	5257	ACAGAGCAAGUUAUUAU	293	5279	UAUAAUUAUUAUUAUUAU	618
5275	AAAUUUGAAUUAUUAUUA	294	5275	AAAUUUGAAUUAUUAUUA	294	5297	UAGUUUUGGUUAUUAUUAU	619
5293	ACUUCUUAUUAUUAUUA	295	5293	ACUUCUUAUUAUUAUUA	295	5315	AAAGUUAUUAUUAUUAUUA	620
5311	UGGUCUCCAUUUUUAUUA	296	5311	UGGUCUCCAUUUUUAUUA	296	5333	CUGGGAAAUUAUUAUUAU	621
5329	GGACAGAAAUUAUUAUUA	297	5329	GGACAGAAAUUAUUAUUA	297	5351	GGGACAUUAUUAUUAUUAU	622
5347	CCCUUAUUAUUAUUAUUA	298	5347	CCCUUAUUAUUAUUAUUA	298	5369	GAAGCAAGAAUUAUUAUUA	623
5365	CAAAAUUAUUAUUAUUAU	299	5365	CAAAAUUAUUAUUAUUAU	299	5387	UGGUGAAUUAUUAUUAUUA	624
5383	AUCCAGAUUAUUAUUAU	300	5383	AUCCAGAUUAUUAUUAU	300	5405	UGUAGAAUUAUUAUUAUUA	625
5401	AAGUUAUUAUUAUUAUUA	301	5401	AAGUUAUUAUUAUUAUUA	301	5423	UGUUGUUAUUAUUAUUAU	626
5419	AUCUCCUACCCAGUUGCC	302	5419	AUCUCCUACCCAGUUGCC	302	5441	GGCACUUGGGUGAGGAGAU	627
5437	CUUCUUGGAGCUCACCAA	303	5437	CUUCUUGGAGCUCACCAA	303	5459	UUGGUGAGCUCACGAGAG	628
5455	AGUACACCAUUAUUAUUA	304	5455	AGUACACCAUUAUUAUUA	304	5477	CCAAGUUAUUAUUAUUAU	629
5473	GUUGUAAACCAUUAUUAU	305	5473	GUUGUAAACCAUUAUUAU	305	5495	AAGGCAAGUUAUUAUUAU	630
5491	UAACCUUUGGGAGGAGG	306	5491	UAACCUUUGGGAGGAGG	306	5513	CCCUUCCUUAUUAUUAUUA	631
5509	GGAUUAGCUUUAUUAUUA	307	5509	GGAUUAGCUUUAUUAUUA	307	5531	CUCCUAGCUUUAUUAUUAU	632
5527	GACAGAGUUAUUAUUAU	308	5527	GACAGAGUUAUUAUUAU	308	5549	UUCUUAUUAUUAUUAUUAU	633
5545	AAGGUGAGGACUUAUUA	309	5545	AAGGUGAGGACUUAUUAU	309	5567	UUGUAGAGUUAUUAUUAU	634
5563	AUGUUGGCUUUAUUAUUA	310	5563	AUGUUGGCUUUAUUAUUA	310	5585	AGCUCUAGAGGCAUUAUUA	635
5581	UUGAUUAGAGCAUUAUUA	311	5581	UUGAUUAGAGCAUUAUUA	311	5603	UGUUCUUGGCUUUAUUAU	636
5599	AGUGGACCAAGGAGAGAC	312	5599	AGUGGACCAAGGAGAGAC	312	5621	GUUUCUUAUUAUUAUUAU	637
5617	CUUGGCCAGGAAUUAUUA	313	5617	CUUGGCCAGGAAUUAUUA	313	5639	AGGUUUUUAUUAUUAUUAU	638
5635	UGUGGUUUGUUAUUAUUA	314	5635	UGUGGUUUGUUAUUAUUA	314	5657	GAUUUAUUAUUAUUAUUAU	639
5653	CUUGCCAGAAUUAUUAUUA	315	5653	CUUGCCAGAAUUAUUAUUA	315	5675	CACCUUAUUAUUAUUAUUA	640
5671	GGACAGAGCUUUAUUAUUA	316	5671	GGACAGAGCUUUAUUAUUA	316	5693	ACCCCAUUAUUAUUAUUAU	641
5689	UGCAUGGAGAAUUAUUAU	317	5689	UGCAUGGAGAAUUAUUAU	317	5711	GUCCCAUUAUUAUUAUUAU	642
5707	CCUGGUUAUUAUUAUUAU	318	5707	CCUGGUUAUUAUUAUUAU	318	5729	GAUUAUUAUUAUUAUUAU	643
5725	CUUGGACUUGAAUUAUUAU	319	5725	CUUGGACUUGAAUUAUUAU	319	5747	CCAAAUUAUUAUUAUUAU	644
5743	GUGAUUUAUUAUUAUUAU	320	5743	GUGAUUUAUUAUUAUUAU	320	5765	AUAUUAUUAUUAUUAUUAU	645

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5761	UUCUGUAAACCCUAAUGUCU	321	5761	UUCUGUAAACCCUAAUGUCU	321	5783	AGACAUUAGGUUUACAGAA	646
5779	UGUAUAAAUAAUGAGCGUU	322	5779	UGUAUAAAUAAUGAGCGUU	322	5801	AACGGUCAUUUAUUAACA	647
5797	UACACAGUAAAAUUAUCA	323	5797	UACACAGUAAAAUUAUCA	323	5819	UGAAUUAUUUACUGUGUUA	648
5815	AUUAAGAAAGUCAAAAAAA	324	5815	AUUAAGAAAGUCAAAAAAA	324	5837	UUUUUUUUGACUUCUUAUU	649
5821	AAGUCAAAAAUAUUUUUUUU	325	5821	AAGUCAAAAAUAUUUUUUUU	325	5843	UUUUUUUUUUUUUUGACUU	650

The 3'-ends of the Upper sequence and the Lower sequence of the siNA construct can include an overhang sequence, for example about 1, 2, 3, or 4 nucleotides in length, preferably 2 nucleotides in length, wherein the overhanging sequence of the lower sequence is optionally complementary to a portion of the target sequence. The upper sequence is also referred to as the sense strand, whereas the lower sequence is also referred to as the antisense strand. The upper and lower sequences in the Table can further comprise a chemical modification having Formulae I-VII or any combination thereof

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Table III: BACE Synthetic Modified siRNA constructs

Target Pos	Target	Seq ID	RPI #	Aliases	Sequence	Seq ID
1480	AAUGGUGAGGUAUCCAAACAGU	651	31005	BACE:1482U21 siRNA sense	UGGUGAGGUAUCCAAACAGU	655
1753	UCACUUGGACAUUGGAAGACUGU	652	31006	BACE:1755U21 siRNA sense	ACCUUGGACAUUGGAAGACU	656
2457	CCUAACAUUGGUGCAAGAGAUUGC	653	31007	BACE:2459U21 siRNA sense	UAACAUUGGUGCAAGAGAU	657
3583	UAUGGGACCUUGCAAGAGUUGGAA	654	31008	BACE:3585U21 siRNA sense	UGGACCUUGCAAGAGUUGG	658
1480	AAUGGUGAGGUAUCCAAACAGU	651	31081	BACE:1510L21 siRNA (1492C) antisense	UGGUUGUAACCUACCCAGT	659
1753	UCACUUGGACAUUGGAAGACUGU	652	31082	BACE:1773L21 siRNA (1735C) antisense	AGUCUUGGACAUUGGAAGG	660
2457	CCUAACAUUGGUGCAAGAGAUUGC	653	31083	BACE:2477L21 siRNA (2459C) antisense	AAUCUUGGACAUUGGAAG	661
3583	UAUGGGACCUUGCAAGAGUUGGAA	654	31084	BACE:3583L21 siRNA (3585C) antisense	CCACACUUGGACCUUGGAA	662
1480	AAUGGUGAGGUAUCCAAACAGU	651	30729	BACE:1492U21 siRNA stab04 sense	B UGGUGAGGUAUCCAAACATT B	663
1753	UCACUUGGACAUUGGAAGACUGU	652	30730	BACE:1755U21 siRNA stab04 sense	B ACCUUGGACAUUGGAAGACU	664
2457	CCUAACAUUGGUGCAAGAGUUGGAA	653	31378	BACE:2459U21 siRNA stab04 sense	B UAACAUUGGUGCAAGAGU	665
3583	UAUGGGACCUUGCAAGAGUUGGAA	654	30732	BACE:3585U21 siRNA stab04 sense	B UGGGACCUUGCAAGAGU	666
1480	AAUGGUGAGGUAUCCAAACAGU	651	30733	BACE:1510L21 siRNA (1492C) antisense	UGGUUGUAACCUACCCAGT	667
1753	UCACUUGGACAUUGGAAGACUGU	652	30734	BACE:1773L21 siRNA (1735C) antisense	AGUCUUGGACAUUGGAAGG	668
2457	CCUAACAUUGGUGCAAGAGAUUGC	653	31381	BACE:2477L21 siRNA (2459C) antisense	AAUCUUGGACAUUGGAAG	669
3583	UAUGGGACCUUGCAAGAGUUGGAA	654	30736	BACE:3583L21 siRNA (3585C) antisense	CCACACUUGGACCUUGGAA	670
1480	AAUGGUGAGGUAUCCAAACAGU	651		BACE:1492U21 siRNA stab07 sense	B UGGUGAGGUAUCCAAACATT B	671
1753	UCACUUGGACAUUGGAAGACUGU	652		BACE:1755U21 siRNA stab07 sense	B ACCUUGGACAUUGGAAGACU	672
2457	CCUAACAUUGGUGCAAGAGUUGGAA	653	31384	BACE:2459U21 siRNA stab07 sense	B UAACAUUGGUGCAAGAGU	673
3583	UAUGGGACCUUGCAAGAGUUGGAA	654		BACE:3585U21 siRNA stab07 sense	B UGGGACCUUGCAAGAGU	674
1480	AAUGGUGAGGUAUCCAAACAGU	651		BACE:1510L21 siRNA (1492C) antisense	UGGUUGUAACCUACCCAGT	675
1753	UCACUUGGACAUUGGAAGACUGU	652		BACE:1773L21 siRNA (1735C) antisense	AGUCUUGGACAUUGGAAG	676
2457	CCUAACAUUGGUGCAAGAGUUGGAA	653	31387	BACE:2477L21 siRNA (2459C) antisense	AAUCUUGGACAUUGGAAG	677
3583	UAUGGGACCUUGCAAGAGUUGGAA	654		BACE:3583L21 siRNA (3585C) antisense	CCACACUUGGACCUUGGAA	678
2457	CCUAACAUUGGUGCAAGAGUUGGAA	653	31390	BACE:2459U21 siRNA inv stab04	B UAACAUUGGUGCAAGAGU	679
2457	CCUAACAUUGGUGCAAGAGUUGGAA	653	31393	BACE:2477L21 siRNA (2459C) inv stab05	AAUCUUGGACAUUGGAAG	680
2457	CCUAACAUUGGUGCAAGAGUUGGAA	653	31398	BACE:2459U21 siRNA inv stab07	B UAACAUUGGUGCAAGAGU	681
2457	CCUAACAUUGGUGCAAGAGUUGGAA	653	31399	BACE:2477L21 siRNA (2459C) inv stab11	AAUCUUGGACAUUGGAAG	682

Uppercase = ribonucleotide

u,e = 2'-deoxy-2'-fluoro U,C

T = thymidine

B = inverted deoxy abasic

s = phosphorothioate linkage

A = deoxy Adenosine

G = deoxy Guanosine

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Table IV
Non-limiting examples of Stabilization Chemistries for chemically modified siNA constructs

Chemistry	pyrimidine	Purine	Cap	p=S	Strand
"Stab 1"	Ribo	Ribo	-	5 at 5'-end 1 at 3'-end	S/AS
"Stab 2"	Ribo	Ribo	-	All linkages	Usually AS
"Stab 3"	2'-fluoro	Ribo	-	4 at 5'-end 4 at 3'-end	Usually S
"Stab 4"	2'-fluoro	Ribo	5' and 3'-ends	-	Usually S
"Stab 5"	2'-fluoro	Ribo	-	1 at 3'-end	Usually AS
"Stab 6"	2'-O-Methyl	Ribo	5' and 3'-ends	-	Usually S
"Stab 7"	2'-fluoro	2'-deoxy	5' and 3'-ends	-	Usually S
"Stab 8"	2'-fluoro	2'-O-Methyl	-	1 at 3'-end	Usually AS
"Stab 9"	Ribo	Ribo	5' and 3'-ends	-	Usually S
"Stab 10"	Ribo	Ribo	-	1 at 3'-end	Usually AS
"Stab 11"	2'-fluoro	2'-deoxy	-	1 at 3'-end	Usually AS

Cap = any terminal cap, see for example **Figure 10**.

All Stab 1-11 chemistries can comprise 3'-terminal thymidine (TT) residues

All Stab 1-11 chemistries typically comprise 21 nucleotides, but can vary as described herein.

S = sense strand

AS = antisense strand

Table V

A. 2.5 μ mol Synthesis Cycle ABI 394 Instrument

Reagent	Equivalents	Amount	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time*RNA
Phosphoramidites	6.5	163 μ L	45 sec	2.5 min	7.5 min
S-Ethyl Tetrazole	23.8	238 μ L	45 sec	2.5 min	7.5 min
Acetic Anhydride	100	233 μ L	5 sec	5 sec	5 sec
N-Methyl Imidazole	186	233 μ L	5 sec	5 sec	5 sec
TCA	176	2.3 mL	21 sec	21 sec	21 sec
Iodine	11.2	1.7 mL	45 sec	45 sec	45 sec
Beaucage	12.9	645 μ L	100 sec	300 sec	300 sec
Acetonitrile	NA	6.67 mL	NA	NA	NA

B. 0.2 μ mol Synthesis Cycle ABI 394 Instrument

Reagent	Equivalents	Amount	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time*RNA
Phosphoramidites	15	31 μ L	45 sec	233 sec	465 sec
S-Ethyl Tetrazole	38.7	31 μ L	45 sec	233 min	465 sec
Acetic Anhydride	655	124 μ L	5 sec	5 sec	5 sec
N-Methyl Imidazole	1245	124 μ L	5 sec	5 sec	5 sec
TCA	700	732 μ L	10 sec	10 sec	10 sec
Iodine	20.6	244 μ L	15 sec	15 sec	15 sec
Beaucage	7.7	232 μ L	100 sec	300 sec	300 sec
Acetonitrile	NA	2.64 mL	NA	NA	NA

C. 0.2 μ mol Synthesis Cycle 96 well Instrument

Reagent	Equivalents:DNA/ 2'-O-methyl/Ribo	Amount: DNA/2'-O- methyl/Ribo	Wait Time* DNA	Wait Time* 2'-O- methyl	Wait Time* Ribo
Phosphoramidites	22/33/66	40/60/120 μ L	60 sec	180 sec	360sec
S-Ethyl Tetrazole	70/105/210	40/60/120 μ L	60 sec	180 min	360 sec
Acetic Anhydride	265/265/265	50/50/50 μ L	10 sec	10 sec	10 sec
N-Methyl Imidazole	502/502/502	50/50/50 μ L	10 sec	10 sec	10 sec
TCA	236/475/475	250/500/500 μ L	15 sec	15 sec	15 sec
Iodine	6.8/6.8/6.8	80/80/80 μ L	30 sec	30 sec	30 sec
Beaucage	34/51/51	80/120/120	100 sec	200 sec	200 sec
Acetonitrile	NA	1150/1150/1150 μ L	NA	NA	NA

- 5
- Wait time does not include contact time during delivery.
 - Tandem synthesis utilizes double coupling of linker molecule

The claims defining the invention are as follows:

1. A chemically synthesized double stranded short interfering nucleic acid (siNA) molecule that directs cleavage of a beta secretase (BACE) RNA via RNA interference (RNAi), wherein:
 - (a) each strand of said siNA molecule is about 19 to about 23 nucleotides in length;
 - (b) one strand of said siNA molecule comprises nucleotide sequence that is complementary to said BACE RNA such that the siNA molecule directs cleavage of the BACE RNA via RNA interference; and
 - (c) said siNA molecule comprises at least one chemically modified nucleotide or non-nucleotide.
2. The siNA molecule of claim 1, wherein said siNA molecule comprises no ribonucleotides.
3. The siNA molecule of claim 1, wherein said siNA molecule comprises one or more ribonucleotides.
4. The siNA molecule of claim 1, wherein said chemically modified nucleotide comprises a 2'-deoxy nucleotide.
5. The siNA molecule of claim 1, wherein said chemically modified nucleotide comprises a 2'-deoxy-2'-fluoro nucleotide.
6. The siNA molecule of claim 1, wherein said chemically modified nucleotide comprises a 2'-O-methyl nucleotide.
7. The siNA molecule of claim 1, wherein said chemically modified nucleotide comprises a phosphorothioate internucleotide linkage.
8. The siNA molecule of claim 1, wherein said non-nucleotide comprises an abasic moiety.
9. The siNA molecule of claim 8, wherein said abasic moiety comprises an inverted deoxyabasic moiety.
10. The siNA molecule of claim 1, wherein said non-nucleotide comprises a glyceryl moiety.
11. The siNA molecule of claim 1, wherein one strand of said double-stranded siNA molecule comprises a nucleotide sequence that is complementary to a nucleotide sequence of a BACE gene or a portion thereof, and wherein a second strand of said double-stranded siNA molecule comprises a nucleotide sequence that is the same as the nucleotide sequence or a portion thereof said BACE RNA.

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12. The siNA molecule of claim 11, wherein each strand of the siNA molecule comprises about 19 to about 23 nucleotides, and wherein each strand comprises at least about 19 nucleotides that are complementary to the nucleotides of the other strand.
13. The siNA molecule of claim 1, wherein said siNA molecule comprises an
 5 antisense region comprising a nucleotide sequence that is complementary to a nucleotide sequence of a BACE gene or a portion thereof, and wherein said siNA further comprises a sense region, wherein said sense region comprises a nucleotide sequence that is the same as the nucleotide sequence of said BACE gene or a portion thereof.
14. The siNA molecule of claim 13, wherein said antisense region and said sense
 10 region comprises about 19 to about 23 nucleotides, and wherein said antisense region comprises at least about 19 nucleotides that are complementary to nucleotides of the sense region.
15. The siNA molecule of claim 1, wherein said siNA molecule comprises a sense region and an antisense region, and wherein said antisense region comprises a nucleotide
 15 sequence that is complementary to a nucleotide sequence of RNA encoded by a BACE gene, or a portion thereof, and said sense region comprises a nucleotide sequence that is complementary to said antisense region.
16. The siNA molecule of claim 13, wherein said siNA molecule is assembled from two separate oligonucleotide fragments wherein one fragment comprises the sense region
 20 and a second fragment comprises the antisense region of said siNA molecule.
17. The siNA molecule of claim 13, wherein said sense region is connected to the antisense region via a linker molecule.
18. The siNA molecule of claim 17, wherein said linker molecule is a polynucleotide linker.
- 25 19. The siNA molecule of claim 17, wherein said linker molecule is a non-nucleotide linker.
20. The siNA molecule of claim 13, wherein pyrimidine nucleotides in the sense region are 2'-O-methyl pyrimidine nucleotides.
21. The siNA molecule of claim 13, wherein purine nucleotides in the sense region
 30 are 2'-deoxy purine nucleotides.
22. The siNA molecule of claim 13, wherein pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides.
23. The siNA molecule of claim 16, wherein the fragment comprising said sense region includes a terminal cap moiety at the 5'-end, the 3'-end, or both of the 5' and 3'
 35 ends of the fragment comprising said sense region.

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24. The siNA molecule of claim 23, wherein said terminal cap moiety is an inverted deoxy abasic moiety.

25. The siNA molecule of claim 13, wherein pyrimidine nucleotides of said antisense region at 2'-deoxy-2'-fluoro pyrimidine nucleotides.

5 26. The siNA molecule of claim 13, wherein purine nucleotides of said antisense region are 2'-O-methyl purine nucleotides.

27. The siNA molecule of claim 13, wherein purine nucleotides present in said antisense region comprise 2'-deoxy-purine nucleotides.

10 28. The siNA molecule of claim 13, wherein said antisense region comprises a phosphorothioate internucleotide linkage at the 3' end of said antisense region.

29. The siNA molecule of claim 13, wherein said antisense region comprises a glyceryl modification at the 3' end of said antisense region.

30. The siNA molecule of claim 16, wherein each of the two fragments of said siNA molecule comprise 21 nucleotides.

15 31. The siNA molecule of claim 30, wherein about 19 nucleotides of each fragment of the siNA molecule are base-paired to the complementary nucleotides of the other fragment of the siNA molecule and wherein at least two 3' terminal nucleotides of each fragment of the siNA molecule are not base-paired to the nucleotides of the other fragment of the siNA molecule.

20 32. The siNA molecule of claim 31, wherein each of the two 3' terminal nucleotides of each fragment of the siNA molecule are 2'-deoxy-pyrimidines.

33. The siNA molecule of claim 32, wherein said 2'-deoxy-pyrimidine is 2'-deoxy-thymidine.

25 34. The siNA molecule of claim 30, wherein all 21 nucleotides of each fragment of the siNA molecule are base-paired to the complementary nucleotides of the other fragment of the siNA molecule.

35. The siNA molecule of claim 30, wherein about 19 nucleotides of the antisense region are base-paired to the nucleotide sequence of the RNA encoded by a BACE gene or a portion thereof.

30 36. The siNA molecule of claim 30, wherein 21 nucleotides of the antisense region are base-paired to the nucleotide sequence of the RNA encoded by a BACE gene or a portion thereof.

37. The siNA molecule of claim 16, wherein the 5'-end of the fragment comprising said antisense region optionally includes a phosphate group.

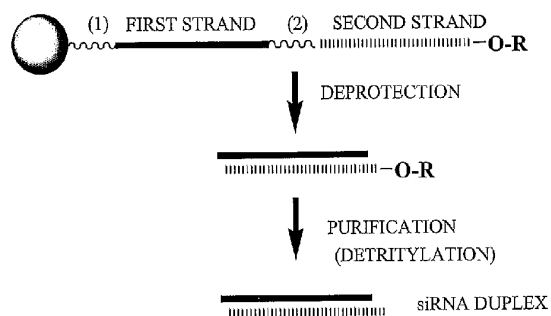
38. A chemically synthesized double stranded short interfering nucleic acid (siNA) molecule that directs cleavage of a beta secretase (BACE) RNA via RNA interference (RNAi), substantially as hereinbefore described with reference to any one of the examples.

- 5 39. A pharmaceutical composition comprising the siNA molecule according to any one of claims 1 to 38 in an acceptable carrier or diluent.

Dated 28 April, 2004
Sirna Therapeutics, Inc.

Patent Attorneys for the Applicant/Nominated Person
SPRUSON & FERGUSON

10

Figure 1

= SOLID SUPPORT

R = TERMINAL PROTECTING GROUP

FOR EXAMPLE:

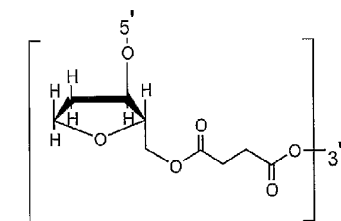
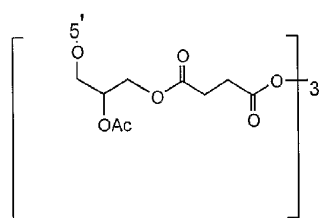
DIMETHOXYTRITYL (DMT)



(1) = CLEAVABLE LINKER

(FOR EXAMPLE: NUCLEOTIDE SUCCINATE OR
INVERTED DEOXYABASIC SUCCINATE)

(2) = CLEAVABLE LINKER

(FOR EXAMPLE: NUCLEOTIDE SUCCINATE OR
INVERTED DEOXYABASIC SUCCINATE)INVERTED DEOXYABASIC SUCCINATE
LINKAGE

GLYCERYL SUCCINATE LINKAGE

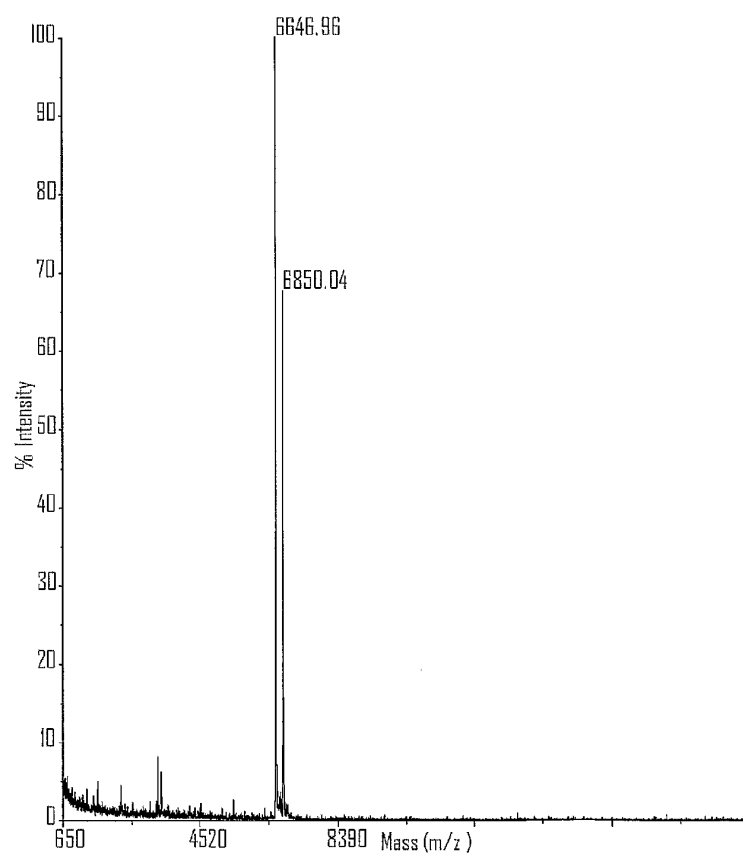
Figure 2

Figure 3

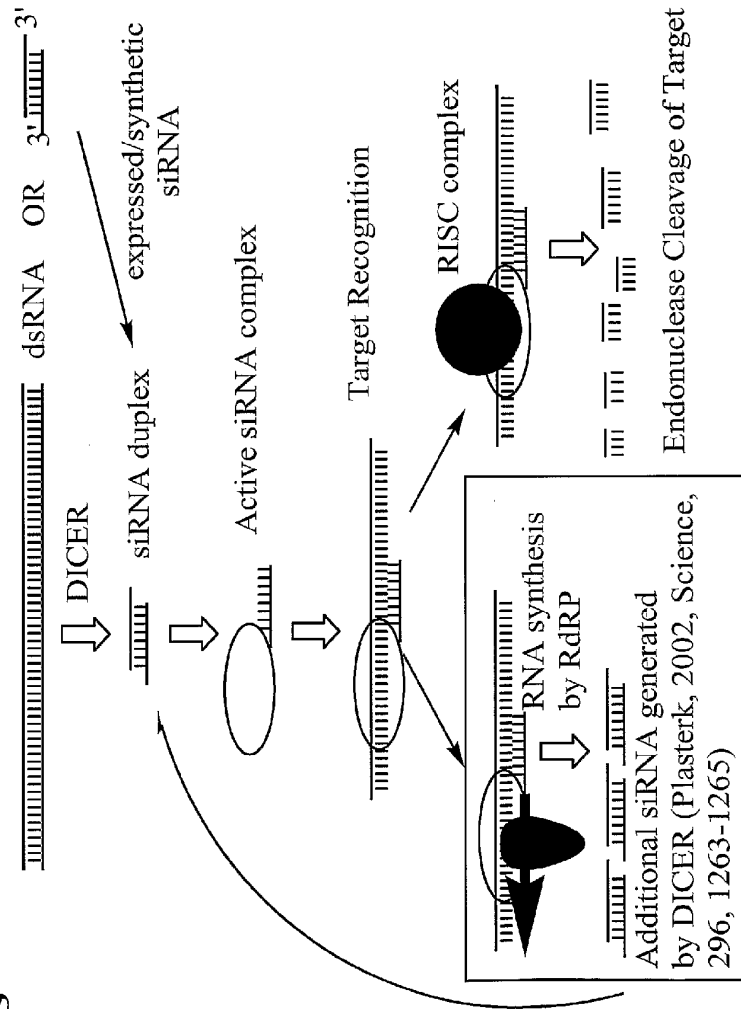
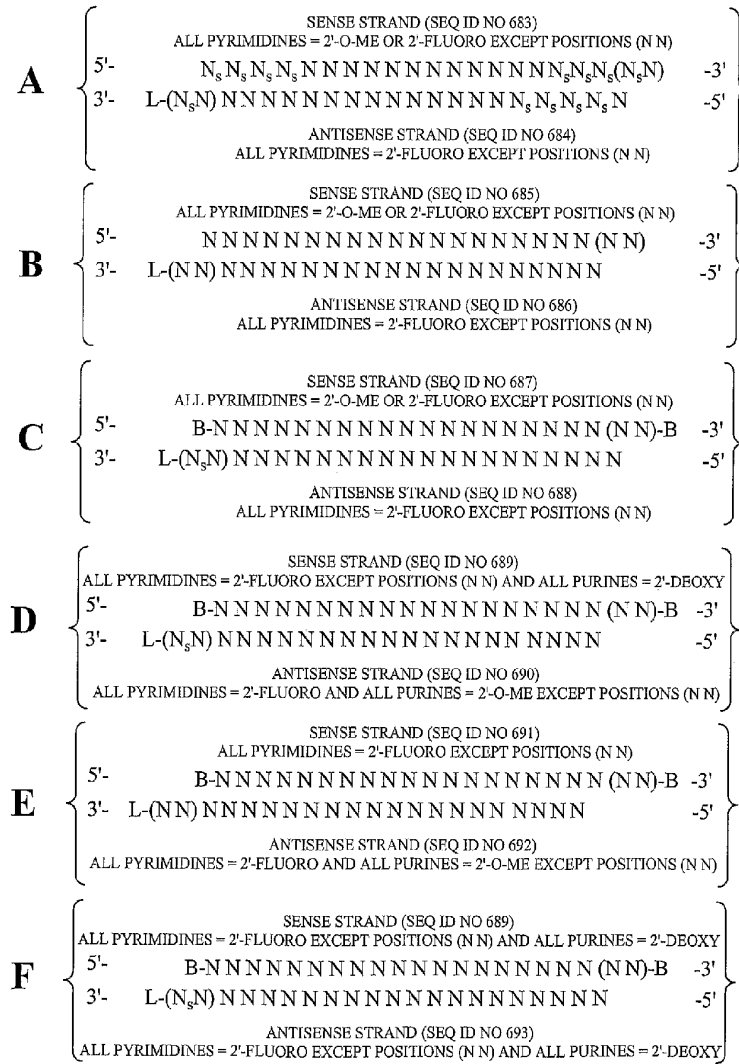
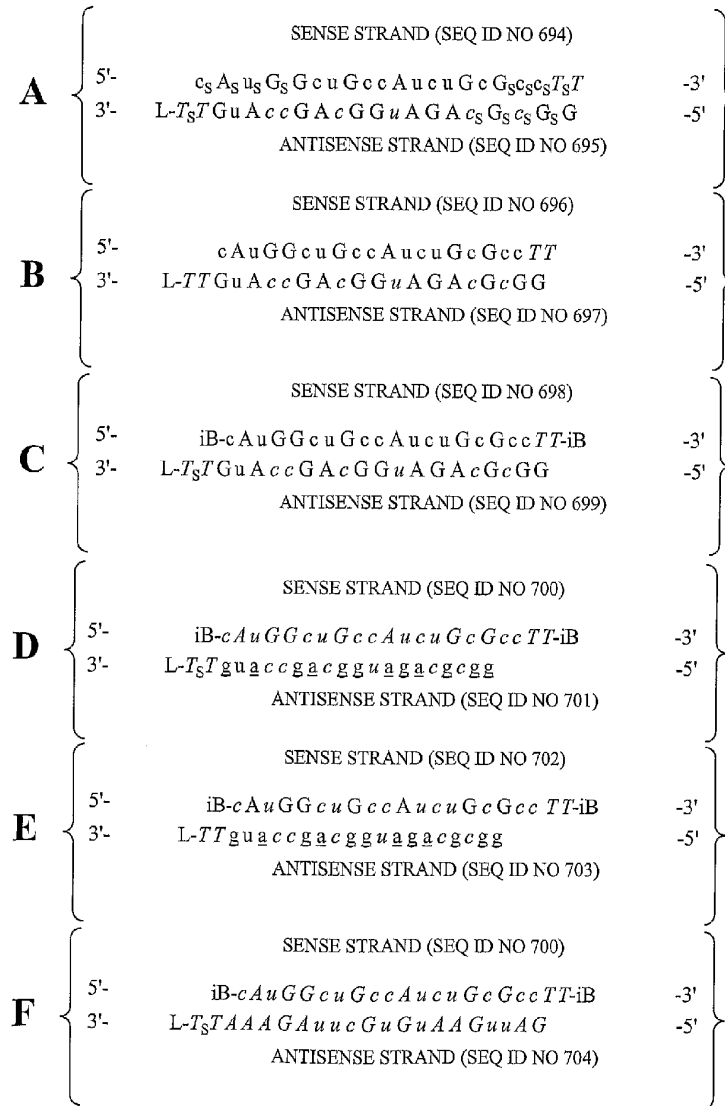


Figure 4

POSITIONS (NN) CAN COMPRISE ANY NUCLEOTIDE, SUCH AS DEOXYNUCLEOTIDES (eg. THYMIDINE) OR UNIVERSAL BASES
 B = ABASIC, INVERTED ABASIC, INVERTED NUCLEOTIDE OR OTHER TERMINAL CAP THAT IS OPTIONALLY PRESENT
 L = GLYCERYL MOIETY THAT IS OPTIONALLY PRESENT
 S = PHOSPHOROTHIOATE OR PHOSPHORODITHIOATE

Figure 5

lower case = 2'-O-Methyl or 2'-deoxy-2'-fluoro

italic lower case = 2'-deoxy-2'-fluorounderline = 2'-O-methyl*ITALIC UPPER CASE* = DEOXY

B = INVERTED DEOXYABASIC

L = GLYCERYL MOIETY OPTIONALLY PRESENT

S = PHOSPHOROTHIOATE OR

PHOSPHORODITHIOATE

Figure 6

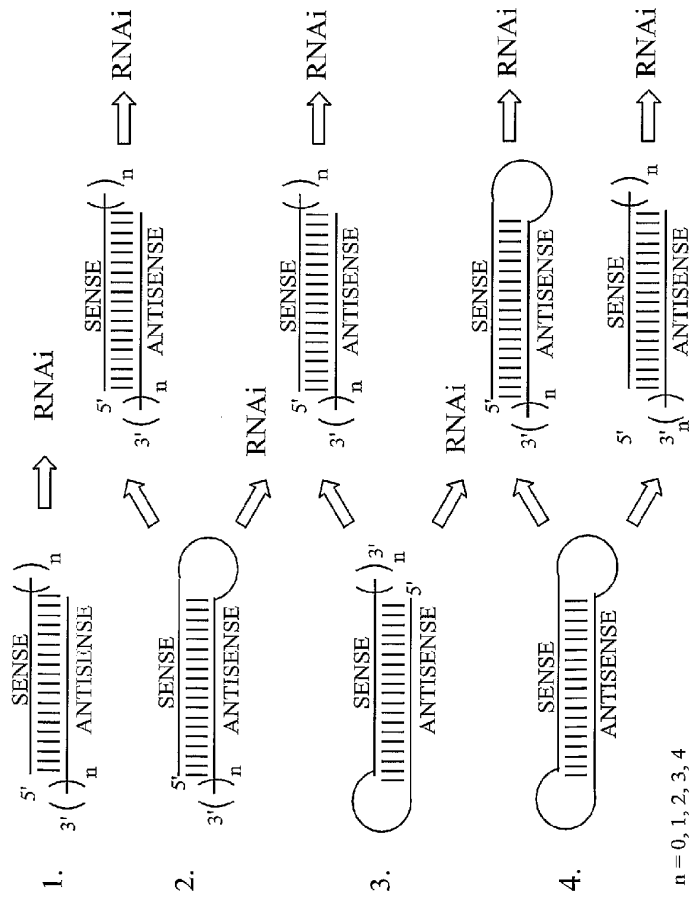


Figure 7

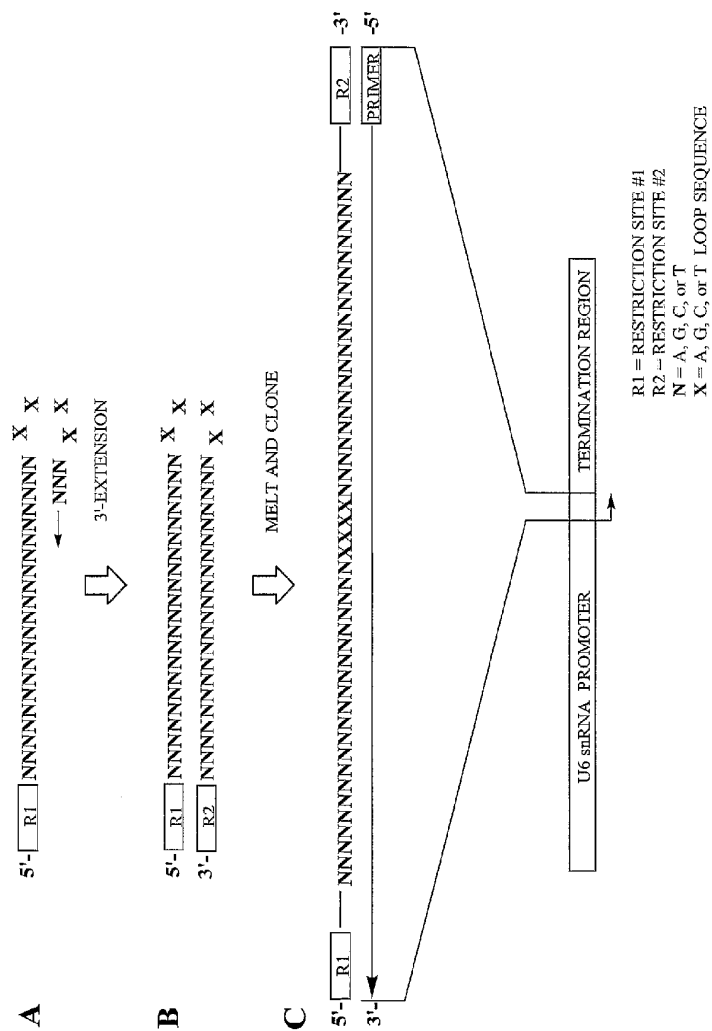


Figure 8

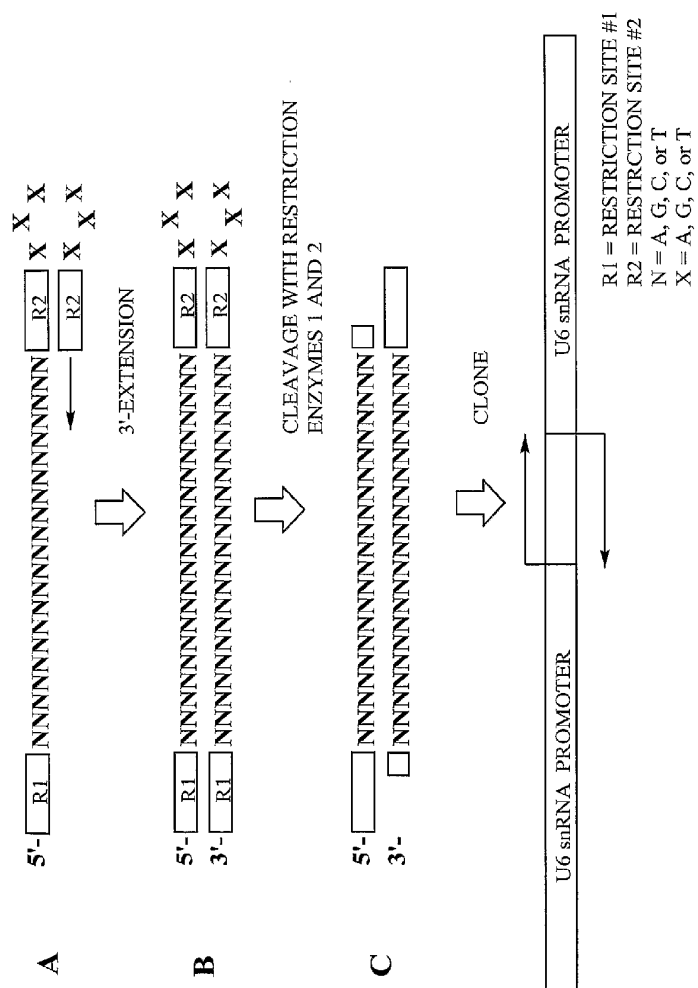


Figure 9: Target site Selection using siRNA

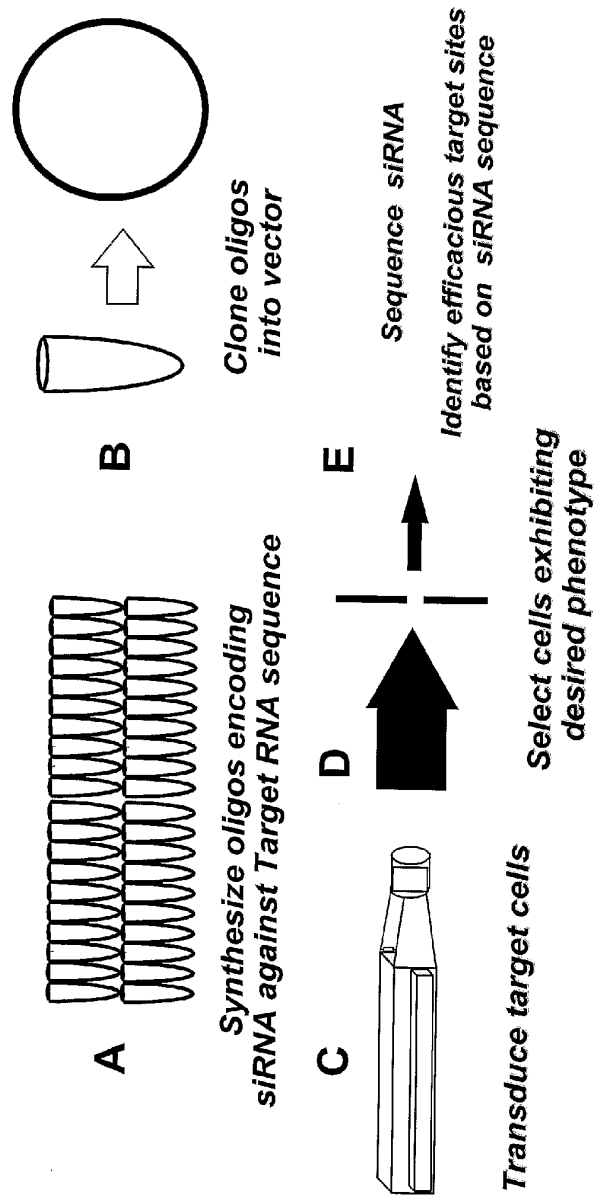
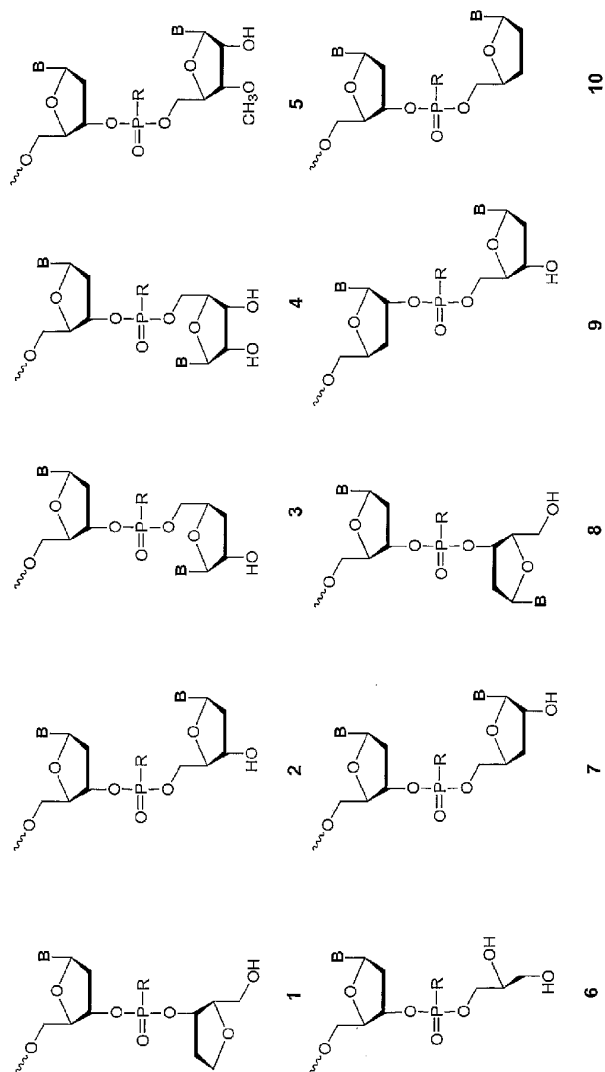


Figure 10

R = O, S, N, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, or aralkyl
 B = Independently any nucleotide base, either naturally occurring or chemically modified, or optionally H (abasic).

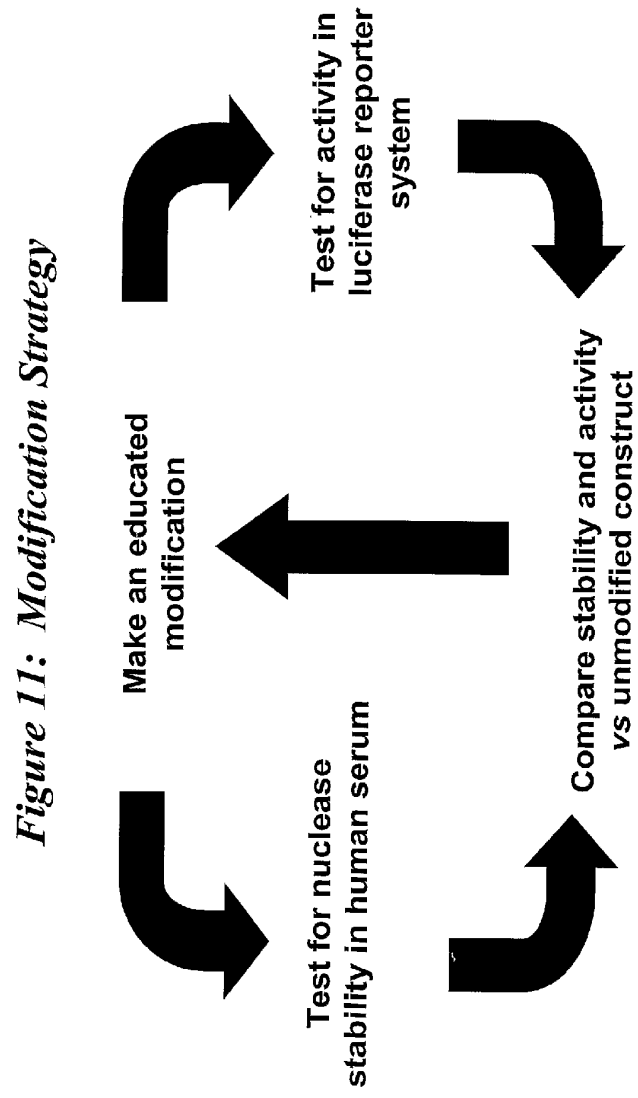


Figure 12: A549 24h BACE mRNA Expression

