CLAIMS

We claim:

1. A modified antisense oligomer capable of binding a selected target to induce exon skipping in the human dystrophin gene, wherein the modified antisense oligomer comprises a sequence of bases that is complementary to an exon 2, intron 1, or intron 2 target region of the dystrophin pre-mRNA designated as an annealing site; wherein the base sequence and/or annealing site are selected from one of the following:

Annealing Site	**Base Sequence [5' to 3']**	**SEQ ID NO.**
H2.SA.(-20+05)	TTC ATC TAA AAT GCA AAA TAA AAA A	SEQ ID NO. 1
H2.SA.(-14+11)	TTC TCT TTC ATC TAA AAT GCA AAA T	SEQ ID NO. 2
H2.SA.(-11+14)	ATC TTC TCT TTC ATC TAA AAT GCA A	SEQ ID NO. 3
H2.SA.(-08+17)	AAC ATC TTC TCT TTC ATC TAA AAT G	SEQ ID NO. 4
H2.SA.(-05+20)	TTG AAC ATC TTC TCT TTC ATC TAA A	SEQ ID NO. 5
~~H2.SA.(-02+23)~~	~~CTT TTG AAC ATC TTC TCT TTC ATC T~~	~~SEQ ID NO. 6~~
~~H2.SA.(+02+26)~~	~~TTT CTT TTG AAC ATC TTC TCT TTC A~~	~~SEQ ID NO. 7~~
~~H2.SA.(+05+29)~~	~~TGT TTT CTT TTG AAC ATC TTC TCT T~~	~~SEQ ID NO. 8~~
~~H2.SA.(+08+32)~~	~~GAA TGT TTT CTT TTG AAC ATC TTC T~~	~~SEQ ID NO. 9~~
~~H2.SA.(+11+35)~~	~~TGT GAA TGT TTT CTT TTG AAC ATC T~~	~~SEQ ID NO. 10~~
~~H2.SA.(+14+38)~~	~~TTT TGT GAA TGT TTT CTT TTG AAC A~~	~~SEQ ID NO. 11~~
~~H2.SA.(+17+41)~~	~~CCA TTT TGT GAA TGT TTT CTT TTG A~~	~~SEQ ID NO. 12~~
~~H2.SA.(+20+44)~~	~~TAC CCA TTT TGT GAA TGT TTT CTT T~~	~~SEQ ID NO. 13~~
~~H2.SA.(+23+47)~~	~~ATT TAC CCA TTT TGT GAA TGT TTT C~~	~~SEQ ID NO. 14~~
~~H2.SA.(+26+50)~~	~~TGC ATT TAC CCA TTT TGT GAA TGT T~~	~~SEQ ID NO. 15~~
~~H2.SA.(+29+53)~~	~~TTG TGC ATT TAC CCA TTT TGT GAA T~~	~~SEQ ID NO. 16~~
~~H2.SA.(+32+56)~~	~~AAA TTG TGC ATT TAC CCA TTT TGT G~~	~~SEQ ID NO. 17~~
~~H2.SA.(+35+59)~~	~~AGA AAA TTG TGC ATT TAC CCA TTT T~~	~~SEQ ID NO. 18~~
~~H2.SA.(+38+62)~~	~~CTT AGA AAA TTG TGC ATT TAC CCA T~~	~~SEQ ID NO. 19~~
~~H2.SD.(+22-03)~~	~~TAC CTT AGA AAA TTG TGC ATT TAC C~~	~~SEQ ID NO. 20~~
~~H2.SD.(+19-06)~~	~~TCT TAC CTT AGA AAA TTG TGC ATT T~~	~~SEQ ID NO. 21~~
~~H2.SD.(+16-09)~~	~~CAT TCT TAC CTT AGA AAA TTG TGC A~~	~~SEQ ID NO. 22~~
~~H2.SD.(+13-12)~~	~~AAC CAT TCT TAC CTT AGA AAA TTG T~~	~~SEQ ID NO. 23~~
~~H2.SD.(+10-15)~~	~~ACA AAC CAT TCT TAC CTT AGA AAA T~~	~~SEQ ID NO. 24~~
~~H2A(+06+30)~~	~~ATG TTT TCT TTT GAA CAT CTT CTC T~~	~~SEQ ID NO. 25~~
~~H2A(+07+31)~~	~~AAT GTT TTC TTT TGA ACA TCT TCT C~~	~~SEQ ID NO. 26~~
~~H2A(+09+33)~~	~~TGA ATG TTT TCT TTT GAA CAT CTT C~~	~~SEQ ID NO. 27~~
~~H2A(+10+34)~~	~~GTG AAT GTT TTC TTT TGA ACA TCT T~~	~~SEQ ID NO. 28~~
~~H2A(-23+02)~~	~~ATC TAA AAT GCA AAA TAA AAA AAT A~~	~~SEQ ID NO. 29~~
~~H2A(-26-02)~~	~~TAA AAT GCA AAA TAA AAA AAT AAA A~~	~~SEQ ID NO. 30~~
~~H2A(-29-05)~~	~~AAT GCA AAA TAA AAA AAT AAA AGT T~~	~~SEQ ID NO. 31~~
~~H2A(-32-08)~~	~~GCA AAA TAA AAA AAT AAA AGT TAG G~~	~~SEQ ID NO. 32~~
~~H2A(-35-11)~~	~~AAA TAA AAA AAT AAA AGT TAG GAA G~~	~~SEQ ID NO. 33~~
H2A(-38-14)	TAA AAA AAT AAA AGT TAG GAA GCA A	SEQ ID NO. 34

H2A(-41-17)	AAA AAT AAA AGT TAG GAA GCA ACT T	SEQ ID NO. 35
~~H2A(+11+29)~~	~~TGT TTT CTT TTG AAC ATC T~~	~~SEQ ID NO. 36~~
~~H2D(+15-08)~~	~~ATT CTT ACC TTA GAA AAT TGT GC~~	~~SEQ ID NO. 37~~
~~H2A(+46+62)~~	~~CTT AGA AAA TTG TGC AT~~	~~SEQ ID NO. 38~~
~~H2D(+08-09)~~	~~CAT TCT TAC CTT AGA AA~~	~~SEQ ID NO. 39~~

wherein T is thymine or uracil.

2. The modified antisense oligomer of claim 1, wherein the base sequence and/or annealing site are selected from one of the following:

Annealing Site	**Base Sequence [5' to 3']**	**SEQ ID NO.**
H2.SA.(-20+05)	TTC ATC TAA AAT GCA AAA TAA AAA A	SEQ ID NO. 1
H2.SA.(-14+11)	TTC TCT TTC ATC TAA AAT GCA AAA T	SEQ ID NO. 2
H2.SA.(-11+14)	ATC TTC TCT TTC ATC TAA AAT GCA A	SEQ ID NO. 3
H2.SA.(-08+17)	AAC ATC TTC TCT TTC ATC TAA AAT G	SEQ ID NO. 4
H2.SA.(-05+20)	TTG AAC ATC TTC TCT TTC ATC TAA A	SEQ ID NO. 5
~~H2.SA.(-02+23)~~	~~CTT TTG AAC ATC TTC TCT TTC ATC T~~	~~SEQ ID NO. 6~~
~~H2.SA.(+02+26)~~	~~TTT CTT TTG AAC ATC TTC TCT TTC A~~	~~SEQ ID NO. 7~~
~~H2.SA.(+05+29)~~	~~TGT TTT CTT TTG AAC ATC TTC TCT T~~	~~SEQ ID NO. 8~~
~~H2.SA.(+08+32)~~	~~GAA TGT TTT CTT TTG AAC ATC TTC T~~	~~SEQ ID NO. 9~~
~~H2.SA.(+11+35)~~	~~TGT GAA TGT TTT CTT TTG AAC ATC T~~	~~SEQ ID NO. 10~~
~~H2.SA.(+14+38)~~	~~TTT TGT GAA TGT TTT CTT TTG AAC A~~	~~SEQ ID NO. 11~~
~~H2.SA.(+17+41)~~	~~CCA TTT TGT GAA TGT TTT CTT TTG A~~	~~SEQ ID NO. 12~~
~~H2.SA.(+20+44)~~	~~TAC CCA TTT TGT GAA TGT TTT CTT T~~	~~SEQ ID NO. 13~~
~~H2.SA.(+23+47)~~	~~ATT TAC CCA TTT TGT GAA TGT TTT C~~	~~SEQ ID NO. 14~~
~~H2.SA.(+26+50)~~	~~TGC ATT TAC CCA TTT TGT GAA TGT T~~	~~SEQ ID NO. 15~~
~~H2.SA.(+29+53)~~	~~TTG TGC ATT TAC CCA TTT TGT GAA T~~	~~SEQ ID NO. 16~~
~~H2.SA.(+32+56)~~	~~AAA TTG TGC ATT TAC CCA TTT TGT G~~	~~SEQ ID NO. 17~~
~~H2.SA.(+35+59)~~	~~AGA AAA TTG TGC ATT TAC CCA TTT T~~	~~SEQ ID NO. 18~~
~~H2.SD.(+22-03)~~	~~TAC CTT AGA AAA TTG TGC ATT TAC C~~	~~SEQ ID NO. 20~~
~~H2.SD.(+19-06)~~	~~TCT TAC CTT AGA AAA TTG TGC ATT T~~	~~SEQ ID NO. 21~~
~~H2.SD.(+16-09)~~	~~CAT TCT TAC CTT AGA AAA TTG TGC A~~	~~SEQ ID NO. 22~~
~~H2.SD.(+13-12)~~	~~AAC CAT TCT TAC CTT AGA AAA TTG T~~	~~SEQ ID NO. 23~~
~~H2.SD.(+10-15)~~	~~ACA AAC CAT TCT TAC CTT AGA AAA T~~	~~SEQ ID NO. 24~~
~~H2A(+06+30)~~	~~ATG TTT TCT TTT GAA CAT CTT CTC T~~	~~SEQ ID NO. 25~~
~~H2A(+07+31)~~	~~AAT GTT TTC TTT TGA ACA TCT TCT C~~	~~SEQ ID NO. 26~~
~~H2A(+09+33)~~	~~TGA ATG TTT TCT TTT GAA CAT CTT C~~	~~SEQ ID NO. 27~~
~~H2A(+10+34)~~	~~GTG AAT GTT TTC TTT TGA ACA TCT T~~	~~SEQ ID NO. 28~~
~~H2A(-23+02)~~	~~ATC TAA AAT GCA AAA TAA AAA AAT A~~	~~SEQ ID NO. 29~~
~~H2A(-26-02)~~	~~TAA AAT GCA AAA TAA AAA AAT AAA A~~	~~SEQ ID NO. 30~~
~~H2A(-29-05)~~	~~AAT GCA AAA TAA AAA AAT AAA AGT T~~	~~SEQ ID NO. 31~~
~~H2A(-32-08)~~	~~GCA AAA TAA AAA AAT AAA AGT TAG G~~	~~SEQ ID NO. 32~~
~~H2A(-35-11)~~	~~AAA TAA AAA AAT AAA AGT TAG GAA G~~	~~SEQ ID NO. 33~~
H2A(-38-14)	TAA AAA AAT AAA AGT TAG GAA GCA A	SEQ ID NO. 34
H2A(-41-17)	AAA AAT AAA AGT TAG GAA GCA ACT T	SEQ ID NO. 35
~~H2A(+11+29)~~	~~TGT TTT CTT TTG AAC ATC T~~	~~SEQ ID NO. 36~~

~~H2D(+15-08)~~	~~ATT CTT ACC TTA GAA AAT TGT GC~~	~~SEQ ID NO. 37~~
~~H2A(+46+62)~~	~~CTT AGA AAA TTG TGC AT~~	~~SEQ ID NO. 38~~
~~H2D(+08-09)~~	~~CAT TCT TAC CTT AGA AA~~	~~SEQ ID NO. 39~~

3. The modified antisense oligomer of claim 1, wherein the base sequence and/or annealing site are selected from one of the following:

Annealing Site	**Base Sequence [5' to 3']**	**SEQ ID NO.**
H2.SA.(-20+05)	TTC ATC TAA AAT GCA AAA TAA AAA A	SEQ ID NO. 1
H2.SA.(-14+11)	TTC TCT TTC ATC TAA AAT GCA AAA T	SEQ ID NO. 2
H2.SA.(-11+14)	ATC TTC TCT TTC ATC TAA AAT GCA A	SEQ ID NO. 3
H2.SA.(-08+17)	AAC ATC TTC TCT TTC ATC TAA AAT G	SEQ ID NO. 4
H2.SA.(-05+20)	TTG AAC ATC TTC TCT TTC ATC TAA A	SEQ ID NO. 5
~~H2.SA.(-02+23)~~	~~CTT TTG AAC ATC TTC TCT TTC ATC T~~	~~SEQ ID NO. 6~~
~~H2.SA.(+02+26)~~	~~TTT CTT TTG AAC ATC TTC TCT TTC A~~	~~SEQ ID NO. 7~~
~~H2.SA.(+05+29)~~	~~TGT TTT CTT TTG AAC ATC TTC TCT T~~	~~SEQ ID NO. 8~~
~~H2.SA.(+08+32)~~	~~GAA TGT TTT CTT TTG AAC ATC TTC T~~	~~SEQ ID NO. 9~~
~~H2.SA.(+11+35)~~	~~TGT GAA TGT TTT CTT TTG AAC ATC T~~	~~SEQ ID NO. 10~~
~~H2.SA.(+14+38)~~	~~TTT TGT GAA TGT TTT CTT TTG AAC A~~	~~SEQ ID NO. 11~~
~~H2.SA.(+17+41)~~	~~CCA TTT TGT GAA TGT TTT CTT TTG A~~	~~SEQ ID NO. 12~~
~~H2.SA.(+20+44)~~	~~TAC CCA TTT TGT GAA TGT TTT CTT T~~	~~SEQ ID NO. 13~~
~~H2.SA.(+38+62)~~	~~CTT AGA AAA TTG TGC ATT TAC CCA T~~	~~SEQ ID NO. 19~~
~~H2.SD.(+22-03)~~	~~TAC CTT AGA AAA TTG TGC ATT TAC C~~	~~SEQ ID NO. 20~~
~~H2.SD.(+19-06)~~	~~TCT TAC CTT AGA AAA TTG TGC ATT T~~	~~SEQ ID NO. 21~~
~~H2A(+06+30)~~	~~ATG TTT TCT TTT GAA CAT CTT CTC T~~	~~SEQ ID NO. 25~~
~~H2A(+07+31)~~	~~AAT GTT TTC TTT TGA ACA TCT TCT C~~	~~SEQ ID NO. 26~~
~~H2A(+09+33)~~	~~TGA ATG TTT TCT TTT GAA CAT CTT C~~	~~SEQ ID NO. 27~~
~~H2A(+10+34)~~	~~GTG AAT GTT TTC TTT TGA ACA TCT T~~	~~SEQ ID NO. 28~~
H2A(-38-14)	TAA AAA AAT AAA AGT TAG GAA GCA A	SEQ ID NO. 34
H2A(-41-17)	AAA AAT AAA AGT TAG GAA GCA ACT T	SEQ ID NO. 35
~~H2A(+11+29)~~	~~TGT TTT CTT TTG AAC ATC T~~	~~SEQ ID NO. 36~~

4. The modified antisense oligomer of claim 1, wherein the base sequence and/or annealing site are selected from one of the following:

Annealing Site	**Base Sequence [5' to 3']**	**SEQ ID NO.**
H2.SA.(-20+05)	TTC ATC TAA AAT GCA AAA TAA AAA A	SEQ ID NO. 1
H2.SA.(-14+11)	TTC TCT TTC ATC TAA AAT GCA AAA T	SEQ ID NO. 2
H2.SA.(-11+14)	ATC TTC TCT TTC ATC TAA AAT GCA A	SEQ ID NO. 3
H2.SA.(-08+17)	AAC ATC TTC TCT TTC ATC TAA AAT G	SEQ ID NO. 4
H2.SA.(-05+20)	TTG AAC ATC TTC TCT TTC ATC TAA A	SEQ ID NO. 5
~~H2.SA.(-02+23)~~	~~CTT TTG AAC ATC TTC TCT TTC ATC T~~	~~SEQ ID NO. 6~~
~~H2.SA.(+02+26)~~	~~TTT CTT TTG AAC ATC TTC TCT TTC A~~	~~SEQ ID NO. 7~~
~~H2.SA.(+05+29)~~	~~TGT TTT CTT TTG AAC ATC TTC TCT T~~	~~SEQ ID NO. 8~~

~~H2.SA.(+08+32)~~	~~GAA TGT TTT CTT TTG AAC ATC TTC T~~	~~SEQ ID NO. 9~~
~~H2.SA.(+11+35)~~	~~TGT GAA TGT TTT CTT TTG AAC ATC T~~	~~SEQ ID NO. 10~~
~~H2.SA.(+14+38)~~	~~TTT TGT GAA TGT TTT CTT TTG AAC A~~	~~SEQ ID NO. 11~~
~~H2.SA.(+17+41)~~	~~CCA TTT TGT GAA TGT TTT CTT TTG A~~	~~SEQ ID NO. 12~~
~~H2.SA.(+20+44)~~	~~TAC CCA TTT TGT GAA TGT TTT CTT T~~	~~SEQ ID NO. 13~~
~~H2.SD.(+22-03)~~	~~TAC CTT AGA AAA TTG TGC ATT TAC C~~	~~SEQ ID NO. 20~~
~~H2.SD.(+19-06)~~	~~TCT TAC CTT AGA AAA TTG TGC ATT T~~	~~SEQ ID NO. 21~~
~~H2A(+06+30)~~	~~ATG TTT TCT TTT GAA CAT CTT CTC T~~	~~SEQ ID NO. 25~~
~~H2A(+07+31)~~	~~AAT GTT TTC TTT TGA ACA TCT TCT C~~	~~SEQ ID NO. 26~~
~~H2A(+09+33)~~	~~TGA ATG TTT TCT TTT GAA CAT CTT C~~	~~SEQ ID NO. 27~~
~~H2A(+10+34)~~	~~GTG AAT GTT TTC TTT TGA ACA TCT T~~	~~SEQ ID NO. 28~~
H2A(-38-14)	TAA AAA AAT AAA AGT TAG GAA GCA A	SEQ ID NO. 34
H2A(-41-17)	AAA AAT AAA AGT TAG GAA GCA ACT T	SEQ ID NO. 35
~~H2A(+11+29)~~	~~TGT TTT CTT TTG AAC ATC T~~	~~SEQ ID NO. 36~~

5. The modified antisense oligomer of claim 1, wherein the base sequence is selected from one of the following: SEQ ID NO. 3, SEQ ID NO. 4, SEQ ID NO. 5, ~~SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 8, SEQ ID NO. 9, SEQ ID NO. 10, SEQ ID NO. 19, SEQ ID NO. 20, SEQ ID NO. 21, SEQ ID NO. 25, SEQ ID NO. 26, SEQ ID NO. 27, SEQ ID NO. 28,~~ or SEQ ID NO. 35.

6. The modified antisense oligomer of claim 1, wherein the base sequence is selected from one of the following: SEQ ID NO. 3, SEQ ID NO. 4, SEQ ID NO. 5, ~~SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 8, SEQ ID NO. 9, SEQ ID NO. 10, SEQ ID NO. 20, SEQ ID NO. 21, SEQ ID NO. 25, SEQ ID NO. 26, SEQ ID NO. 27, SEQ ID NO. 28,~~ or SEQ ID NO. 35.

7. The modified antisense oligomer of claim 1, wherein the base sequence is selected from one of the following: SEQ ID NO. 3[[,]] or SEQ ID NO. 5, ~~SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 8, SEQ ID NO. 9, SEQ ID NO. 10, SEQ ID NO. 20, SEQ ID NO. 21, SEQ ID NO. 25, SEQ ID NO. 26, SEQ ID NO. 27, or SEQ ID NO. 28~~.

~~8. The modified antisense oligomer of claim 1, wherein the base sequence is selected from one of the following: SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 25, or SEQ ID NO. 28.~~

~~9. The modified antisense oligomer of claim 1, wherein the base sequence is SEQ ID NO. 19.~~

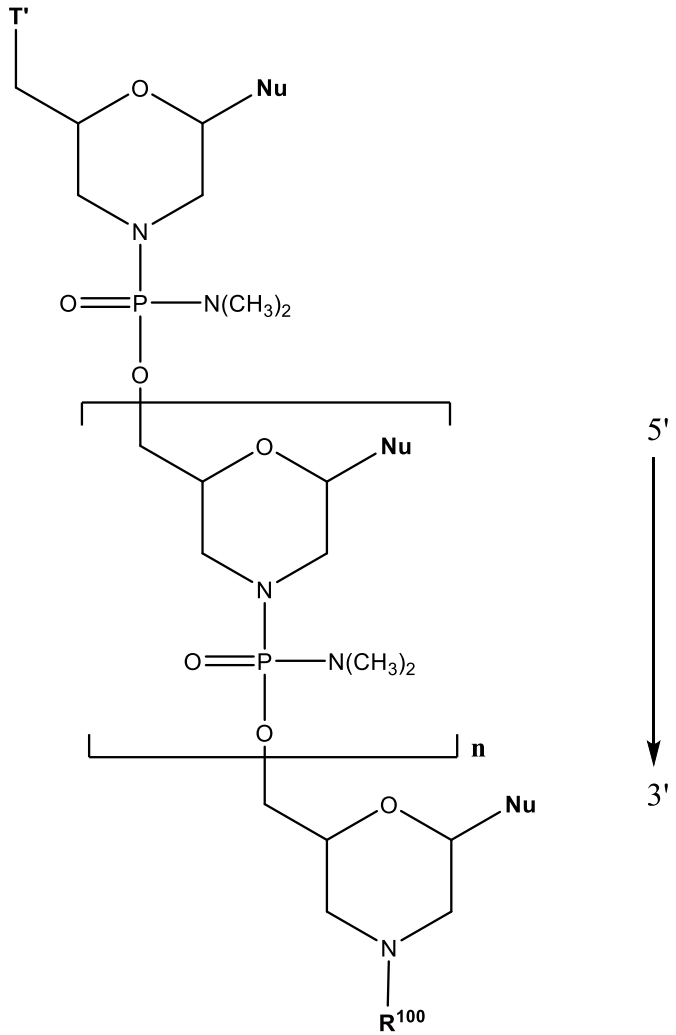
~~10. The modified antisense oligomer of claim 1, wherein the base sequence of the annealing site is SEQ ID NO. 37~~

~~11~~8. The modified antisense oligomer of any of claims 1-~~10~~7, wherein T is thymine.

~~12~~9. The modified antisense oligomer of ~~any one of claims 1-11~~ claim ~~11~~8, wherein the nucleobases of the modified antisense oligomer are linked to morpholino ring structures.

~~13~~10. The modified antisense oligomer of claim ~~12~~9, wherein the morpholino ring structures are joined by phosphorous-containing intersubunit linkages joining a morpholino nitrogen of one ring structure to a 5' exocyclic carbon of an adjacent ring structure.

~~14~~11. An antisense oligomer according to Formula (I):

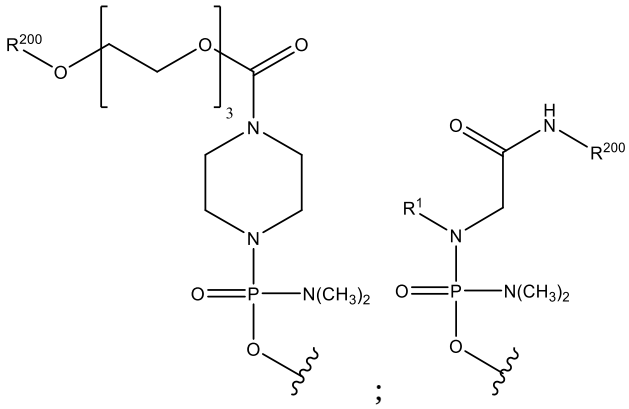


(I)

or a pharmaceutically acceptable salt thereof, wherein:

each **Nu** is a nucleobase which taken together form a targeting sequence;

T' in Formula (I) is a moiety selected from:



$\mathbf{R^{100}}$ and $\mathbf{R^{200}}$ are each independently hydrogen or a cell-penetrating peptide and $\mathbf{R^{1}}$ is C_1-C_6 alkyl;

each **Nu** from 1 to (**n**+1) and 5' to 3' corresponds to the nucleobases in one of the following:

Annealing Site	**Base Sequence [5' to 3']**	**SEQ ID NO.**
H2.SA.(-20+05)	TTC ATC TAA AAT GCA AAA TAA AAA A	SEQ ID NO. 1
H2.SA.(-14+11)	TTC TCT TTC ATC TAA AAT GCA AAA T	SEQ ID NO. 2
H2.SA.(-11+14)	ATC TTC TCT TTC ATC TAA AAT GCA A	SEQ ID NO. 3
H2.SA.(-08+17)	AAC ATC TTC TCT TTC ATC TAA AAT G	SEQ ID NO. 4
H2.SA.(-05+20)	TTG AAC ATC TTC TCT TTC ATC TAA A	SEQ ID NO. 5
~~H2.SA.(-02+23)~~	~~CTT TTG AAC ATC TTC TCT TTC ATC T~~	~~SEQ ID NO. 6~~
~~H2.SA.(+02+26)~~	~~TTT CTT TTG AAC ATC TTC TCT TTC A~~	~~SEQ ID NO. 7~~
~~H2.SA.(+05+29)~~	~~TGT TTT CTT TTG AAC ATC TTC TCT T~~	~~SEQ ID NO. 8~~
~~H2.SA.(+08+32)~~	~~GAA TGT TTT CTT TTG AAC ATC TTC T~~	~~SEQ ID NO. 9~~
~~H2.SA.(+11+35)~~	~~TGT GAA TGT TTT CTT TTG AAC ATC T~~	~~SEQ ID NO. 10~~
~~H2.SA.(+14+38)~~	~~TTT TGT GAA TGT TTT CTT TTG AAC A~~	~~SEQ ID NO. 11~~
~~H2.SA.(+17+41)~~	~~CCA TTT TGT GAA TGT TTT CTT TTG A~~	~~SEQ ID NO. 12~~
~~H2.SA.(+20+44)~~	~~TAC CCA TTT TGT GAA TGT TTT CTT T~~	~~SEQ ID NO. 13~~
~~H2.SA.(+23+47)~~	~~ATT TAC CCA TTT TGT GAA TGT TTT C~~	~~SEQ ID NO. 14~~
~~H2.SA.(+26+50)~~	~~TGC ATT TAC CCA TTT TGT GAA TGT T~~	~~SEQ ID NO. 15~~
~~H2.SA.(+29+53)~~	~~TTG TGC ATT TAC CCA TTT TGT GAA T~~	~~SEQ ID NO. 16~~
~~H2.SA.(+32+56)~~	~~AAA TTG TGC ATT TAC CCA TTT TGT G~~	~~SEQ ID NO. 17~~
~~H2.SA.(+35+59)~~	~~AGA AAA TTG TGC ATT TAC CCA TTT T~~	~~SEQ ID NO. 18~~
~~H2.SA.(+38+62)~~	~~CTT AGA AAA TTG TGC ATT TAC CCA T~~	~~SEQ ID NO. 19~~
~~H2.SD.(+22-03)~~	~~TAC CTT AGA AAA TTG TGC ATT TAC C~~	~~SEQ ID NO. 20~~
~~H2.SD.(+19-06)~~	~~TCT TAC CTT AGA AAA TTG TGC ATT T~~	~~SEQ ID NO. 21~~
~~H2.SD.(+16-09)~~	~~CAT TCT TAC CTT AGA AAA TTG TGC A~~	~~SEQ ID NO. 22~~
~~H2.SD.(+13-12)~~	~~AAC CAT TCT TAC CTT AGA AAA TTG T~~	~~SEQ ID NO. 23~~
~~H2.SD.(+10-15)~~	~~ACA AAC CAT TCT TAC CTT AGA AAA T~~	~~SEQ ID NO. 24~~
~~H2A(+06+30)~~	~~ATG TTT TCT TTT GAA CAT CTT CTC T~~	~~SEQ ID NO. 25~~
~~H2A(+07+31)~~	~~AAT GTT TTC TTT TGA ACA TCT TCT C~~	~~SEQ ID NO. 26~~
~~H2A(+09+33)~~	~~TGA ATG TTT TCT TTT GAA CAT CTT C~~	~~SEQ ID NO. 27~~

~~H2A(+10+34)~~	~~GTG AAT GTT TTC TTT TGA ACA TCT T~~	~~SEQ ID NO. 28~~
~~H2A(-23+02)~~	~~ATC TAA AAT GCA AAA TAA AAA AAT A~~	~~SEQ ID NO. 29~~
~~H2A(-26-02)~~	~~TAA AAT GCA AAA TAA AAA AAT AAA A~~	~~SEQ ID NO. 30~~
~~H2A(-29-05)~~	~~AAT GCA AAA TAA AAA AAT AAA AGT T~~	~~SEQ ID NO. 31~~
~~H2A(-32-08)~~	~~GCA AAA TAA AAA AAT AAA AGT TAG G~~	~~SEQ ID NO. 32~~
~~H2A(-35-11)~~	~~AAA TAA AAA AAT AAA AGT TAG GAA G~~	~~SEQ ID NO. 33~~
H2A(-38-14)	TAA AAA AAT AAA AGT TAG GAA GCA A	SEQ ID NO. 34
H2A(-41-17)	AAA AAT AAA AGT TAG GAA GCA ACT T	SEQ ID NO. 35
~~H2A(+11+29)~~	~~TGT TTT CTT TTG AAC ATC T~~	~~SEQ ID NO. 36~~
~~H2D(+15-08)~~	~~ATT CTT ACC TTA GAA AAT TGT GC~~	~~SEQ ID NO. 37~~
~~H2A(+46+62)~~	~~CTT AGA AAA TTG TGC AT~~	~~SEQ ID NO. 38~~
~~H2D(+08-09)~~	~~CAT TCT TAC CTT AGA AA~~	~~SEQ ID NO. 39~~

wherein T is thymine or uracil.

~~15~~12. The antisense oligomer of claim ~~14~~11, or a pharmaceutically acceptable salt thereof, wherein each **Nu** from 1 to (**n**+1) and 5' to 3' of Formula (I) corresponds to the nucleobases in one of the following:

Annealing Site	**Base Sequence [5' to 3']**	**SEQ ID NO.**
H2.SA.(-20+05)	TTC ATC TAA AAT GCA AAA TAA AAA A	SEQ ID NO. 1
H2.SA.(-14+11)	TTC TCT TTC ATC TAA AAT GCA AAA T	SEQ ID NO. 2
H2.SA.(-11+14)	ATC TTC TCT TTC ATC TAA AAT GCA A	SEQ ID NO. 3
H2.SA.(-08+17)	AAC ATC TTC TCT TTC ATC TAA AAT G	SEQ ID NO. 4
H2.SA.(-05+20)	TTG AAC ATC TTC TCT TTC ATC TAA A	SEQ ID NO. 5
~~H2.SA.(-02+23)~~	~~CTT TTG AAC ATC TTC TCT TTC ATC T~~	~~SEQ ID NO. 6~~
~~H2.SA.(+02+26)~~	~~TTT CTT TTG AAC ATC TTC TCT TTC A~~	~~SEQ ID NO. 7~~
~~H2.SA.(+05+29)~~	~~TGT TTT CTT TTG AAC ATC TTC TCT T~~	~~SEQ ID NO. 8~~
~~H2.SA.(+08+32)~~	~~GAA TGT TTT CTT TTG AAC ATC TTC T~~	~~SEQ ID NO. 9~~
~~H2.SA.(+11+35)~~	~~TGT GAA TGT TTT CTT TTG AAC ATC T~~	~~SEQ ID NO. 10~~
~~H2.SA.(+14+38)~~	~~TTT TGT GAA TGT TTT CTT TTG AAC A~~	~~SEQ ID NO. 11~~
~~H2.SA.(+17+41)~~	~~CCA TTT TGT GAA TGT TTT CTT TTG A~~	~~SEQ ID NO. 12~~
~~H2.SA.(+20+44)~~	~~TAC CCA TTT TGT GAA TGT TTT CTT T~~	~~SEQ ID NO. 13~~
~~H2.SA.(+23+47)~~	~~ATT TAC CCA TTT TGT GAA TGT TTT C~~	~~SEQ ID NO. 14~~
~~H2.SA.(+26+50)~~	~~TGC ATT TAC CCA TTT TGT GAA TGT T~~	~~SEQ ID NO. 15~~
~~H2.SA.(+29+53)~~	~~TTG TGC ATT TAC CCA TTT TGT GAA T~~	~~SEQ ID NO. 16~~
~~H2.SA.(+32+56)~~	~~AAA TTG TGC ATT TAC CCA TTT TGT G~~	~~SEQ ID NO. 17~~
~~H2.SA.(+35+59)~~	~~AGA AAA TTG TGC ATT TAC CCA TTT T~~	~~SEQ ID NO. 18~~
~~H2.SD.(+22-03)~~	~~TAC CTT AGA AAA TTG TGC ATT TAC C~~	~~SEQ ID NO. 20~~
~~H2.SD.(+19-06)~~	~~TCT TAC CTT AGA AAA TTG TGC ATT T~~	~~SEQ ID NO. 21~~
~~H2.SD.(+16-09)~~	~~CAT TCT TAC CTT AGA AAA TTG TGC A~~	~~SEQ ID NO. 22~~
~~H2.SD.(+13-12)~~	~~AAC CAT TCT TAC CTT AGA AAA TTG T~~	~~SEQ ID NO. 23~~
~~H2.SD.(+10-15)~~	~~ACA AAC CAT TCT TAC CTT AGA AAA T~~	~~SEQ ID NO. 24~~
~~H2A(+06+30)~~	~~ATG TTT TCT TTT GAA CAT CTT CTC T~~	~~SEQ ID NO. 25~~
~~H2A(+07+31)~~	~~AAT GTT TTC TTT TGA ACA TCT TCT C~~	~~SEQ ID NO. 26~~
~~H2A(+09+33)~~	~~TGA ATG TTT TCT TTT GAA CAT CTT C~~	~~SEQ ID NO. 27~~
~~H2A(+10+34)~~	~~GTG AAT GTT TTC TTT TGA ACA TCT T~~	~~SEQ ID NO. 28~~

~~H2A(-23+02)~~	~~ATC TAA AAT GCA AAA TAA AAA AAT A~~	~~SEQ ID NO. 29~~
~~H2A(-26-02)~~	~~TAA AAT GCA AAA TAA AAA AAT AAA A~~	~~SEQ ID NO. 30~~
~~H2A(-29-05)~~	~~AAT GCA AAA TAA AAA AAT AAA AGT T~~	~~SEQ ID NO. 31~~
~~H2A(-32-08)~~	~~GCA AAA TAA AAA AAT AAA AGT TAG G~~	~~SEQ ID NO. 32~~
~~H2A(-35-11)~~	~~AAA TAA AAA AAT AAA AGT TAG GAA G~~	~~SEQ ID NO. 33~~
H2A(-38-14)	TAA AAA AAT AAA AGT TAG GAA GCA A	SEQ ID NO. 34
H2A(-41-17)	AAA AAT AAA AGT TAG GAA GCA ACT T	SEQ ID NO. 35
~~H2A(+11+29)~~	~~TGT TTT CTT TTG AAC ATC T~~	~~SEQ ID NO. 36~~
~~H2A(+46+62)~~	~~CTT AGA AAA TTG TGC AT~~	~~SEQ ID NO. 38~~
~~H2D(+08-09)~~	~~CAT TCT TAC CTT AGA AA~~	~~SEQ ID NO. 39~~

~~16~~13. The antisense oligomer of claim ~~14~~11, or a pharmaceutically acceptable salt thereof, wherein each **Nu** from 1 to (**n**+1) and 5' to 3' of Formula (I) corresponds to the nucleobases in one of the following:

Annealing Site	**Base Sequence [5' to 3']**	**SEQ ID NO.**
H2.SA.(-20+05)	TTC ATC TAA AAT GCA AAA TAA AAA A	SEQ ID NO. 1
H2.SA.(-14+11)	TTC TCT TTC ATC TAA AAT GCA AAA T	SEQ ID NO. 2
H2.SA.(-11+14)	ATC TTC TCT TTC ATC TAA AAT GCA A	SEQ ID NO. 3
H2.SA.(-08+17)	AAC ATC TTC TCT TTC ATC TAA AAT G	SEQ ID NO. 4
H2.SA.(-05+20)	TTG AAC ATC TTC TCT TTC ATC TAA A	SEQ ID NO. 5
~~H2.SA.(-02+23)~~	~~CTT TTG AAC ATC TTC TCT TTC ATC T~~	~~SEQ ID NO. 6~~
~~H2.SA.(+02+26)~~	~~TTT CTT TTG AAC ATC TTC TCT TTC A~~	~~SEQ ID NO. 7~~
~~H2.SA.(+05+29)~~	~~TGT TTT CTT TTG AAC ATC TTC TCT T~~	~~SEQ ID NO. 8~~
~~H2.SA.(+08+32)~~	~~GAA TGT TTT CTT TTG AAC ATC TTC T~~	~~SEQ ID NO. 9~~
~~H2.SA.(+11+35)~~	~~TGT GAA TGT TTT CTT TTG AAC ATC T~~	~~SEQ ID NO. 10~~
~~H2.SA.(+14+38)~~	~~TTT TGT GAA TGT TTT CTT TTG AAC A~~	~~SEQ ID NO. 11~~
~~H2.SA.(+17+41)~~	~~CCA TTT TGT GAA TGT TTT CTT TTG A~~	~~SEQ ID NO. 12~~
~~H2.SA.(+20+44)~~	~~TAC CCA TTT TGT GAA TGT TTT CTT T~~	~~SEQ ID NO. 13~~
~~H2.SA.(+38+62)~~	~~CTT AGA AAA TTG TGC ATT TAC CCA T~~	~~SEQ ID NO. 19~~
~~H2.SD.(+22-03)~~	~~TAC CTT AGA AAA TTG TGC ATT TAC C~~	~~SEQ ID NO. 20~~
~~H2.SD.(+19-06)~~	~~TCT TAC CTT AGA AAA TTG TGC ATT T~~	~~SEQ ID NO. 21~~
~~H2A(+06+30)~~	~~ATG TTT TCT TTT GAA CAT CTT CTC T~~	~~SEQ ID NO. 25~~
~~H2A(+07+31)~~	~~AAT GTT TTC TTT TGA ACA TCT TCT C~~	~~SEQ ID NO. 26~~
~~H2A(+09+33)~~	~~TGA ATG TTT TCT TTT GAA CAT CTT C~~	~~SEQ ID NO. 27~~
~~H2A(+10+34)~~	~~GTG AAT GTT TTC TTT TGA ACA TCT T~~	~~SEQ ID NO. 28~~
H2A(-38-14)	TAA AAA AAT AAA AGT TAG GAA GCA A	SEQ ID NO. 34
H2A(-41-17)	AAA AAT AAA AGT TAG GAA GCA ACT T	SEQ ID NO. 35
~~H2A(+11+29)~~	~~TGT TTT CTT TTG AAC ATC T~~	~~SEQ ID NO. 36~~

~~17~~14. The antisense oligomer of claim ~~14~~11, or a pharmaceutically acceptable salt thereof, wherein each **Nu** from 1 to (**n**+1) and 5' to 3' of Formula (I) corresponds to the nucleobases in one of the following:

Annealing Site	**Base Sequence [5' to 3']**	**SEQ ID NO.**

H2.SA.(-20+05)	TTC ATC TAA AAT GCA AAA TAA AAA A	SEQ ID NO. 1
H2.SA.(-14+11)	TTC TCT TTC ATC TAA AAT GCA AAA T	SEQ ID NO. 2
H2.SA.(-11+14)	ATC TTC TCT TTC ATC TAA AAT GCA A	SEQ ID NO. 3
H2.SA.(-08+17)	AAC ATC TTC TCT TTC ATC TAA AAT G	SEQ ID NO. 4
H2.SA.(-05+20)	TTG AAC ATC TTC TCT TTC ATC TAA A	SEQ ID NO. 5
~~H2.SA.(-02+23)~~	~~CTT TTG AAC ATC TTC TCT TTC ATC T~~	~~SEQ ID NO. 6~~
~~H2.SA.(+02+26)~~	~~TTT CTT TTG AAC ATC TTC TCT TTC A~~	~~SEQ ID NO. 7~~
~~H2.SA.(+05+29)~~	~~TGT TTT CTT TTG AAC ATC TTC TCT T~~	~~SEQ ID NO. 8~~
~~H2.SA.(+08+32)~~	~~GAA TGT TTT CTT TTG AAC ATC TTC T~~	~~SEQ ID NO. 9~~
~~H2.SA.(+11+35)~~	~~TGT GAA TGT TTT CTT TTG AAC ATC T~~	~~SEQ ID NO. 10~~
~~H2.SA.(+14+38)~~	~~TTT TGT GAA TGT TTT CTT TTG AAC A~~	~~SEQ ID NO. 11~~
~~H2.SA.(+17+41)~~	~~CCA TTT TGT GAA TGT TTT CTT TTG A~~	~~SEQ ID NO. 12~~
~~H2.SA.(+20+44)~~	~~TAC CCA TTT TGT GAA TGT TTT CTT T~~	~~SEQ ID NO. 13~~
~~H2.SD.(+22-03)~~	~~TAC CTT AGA AAA TTG TGC ATT TAC C~~	~~SEQ ID NO. 20~~
~~H2.SD.(+19-06)~~	~~TCT TAC CTT AGA AAA TTG TGC ATT T~~	~~SEQ ID NO. 21~~
~~H2A(+06+30)~~	~~ATG TTT TCT TTT GAA CAT CTT CTC T~~	~~SEQ ID NO. 25~~
~~H2A(+07+31)~~	~~AAT GTT TTC TTT TGA ACA TCT TCT C~~	~~SEQ ID NO. 26~~
~~H2A(+09+33)~~	~~TGA ATG TTT TCT TTT GAA CAT CTT C~~	~~SEQ ID NO. 27~~
~~H2A(+10+34)~~	~~GTG AAT GTT TTC TTT TGA ACA TCT T~~	~~SEQ ID NO. 28~~
H2A(-38-14)	TAA AAA AAT AAA AGT TAG GAA GCA A	SEQ ID NO. 34
H2A(-41-17)	AAA AAT AAA AGT TAG GAA GCA ACT T	SEQ ID NO. 35
~~H2A(+11+29)~~	~~TGT TTT CTT TTG AAC ATC T~~	~~SEQ ID NO. 36~~

~~18~~15. The antisense oligomer of claim ~~14~~11, wherein each **Nu** from 1 to (**n**+1) and 5' to 3' of Formula (I) corresponds to one of the following: SEQ ID NO. 3, SEQ ID NO. 4, SEQ ID NO. 5, ~~SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 8, SEQ ID NO. 9, SEQ ID NO. 10, SEQ ID NO. 19, SEQ ID NO. 20, SEQ ID NO. 21, SEQ ID NO. 25, SEQ ID NO. 26, SEQ ID NO. 27, SEQ ID NO. 28,~~ or SEQ ID NO. 35.

~~19~~16. The antisense oligomer of claim ~~14~~11, wherein each **Nu** from 1 to (**n**+1) and 5' to 3' of Formula (I) corresponds to one of the following: SEQ ID NO. 3, SEQ ID NO. 4, SEQ ID NO. 5, ~~SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 8, SEQ ID NO. 9, SEQ ID NO. 10, SEQ ID NO. 20, SEQ ID NO. 21, SEQ ID NO. 25, SEQ ID NO. 26, SEQ ID NO. 27, SEQ ID NO. 28,~~ or SEQ ID NO. 35.

~~20~~17. The antisense oligomer of claim ~~14~~11, wherein each **Nu** from 1 to (**n**+1) and 5' to 3' of Formula (I) corresponds to one of the following: SEQ ID NO. 3[[,]] or SEQ ID NO. 5, ~~SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 8, SEQ ID NO. 9, SEQ ID NO. 10, SEQ ID NO. 20, SEQ ID NO. 21, SEQ ID NO. 25, SEQ ID NO. 26, SEQ ID NO. 27, or SEQ ID NO. 28~~.

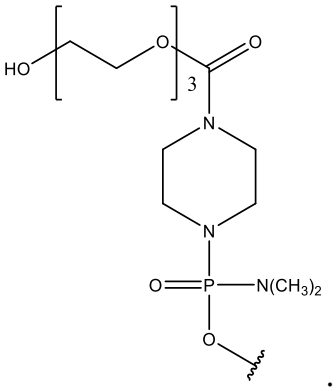
~~21. The antisense oligomer of claim 14, wherein each **Nu** from 1 to (**n**+1) and 5' to 3' of Formula (I) corresponds to one of the following: SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 25, or SEQ ID NO. 28.~~

~~22. The antisense oligomer of claim 14, wherein each **Nu** from 1 to (**n**+1) and 5' to 3' of Formula (I) corresponds to the nucleobases in SEQ ID NO. 19.~~

~~23. The antisense oligomer of claim 14, wherein each **Nu** from 1 to (**n**+1) and 5' to 3' of Formula (I) corresponds to the nucleobases in SEQ ID NO. 37.~~

~~24~~18. The antisense oligomer of any one of claims ~~14-23~~11-17, wherein T is thymine.

~~25~~19. The antisense oligomer of ~~any one of claims 14-24~~ claim ~~24~~18, wherein:

T' is 

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