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
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

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
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

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
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

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
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

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 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 or SEQ ID NO. 35.

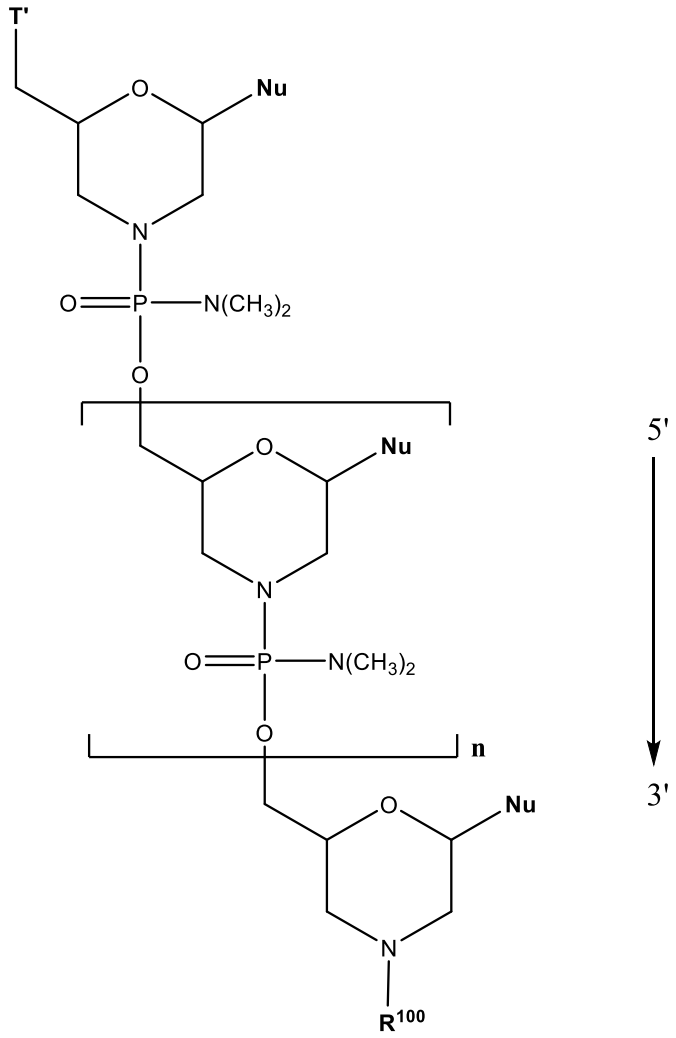
7. The modified antisense oligomer of claim 1, wherein the base sequence is selected from one of the following: SEQ ID NO. 3 or SEQ ID NO. 5.

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

9. The modified antisense oligomer of claim 8, wherein the nucleobases of the modified antisense oligomer are linked to morpholino ring structures.

10. The modified antisense oligomer of claim 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.

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

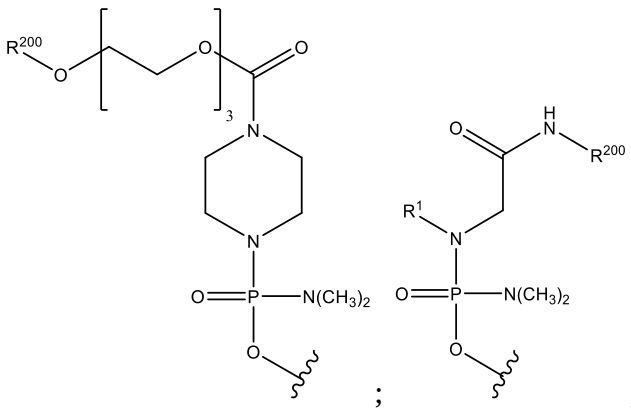


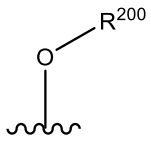
(I)

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:



; ; and  ;

R^{100} and **R**^{200} are each independently hydrogen or a cell-penetrating peptide and **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
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

wherein T is thymine or uracil.

12. The antisense oligomer of claim 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
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

13. The antisense oligomer of claim 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
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

14. The antisense oligomer of claim 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
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

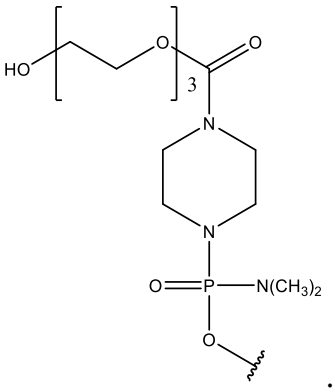
15. The antisense oligomer of claim 11, wherein each **Nu** from 1 to (**n**+1) and 5' to 3' of Formula (I) corresponds to one of the following: SEQ ID NO. 3, SEQ ID NO. 4, SEQ ID NO. 5, or SEQ ID NO. 35.

16. The antisense oligomer of claim 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 or SEQ ID NO. 35.

17. The antisense oligomer of claim 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.

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

19. The antisense oligomer of claim 18, wherein:

T' is 

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