(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
12 February 2015 (12.02.2015)

WIPO | PCT

(10) International Publication Number
WO 2015/021457 A2

(51) International Patent Classification:
A61K 48/00 (2006.01) *C07H 21/02* (2006.01)

(21) International Application Number: PCT/US2014/050481

(22) International Filing Date: 11 August 2014 (11.08.2014)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
61/864,439 9 August 2013 (09.08.2013) US
61/889,337 10 October 2013 (10.10.2013) US

(71) Applicant: **ISIS PHARMACEUTICALS, INC.** [US/US]; 2855 Gazelle Court, Carlsbad, CA 92010 (US).

(72) Inventors: **PANDEY, Sanjay, K.**; 2855 Gazelle Court, Carlsbad, CA 92010 (US). **MACLEOD, Robert, A.**; 2855 Gazelle Court, Carlsbad, CA 92010 (US). **SWAYZE, Eric, E.**; 2855 Gazelle Court, Carlsbad, CA 92010 (US). **BENNETT, C., Frank**; 2855 Gazelle Court, Carlsbad, CA 92010 (US).

(74) Agents: **GINGRICH, Brenden** et al.; Knobbe Martens LLP, 2040 Main Street, 14th Floor, Irvine, CA 92614 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report (Rule 48.2(g))*

— *with sequence listing part of description (Rule 5.2(a))*

(54) **Title**: COMPOUNDS AND METHODS FOR MODULATION OF DYSTROPHIA MYOTONICA-PROTEIN KINASE (DMPK) EXPRESSION

(57) **Abstract**: Provided herein are methods, compounds, and compositions for reducing expression of a DMPK mRNA and protein in an animal. Also provided herein are methods, compounds, and compositions for preferentially reducing CUGexp DMPK RNA, reducing myotonia or reducing spliceopathy in an animal. Such methods, compounds, and compositions are useful to treat, prevent, delay, or ameliorate type 1 myotonic dystrophy, or a symptom thereof.

WO 2015/021457 A2

COMPOUNDS AND METHODS FOR MODULATION OF DYSTROPHIA MYOTONICA-PROTEIN KINASE (DMPK) EXPRESSION

Sequence Listing

The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled BIOL0171WOSEQ_ST25.txt created August 1, 2014, which is approximately 276 Kb in size. The information in the electronic format of the sequence listing is incorporated herein by reference in its entirety.

Field

Provided herein are methods, compounds, and compositions for reducing expression of DMPK mRNA and protein in an animal. Also, provided herein are methods, compounds, and compositions comprising a DMPK inhibitor for preferentially reducing CUGexp DMPK RNA, reducing myotonia, or reducing spliceopathy in an animal. Such methods, compounds, and compositions are useful, for example, to treat, prevent, or ameliorate type 1 myotonic dystrophy (DM1) in an animal.

Background

Myotonic dystrophy type 1 (DM1) is the most common form of muscular dystrophy in adults with an estimated frequency of 1 in 7,500 (Harper PS., Myotonic Dystrophy. London: W.B. Saunders Company; 2001). DM1 is an autosomal dominant disorder caused by expansion of a non-coding CTG repeat in DMPK1. DMPK1 is a gene encoding a cytosolic serine/threonine kinase (Brook JD, et al., *Cell.*, **1992**, *68*(4):799-808). The physiologic functions and substrates of this kinase have not been fully determined. The expanded CTG repeat is located in the 3′ untranslated region (UTR) of DMPK1. This mutation leads to RNA dominance, a process in which expression of RNA containing an expanded CUG repeat (CUGexp) induces cell dysfunction (Osborne RJ and Thornton CA., *Human Molecular Genetics.*, **2006**, *15*(2): R162-R169).

The DMPK gene normally has 5-37 CTG repeats in the 3’ untranslated region. In myotonic dystrophy type I, this number is significantly expanded and is, for example, in the range of 50 to greater than 3,500 (Harper, Myotonic Dystrophy (Saunders, London, ed.3, 2001); Annu. Rev. Neurosci. 29: 259, 2006; EMBO J. 19: 4439, 2000; Curr Opin Neurol. 20: 572, 2007).

The CUGexp tract interacts with RNA binding proteins including muscleblind-like (MBNL) protein, a splicing factor, and causes the mutant transcript to be retained in nuclear foci. The toxicity of this RNA stems from sequestration of RNA binding proteins and activation of signaling pathways. Studies in animal models have shown that phenotypes of DM1 can be reversed if toxicity of CUGexp RNA is reduced (Wheeler TM, et al., *Science.*, **2009**, *325*(5938):336-339; Mulders SA, et al., *Proc Natl Acad Sci U S A.*, **2009**, *106*(33):13915-13920).

In DM1, skeletal muscle is the most severely affected tissue, but the disease also has important effects on cardiac and smooth muscle, ocular lens, and brain. The cranial, distal limb, and diaphragm muscles are preferentially affected. Manual dexterity is compromised early, which causes several decades of severe disability. The median age at death is 55 years, usually from respiratory failure (de Die-Smulders CE, et al., *Brain.*, **1998**, *121*(Pt 8):1557-1563).

Antisense technology is emerging as an effective means for modulating expression of certain gene products and may therefore prove to be uniquely useful in a number of therapeutic, diagnostic, and research applications for the modulation of DMPK1. Intramuscular injection of fully modified oligonucleotides targeting with the CAG-repeat were shown in mice to block formation of CUGexp-MBNL1 complexes, disperse nuclear foci of CUGexp transcripts, enhance the nucleocytoplasmic transport and translation of CUGexp transcripts, release MBNL proteins to the nucleoplasm, normalize alternative splicing of MBNL-dependent exons, and eliminate myotonia in CUGexp-expressing transgenic mice (Wheeler TM, et al., *Science.*, **2009**, *325*(5938):336-339; WO2008/036406).

Presently there is no treatment that can modify the course of DM1. The burden of disease, therefore, is significant. It is, therefore, an object herein to provide compounds, compositions, and methods for treating DM1

Summary

Provided herein are methods, compounds, and compositions for inhibiting expression of DMPK and treating, preventing, delaying or ameliorating a DMPK related disease and or a symptom thereof. In certain embodiments, the compounds and compositions disclosed herein inhibit mutant DMPK or CUGexp DMPK.

Certain embodiments provide a method of reducing DMPK expression in an animal comprising administering to the animal a compound comprising a modified oligonucleotide as further described herein targeted to DMPK.

Certain embodiments provide a method of preferentially reducing CUGexp DMPK relative to wild-type DMPK, reducing myotonia, or reducing spliceopathy in an animal comprising administering to the animal a compound comprising a modified oligonucleotide, as further described herein, targeted to CUGexp DMPK. In certain instances, CUGexp DMPK transcripts are believed to be particularly sensitive to antisense knockdown via nuclear ribonucleases (such as RNase H), because of their longer residence time in the nucleus, and this sensitivity is thought to permit effective antisense inhibition of CUGexp DMPK transcripts in relevant tissues such as muscle despite the biodistribution barriers to tissue uptake of antisense oligonucleotides. Antisense mechanisms that do not elicit cleavage via nuclear ribonucleases, such as the CAG-repeat ASOs described in, for example, Wheeler TM, et al., Science., 2009, 325(5938):336-339 and WO2008/036406, do not provide the same therapeutic advantage.

Certain embodiments provide a method of treating an animal having type 1 myotonic dystrophy. In certain embodiments, the method includes administering to the animal a therapeutically effective amount of a compound comprising a modified oligonucleotide as further described herein targeted to DMPK. In certain embodiments, the method includes identifying an animal with type 1 myotonic dystrophy.

Certain embodiments provide a method of treating, preventing, delaying, or ameliorating symptoms and outcomes associated with development of DM1 including muscle stiffness, myotonia, disabling distal weakness, weakness in face and jaw muscles, difficulty in swallowing, drooping of the eyelids (ptosis), weakness of neck muscles, weakness in arm and leg muscles, persistent muscle pain, hypersomnia, muscle wasting, dysphagia, respiratory insufficiency, irregular heartbeat, heart muscle damage, apathy, insulin resistance, and cataracts. Certain embodiments provide a method of treating, preventing, delaying, or ameliorating symptoms and outcomes associated with development of DM1 in children, including, developmental delays, learning problems, language and speech issues, and personality development issues.

Certain embodiments provide a method of administering an antisense oligonucleotide to counteract RNA dominance by directing the cleavage of pathogenic transcripts.

In certain embodiments, the DMPK has a sequence as set forth in GenBank Accession No. NM_001081560.1 (incorporated herein as SEQ ID NO: 1). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. NT_011109.15 truncated from nucleotides 18540696 to 18555106 (incorporated herein as SEQ ID NO: 2). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. NT_039413.7 truncated from nucleotides 16666001 to 16681000 (incorporated herein as SEQ ID NO: 3). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. NM_032418.1 (incorporated herein as SEQ ID NO: 4). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. AI007148.1 (incorporated herein as SEQ ID NO: 5). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. AI304033.1 (incorporated herein as SEQ ID NO: 6). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. BC024150.1 (incorporated herein as SEQ ID NO: 7). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. BC056615.1 (incorporated herein as SEQ ID NO: 8). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. BC075715.1 (incorporated herein as SEQ ID NO: 9). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. BU519245.1 (incorporated herein as SEQ ID NO: 10). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. CB247909.1 (incorporated herein as SEQ ID NO: 11). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. CX208906.1 (incorporated herein as SEQ ID NO: 12). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. CX732022.1 (incorporated herein as SEQ ID NO: 13). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. S60315.1 (incorporated herein as SEQ ID NO: 14). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. S60316.1 (incorporated herein as SEQ ID NO: 15). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. NM_001081562.1 (incorporated herein as SEQ ID NO: 16). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. NM_001100.3 (incorporated herein as SEQ ID NO: 17).

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

Embodiment 1. A compound comprising a modified oligonucleotide consisting of 10-30 linked nucleosides and having a nucleobase sequence comprising a complementary region comprising at least 8 contiguous nucleobases complementary to a target region of equal length of a DMPK nucleic acid.

Embodiment 2. The compound of embodiment 1, wherein at least one nucleoside of the modified oligonucleotide comprises a bicyclic sugar selected from among cEt, LNA, α-L-LNA, ENA and 2'-thio LNA.

Embodiment 3. The compound of any of embodiments 1 to 2, wherein the target region is exon 9 of a DMPK nucleic acid.

Embodiment 4. The compound of any of embodiments 1 to 3, wherein the complementary region comprises at least 10 contiguous nucleobases complementary to a target region of equal length of a DMPK transcript.

Embodiment 5. The compound of any of embodiments 1 to 3, wherein the complementary region comprises at least 12 contiguous nucleobases complementary to a target region of equal length of a DMPK nucleic acid.

Embodiment 6. The compound of any of embodiments 1 to 3, wherein the complementary region comprises at least 14 contiguous nucleobases complementary to a target region of equal length of a DMPK nucleic acid.

Embodiment 7. The compound of any of embodiments 1 to 3, wherein the complementary region comprises at least 16 contiguous nucleobases complementary to a target region of equal length of a DMPK nucleic acid.

Embodiment 8. The compound of any of embodiments 1 to 7, wherein the DMPK nucleic acid is a DMPK pre-mRNA

Embodiment 9. The compound of any of embodiments 1 to 7, wherein the DMPK nucleic acid is a DMPK mRNA.

Embodiment 10. The compound of any of embodiments 1 to 9, wherein the DMPK nucleic acid has a nucleobase sequence selected from among SEQ ID NO: 1 and SEQ ID NO: 2.

Embodiment 11. The compound of any of embodiments 1 to 10, wherein the modified oligonucleotide has a nucleobase sequence comprising a complementary region comprising at least 10 contiguous nucleobases complementary to a target region of equal length of SEQ ID NO: 1 or SEQ ID NO: 2.

Embodiment 12. The compound of embodiments 1 to 10, wherein the modified oligonucleotide has a nucleobase sequence comprising a complementary region comprising at least 12 contiguous nucleobases complementary to a target region of equal length of SEQ ID NO: 1 or SEQ ID NO: 2.

Embodiment 13. The compound of embodiments 1 to 10, wherein the modified oligonucleotide has a nucleobase sequence comprising a complementary region comprising at least 14 contiguous nucleobases complementary to a target region of equal length of SEQ ID NO: 1 or SEQ ID NO: 2.

Embodiment 14. The compound of embodiments 1 to 10, wherein the modified oligonucleotide has a nucleobase sequence comprising a complementary region comprising at least 16 contiguous nucleobases complementary to a target region of equal length of SEQ ID NO: 1 or SEQ ID NO: 2.

Embodiment 15. The compound of any of embodiments 1 to 14, wherein the target region is from nucleobase 1343 to nucleobase 1368 of SEQ ID NO.: 1.

Embodiment 16. The compound of any of embodiments 1 to 14, wherein the target region is from nucleobase 1317 to nucleobase 1366 of SEQ ID NO.: 1.

Embodiment 17. The compound of any of embodiments 1 to 14, wherein the target region is from nucleobase 2748 to nucleobase 2791 of SEQ ID NO.: 1.

Embodiment 18. The compound of any of embodiments 1 to 14, wherein the target region is from nucleobase 730 to nucleobase 748 of SEQ ID NO.: 1.

Embodiment 19. The compound of any of embodiments 1 to 14, wherein the target region is from nucleobase 10195 to nucleobase 10294 of SEQ ID NO.: 2.

Embodiment 20. The compound of any of embodiments 1 to 14, wherein the target region is from nucleobase 10195 to nucleobase 10294 of SEQ ID NO.: 2.

Embodiment 21. The compound of any of embodiments 1 to 14, wherein the target region is from nucleobase 10201 to nucleobase 10216 of SEQ ID NO.: 2.

Embodiment 22. The compound of any of embodiments 1 to 14, wherein the target region is from nucleobase 10202 to nucleobase 10218 of SEQ ID NO.: 2.

Embodiment 23. The compound of any of embodiments 1 to 22, wherein the modified oligonucleotide has a nucleobase sequence that is at least 80% complementary to the target region over the entire length of the oligonucleotide.

Embodiment 24. The compound of any of embodiments 1 to 22, wherein the modified oligonucleotide has a nucleobase sequence that is at least 90% complementary to the target region over the entire length of the oligonucleotide.

Embodiment 25. The compound of any of embodiments 1 to 22, wherein the modified oligonucleotide has a nucleobase sequence that is at least 100% complementary to the target region over the entire length of the oligonucleotide.

Embodiment 26. The compound of any of embodiments 1-25 having a nucleobase sequence comprising at least 8 contiguous nucleobases of a sequence recited in any of SEQ ID NOs: 23-874.

Embodiment 27. The compound of any of embodiments 1 to 25, wherein the modified oligonucleotide has a nucleobase sequence comprising at least 10 contiguous nucleobases of sequence recited in SEQ ID NOs: 23-32.

Embodiment 28. The compound of any of embodiments 1 to 25, wherein the modified oligonucleotide has a nucleobase sequence comprising at least 12 contiguous nucleobases of sequence recited in SEQ ID NOs: 23-32.

Embodiment 29. The compound of any of embodiments 1 to 25, wherein the modified oligonucleotide has a nucleobase sequence comprising at least 14 contiguous nucleobases of sequence recited in SEQ ID NOs: 23-32.

Embodiment 30. The compound of any of embodiments 1 to 25, wherein the modified oligonucleotide has a nucleobase sequence comprising at least 16 contiguous nucleobases of sequence recited in SEQ ID NOs: 23-32.

Embodiment 31. The compound of any of embodiments 1 to 30, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 23.

Embodiment 32. The compound of any of embodiments 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 25.

Embodiment 33. The compound of any of embodiments 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 26.

Embodiment 34. The compound of any of embodiments 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 27.

Embodiment 35. The compound of any of embodiments 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 28.

Embodiment 36. The compound of any of embodiments 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 29.

Embodiment 37. The compound of any of embodiments 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 30.

Embodiment 38. The compound of any of embodiments 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 31.

Embodiment 39. The compound of any of embodiments 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 32.

Embodiment 40. The compound of any of embodiments 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence comprising the sequence recited in SEQ ID NO: 23, 24, 25, 26, 27, 28, 29, 30, 31, or 32.

Embodiment 41. The compound of any of embodiments 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence comprising the sequence recited in SEQ ID NO: 23, 25, 26, 27, 28, 29, 30, 31, or 32.

Embodiment 42. The compound of any of embodiments 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence comprising the sequence recited in SEQ ID NO: 33-874.

Embodiment 43. The compound of any of embodiments 1 to 42, wherein the nucleobase sequence of the modified oligonucleotide is at least 90% complementary to SEQ ID NOs: 1-19.

Embodiment 44. The compound of any of embodiments 1 to 34, wherein the nucleobase sequence of the modified oligonucleotide is 100% complementary to SEQ ID NOs: 1-19.

Embodiment 45. The compound of any of embodiments 1 to 30, wherein the modified oligonucleotide consists of 16 linked nucleosides.

Embodiment 46. The compound of any of embodiments 1 to 30, wherein the modified oligonucleotide consists of 17 linked nucleosides.

Embodiment 47. The compound of any of embodiments 1 to 30, wherein the modified oligonucleotide consists of 18 linked nucleosides.

Embodiment 48. The compound of any of embodiments 1 to 30, wherein the modified oligonucleotide consists of 19 linked nucleosides.

Embodiment 49. The compound of any of embodiments 1 to 30, wherein the modified oligonucleotide consists of 20 linked nucleosides.

Embodiment 50. The compound of any of embodiments 1 to 49, wherein the modified oligonucleotide is a single-stranded oligonucleotide.

Embodiment 51. The compound of any of embodiments 1 to 50 wherein at least one nucleoside comprises a modified sugar.

Embodiment 52. The compound of any of embodiments 1 to 51 wherein at least two nucleosides comprise a modified sugar.

Embodiment 53. The compound of embodiment 52, wherein each of the modified sugars have the same modification.

Embodiment 54. The compound of embodiment 52, wherein at least one the modified sugars has a different modification.

Embodiment 55. The compound of any of embodiments 51 to 54, wherein at least one modified sugar is a bicyclic sugar.

Embodiment 56. The compound of embodiment 55, wherein the bicyclic sugar is selected from among cEt, LNA, α-L-LNA, ENA and 2'-thio LNA.

Embodiment 57. The compound of embodiment 56, wherein the bicyclic sugar comprises cEt.

Embodiment 58. The compound of embodiment 56, wherein the bicyclic sugar comprises LNA.

Embodiment 59. The compound of embodiment 56, wherein the bicyclic sugar comprises α-L-LNA.

Embodiment 60. The compound of embodiment 56, wherein the bicyclic sugar comprises ENA.

Embodiment 61. The compound of embodiment 56, wherein the bicyclic sugar comprises 2'-thio LNA.

Embodiment 62. The compound of any of embodiments 1 to 61, wherein at least one modified sugar comprises a 2'-substituted nucleoside.

Embodiment 63. The compound of embodiment 62, wherein the 2'-substituted nucleoside is selected from among: 2'-OCH_3, 2'-F, and 2'-O-methoxyethyl.

Embodiment 64. The compound of any of embodiments 1 to 63, wherein at least one modified sugar comprises a 2'-O-methoxyethyl.

Embodiment 65. The compound of any of embodiments 1 to 64, wherein at least one nucleoside comprises a modified nucleobase.

Embodiment 66. The compound of embodiment 65, wherein the modified nucleobase is a 5-methylcytosine.

Embodiment 67. The compound of any of embodiments 1 to 67, wherein each cytosine is a 5-methylcytosine.

Embodiment 68. The compound of any of embodiments 1 to 67, wherein the modified oligonucleotide comprises:

a. a gap segment consisting of linked deoxynucleosides;
b. a 5’ wing segment consisting of linked nucleosides;
c. a 3’ wing segment consisting of linked nucleosides;
d. wherein the gap segment is positioned between the 5’ wing segment and the 3’ wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

Embodiment 69. The compound of embodiment 68, wherein the modified oligonucleotide consists of 16 linked nucleosides.

Embodiment 70. The compound of embodiment 68, wherein the modified oligonucleotide consists of 17 linked nucleosides.

Embodiment 71. The compound of embodiment 68, wherein the modified oligonucleotide consists of 18 linked nucleosides.

Embodiment 72. The compound of embodiment 68, wherein the modified oligonucleotide consists of 19 linked nucleosides.

Embodiment 73. The compound of embodiment 68, wherein the modified oligonucleotide consists of 20 linked nucleosides.

Embodiment 74. The compound of any of embodiments 68 to 73, wherein the 5’-wing segment consists of two linked nucleosides.

Embodiment 75. The compound of any of embodiments 68 to 73, wherein the 5’-wing segment consists of three linked nucleosides.

Embodiment 76. The compound of any of embodiments 68 to 73, wherein the 5’-wing segment consists of four linked nucleosides.

Embodiment 77. The compound of any of embodiments 68 to 73, wherein the 5'-wing segment consists of five linked nucleosides.

Embodiment 78. The compound of any of embodiments 68 to 73, wherein the 5'-wing segment consists of six linked nucleosides.

Embodiment 79. The compound of any of embodiments 68 to 78, wherein the 3'-wing segment consists of two linked nucleosides.

Embodiment 80. The compound of any of embodiments 68 to 78, wherein the 3'-wing segment consists of three linked nucleosides.

Embodiment 81. The compound of any of embodiments 68 to 78, wherein the 3'-wing segment consists of four linked nucleosides.

Embodiment 82. The compound of any of embodiments 68 to 78, wherein the 3'-wing segment consists of five linked nucleosides.

Embodiment 83. The compound of any of embodiments 68 to 78, wherein the 3'-wing segment consists of six linked nucleosides.

Embodiment 84. The compound of any of embodiments 68 to 83, wherein the gap segment consists of six linked deoxynucleosides.

Embodiment 85. The compound of any of embodiments 68 to 83, wherein the gap segment consists of seven linked deoxynucleosides.

Embodiment 86. The compound of any of embodiments 68 to 83, wherein the gap segment consists of eight linked deoxynucleosides.

Embodiment 87. The compound of any of embodiments 68 to 83, wherein the gap segment consists of nine linked deoxynucleosides.

Embodiment 88. The compound of any of embodiments 68 to 83, wherein the gap segment consists of ten linked deoxynucleosides.

Embodiment 89. The compound of any of embodiments 1 to 31, 34, 37 to 45, or 53 to 88, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:

a. a gap segment consisting of ten linked deoxynucleosides;
b. a 5' wing segment consisting of three linked nucleosides;
c. a 3' wing segment consisting of three linked nucleosides;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each nucleoside of each wing segment comprises a bicyclic sugar.

Embodiment 90. The compound of any of embodiments 1 to 31, 34, 37 to 45, or 53 to 88, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:

a. a gap segment consisting of eight linked deoxynucleosides;
b. a 5' wing segment consisting of four linked nucleosides and having an AABB 5'-wing motif;
c. a 3' wing segment consisting of four linked nucleosides and having a BBAA 3'-wing motif;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment.

Embodiment 91. The compound of any of embodiments 1 to 30, 35, 36, 46, or 50 to 88, wherein the modified oligonucleotide consists of 17 linked nucleosides and comprises:

a. a gap segment consisting of seven linked deoxynucleosides;
b. a 5' wing segment consisting of five linked nucleosides and having an AAABB 5'-wing motif;
c. a 3' wing segment consisting of five linked nucleosides and having a BBAAA 3'-wing motif;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment.

Embodiment 92. The compound of any of embodiments 1 to 31, 34, 37 to 45, or 53 to 88, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:

a. a gap segment consisting of eight linked deoxynucleosides;
b. a 5' wing segment consisting of four linked nucleosides and having a E-E-K-K 5'-wing motif;
c. a 3' wing segment consisting of four linked nucleosides and having a K-K-E-E 3'-wing motif;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each E represents 2'-O-methoxyethyl sugar and each K represents a cEt sugar.

Embodiment 93. The compound of any of embodiments 1 to 30, 35, 36, 46, or 50 to 88, wherein the modified oligonucleotide consists of 17 linked nucleosides and comprises:

a. a gap segment consisting of seven linked deoxynucleosides;
b. a 5' wing segment consisting of five linked nucleosides and having an E-E-E-K-K 5'-wing motif;
c. a 3' wing segment consisting of five linked nucleosides and having a K-K-E-E-E 3'-wing motif;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each E represents 2'-O-methoxyethyl sugar and each K represents a cEt sugar.

Embodiment 94. The compound of any of embodiments 1 to 30, 32, 33, or 49 to 88, wherein the modified oligonucleotide consists of 20 linked nucleosides and comprises:

a. a gap segment consisting of ten linked deoxynucleosides;
b. a 5' wing segment consisting of five linked nucleosides;
c. a 3' wing segment consisting of five linked nucleosides;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each nucleoside of each wing segment comprises a 2'-O-methoxyethyl sugar.

Embodiment 95. The compound of any of embodiments 1 to 31, 34, 37 to 45, or 53 to 88, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:

a. a gap segment consisting of ten linked deoxynucleosides;
b. a 5' wing segment consisting of three linked nucleosides;
c. a 3' wing segment consisting of three linked nucleosides;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each nucleoside of each wing segment comprises a cEt sugar.

Embodiment 96. The compound of any of embodiments 1 to 67, wherein the modified oligonucleotide comprises at least 8 contiguous nucleobases complementary to a target region within nucleobase 1343 and nucleobase 1368 of SEQ ID NO.: 1, and wherein the modified oligonucleotide comprises:

a. a gap segment consisting of linked deoxynucleosides;
b. a 5' wing segment consisting of linked nucleosides;
c. a 3' wing segment consisting of linked nucleosides;

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

Embodiment 97. The compound of embodiment 96, wherein each modified sugar in the 5'-wing segment has the same modifications.

Embodiment 98. The compound of embodiment 96, wherein at least two modified sugars in the 5'-wing segment have different modifications.

Embodiment 99. The compound of any of embodiments 96 to 98 wherein each modified sugar in the 3'-wing segment has the same modifications.

Embodiment 100. The compound of any of embodiments 96 to 98, wherein at least two modified sugars in the 3'-wing segment have different modification.

Embodiment 101. The compound of embodiment 96, wherein at least one modified sugar is a bicyclic sugar selected from among cEt, LNA, α-L-LNA, ENA and 2'-thio LNAs.

Embodiment 102. The compound of embodiment 90 to 91, wherein each B represents a bicyclic sugar selected from among cEt, LNA, α-L-LNA, ENA and 2'-thio LNA.

Embodiment 103. The compound of embodiment 102, wherein the bicyclic sugar comprises BNA.

Embodiment 104. The compound of embodiment 102, wherein the bicyclic sugar comprises cEt.

Embodiment 105. The compound of embodiment 102, wherein the bicyclic sugar comprises LNA.

Embodiment 106. The compound of embodiment 102, wherein the bicyclic sugar comprises α-L-LNA.

Embodiment 107. The compound of embodiment 102, wherein the bicyclic sugar comprises ENA.

Embodiment 108. The compound of embodiment 102, wherein the bicyclic sugar comprises 2'-thio LNA.

Embodiment 109. The compound of embodiment 90 or 91, wherein each A represents a 2'-substituted nucleoside is selected from among: 2'-OCH_3, 2'-F, and 2'-O-methoxyethyl.

Embodiment 110. The compound of embodiment 109, wherein the 2'-substituted nucleoside comprises 2'-O-methoxyethyl.

Embodiment 111. The compound of any of embodiments 1 to 111, wherein at least one internucleoside linkage is a modified internucleoside linkage.

Embodiment 112. The compound of any of embodiments 1 to 111, wherein each internucleoside linkage is a phosphorothioate internucleoside linkage.

Embodiment 113. A compound consisting of ISIS 486178.

Embodiment 114. A compound consisting of ISIS 512497.

Embodiment 115. A compound consisting of ISIS 598768.

Embodiment 116. A compound consisting of ISIS 594300.

Embodiment 117. A compound consisting of ISIS 594292.

Embodiment 118. A compound consisting of ISIS 569473.

Embodiment 119. A compound consisting of ISIS 598769.

Embodiment 120. A compound consisting of ISIS 570808.

Embodiment 121. A compound consisting of ISIS 598777.

Embodiment 122. A compound having a nucleobase sequence as set forth in SEQ ID NO: 23, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:

a. a gap segment consisting of ten linked deoxynucleosides;
b. a 5' wing segment consisting of three linked nucleosides;
c. a 3' wing segment consisting of three linked nucleosides;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment;
e. wherein each nucleoside of each wing segment comprises a bicyclic sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

Embodiment 123. A compound having a nucleobase sequence as set forth in SEQ ID NO: 29, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:

a. a gap segment consisting of ten linked deoxynucleosides;
b. a 5’ wing segment consisting of three linked nucleosides;
c. a 3’ wing segment consisting of three linked nucleosides;
d. wherein the gap segment is positioned between the 5’ wing segment and the 3’ wing segment;
e. wherein each nucleoside of each wing segment comprises a bicyclic sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

Embodiment 124. A compound having a nucleobase sequence as set forth in SEQ ID NO: 31, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:

a. a gap segment consisting of ten linked deoxynucleosides;
b. a 5’ wing segment consisting of three linked nucleosides;
c. a 3’ wing segment consisting of three linked nucleosides;
d. wherein the gap segment is positioned between the 5’ wing segment and the 3’ wing segment;
e. wherein each nucleoside of each wing segment comprises a bicyclic sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

Embodiment 125. A compound having a nucleobase sequence as set forth in SEQ ID NO: 26, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:

a. a gap segment consisting of eight linked deoxynucleosides;
b. a 5’ wing segment consisting of four linked nucleosides and having a E-E-K-K 5’-wing motif;
c. a 3’ wing segment consisting of four linked nucleosides and having a K-K-E-E 3’-wing motif;
d. wherein the gap segment is positioned between the 5’ wing segment and the 3’ wing segment;
e. wherein each E represents 2’-O-methoxyethyl sugar and each K represents a cEt sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

Embodiment 126. A compound having a nucleobase sequence as set forth in SEQ ID NO: 30, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:

a. a gap segment consisting of eight linked deoxynucleosides;
b. a 5' wing segment consisting of four linked nucleosides and having a E-E-K-K 5'-wing motif;
c. a 3' wing segment consisting of four linked nucleosides and having a K-K-E-E 3'-wing motif;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment;
e. wherein each E represents 2'-O-methoxyethyl sugar and each K represents a cEt sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

Embodiment 127. A compound having a nucleobase sequence as set forth in SEQ ID NO: 32, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:

a. a gap segment consisting of eight linked deoxynucleosides;
b. a 5' wing segment consisting of four linked nucleosides and having a E-E-K-K 5'-wing motif;
c. a 3' wing segment consisting of four linked nucleosides and having a K-K-E-E 3'-wing motif;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment;
e. wherein each E represents 2'-O-methoxyethyl sugar and each K represents a cEt sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

Embodiment 128. A compound having a nucleobase sequence as set forth in SEQ ID NO: 27, wherein the modified oligonucleotide consists of 17 linked nucleosides and comprises:

a. a gap segment consisting of seven linked deoxynucleosides;
b. a 5' wing segment consisting of five linked nucleosides and having an E-E-E-K-K 5'-wing motif;
c. a 3' wing segment consisting of five linked nucleosides and having a K-K-E-E-E 3'-wing motif;

d. wherein the gap segment is positioned between the 5’ wing segment and the 3’ wing segment;
e. wherein each E represents 2’-O-methoxyethyl sugar and each K represents a cEt sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

Embodiment 129. A compound having a nucleobase sequence as set forth in SEQ ID NO: 28, wherein the modified oligonucleotide consists of 17 linked nucleosides and comprises:

a. a gap segment consisting of seven linked deoxynucleosides;
b. a 5’ wing segment consisting of five linked nucleosides and having an E-E-E-K-K 5’-wing motif;
c. a 3’ wing segment consisting of five linked nucleosides and having a K-K-E-E-E 3’-wing motif;
d. wherein the gap segment is positioned between the 5’ wing segment and the 3’ wing segment;
e. wherein each E represents 2’-O-methoxyethyl sugar and each K represents a cEt sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

Embodiment 130. A compound having a nucleobase sequence as set forth in SEQ ID NO: 25, wherein the modified oligonucleotide consists of 20 linked nucleosides and comprises:

a. a gap segment consisting of ten linked deoxynucleosides;
b. a 5’ wing segment consisting of five linked nucleosides;
c. a 3’ wing segment consisting of five linked nucleosides;
d. wherein the gap segment is positioned between the 5’ wing segment and the 3’ wing segment;
e. wherein each nucleoside of each wing segment comprises a 2’-O-methoxyethyl sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

Embodiment 131. The compound of any of embodiments 1 to 130 comprising a conjugate.

Embodiment 132. A composition comprising the compound of any of embodiments 1 to 131, and a pharmaceutically acceptable carrier or diluent.

Embodiment 133. A method of treating DM1 in an animal comprising administering to an animal in need thereof a compound according to any of embodiments 1 to 130, or a composition according to embodiment 132.

Embodiment 134. The method of embodiment 133, wherein the compound reduces DMPK mRNA levels.

Embodiment 135. The method of embodiment 133, wherein the compound reduces DMPK protein expression.

Embodiment 136. The method of embodiment 133, wherein the compound reduces CUGexp DMPK.

Embodiment 137. The method of embodiment 133, wherein the compound preferentially reduces CUGexp DMPK.

Embodiment 138. The method of embodiment 133, wherein the compound reduces CUGexp DMPK mRNA.

Embodiment 139. The method of embodiment 133, wherein the compound preferentially reduces CUGexp DMPK mRNA.

Embodiment 140. The method of embodiment 138 or 139, wherein the preferential reduction of CUGexp is in muscle tissue.

Embodiment 141. A method of reducing myotonia in an animal comprising administering to an animal in need thereof a compound according to any of embodiments 1 to 131, or a composition according to embodiment 132.

Embodiment 142. A method of reducing MBLN dependent spliceopathy in an animal comprising administering to an animal in need thereof a compound according to any of embodiments 1 to 131, or a composition according to embodiment 132.

Embodiment 143. The method of embodiment 138, wherein splicing of any of Serca1, m-Titin, Clcn1, and Zasp is corrected.

Embodiment 144. The method of any of embodiments 133 to 143, wherein the administering is systemic administration.

Embodiment 145. The method of any of embodiments 133 to 143, wherein the administering is parenteral administration.

Embodiment 146. The method of embodiment 144, wherein the systemic administration is any of subcutaneous administration, intravenous administration, intracerebroventricular administration, and intrathecal administration.

Embodiment 147. The method of any of embodiments 133 to 143, wherein the administration is not intramuscular administration.

Embodiment 148. The method of any of embodiments 133 to 143, wherein the animal is a human.

Embodiment 149. A method of reducing spliceopathy of *Serca1* in an animal in need thereof by administering a compound according to any of embodiments 1 to 131, or a composition according to embodiment 132, and thereby causing *Serca1* exon 22 inclusion.

Embodiment 150. A method of reducing spliceopathy of *m-Titin* in an animal in need thereof by administering a compound according to any of embodiments 1 to 131, or a composition according to embodiment 132, and thereby causing *m-Titin* exon 5 inclusion.

Embodiment 151. A method of reducing spliceopathy of *Clcn1* in an animal in need thereof by administering a compound according to any of embodiments 1 to 131, or a composition according to embodiment 132, and thereby causing *Clcn1* exon 7a inclusion.

Embodiment 152. A method of reducing spliceopathy of *Zasp* in an animal in need thereof by administering a compound according to any of embodiments 1 to 131, or a composition according to embodiment 132, and thereby causing *Zasp* exon 11 inclusion.

Embodiment 153. A method of reducing DMPK mRNA in a cell, comprising contacting a cell with a compound according to any of embodiments 1 to 131, or a composition according to embodiment 132.

Embodiment 154. A method of reducing DMPK protein in a cell, comprising contacting a cell with a compound according to any of embodiments 1 to 131, or a composition according to embodiment 132.

Embodiment 155. A method of reducing CUGexp mRNA in a cell, comprising contacting a cell with a compound according to any of embodiments 1 to 131, or a composition according to embodiment 132.

Embodiment 156. The method of any of embodiments 149 to 151, wherein the cell is in an animal.

Embodiment 157. The method of embodiment 156, wherein the animal is a human.

Embodiment 158. A method of achieving a preferential reduction of CUGexp DMPK RNA, comprising:

a. selecting a subject having type 1 myotonic dystrophy or having a CUGexp DMPK RNA; and
b. administering to said subject a compound according to any of embodiments 1 to 131, or a composition according to embodiment 132;

wherein said compound according to any of embodiments 1 to 131, or a composition according to embodiment 132, when bound to said CUGexp DMPK RNA, activates a ribonuclease, thereby achieving a preferential reduction of said CUGexp DMPK RNA.

Embodiment 159. A method of achieving a preferential reduction of CUGexp DMPK RNA, comprising:

a. selecting a subject having type 1 myotonic dystrophy or having a CUGexp DMPK RNA; and
b. systemically administering to said subject a compound according to any of embodiments 1 to 131, or a composition according to embodiment 132;

wherein said chemically-modified antisense oligonucleotide, when bound to said CUGexp DMPK RNA, achieves a preferential reduction of said CUGexp DMPK RNA.

Embodiment 160. A method of reducing spliceopathy in a subject suspected of having type 1 myotonic dystrophy or having a nuclear retained CUGexp DMPK RNA, comprising:

administering to said subject a compound according to any of embodiments 1 to 131, or a composition according to embodiment 132,

wherein the compound according to any of embodiments 1 to 131, or a composition according to embodiment 132, when bound to said mutant DMPK RNA, activates a ribonuclease, thereby reducing spliceopathy.

Embodiment 161. A method of preferentially reducing CUGexp DMPK RNA, reducing myotonia or reducing spliceopathy in an animal comprising administering to the animal a compound according to any of embodiments 1 to 131 or a pharmaceutical composition of embodiment 132, wherein the compound reduces DMPK expression in the animal, thereby preferentially reducing CUGexp DMPK RNA, reducing myotonia, or reducing spliceopathy in the animal.

Embodiment 162. A method for treating an animal with type 1 myotonic dystrophy comprising

identifying said animal with type 1 myotonic dystrophy,

administering to said animal a therapeutically effective amount of a compound according to any of embodiments 1 to 131 or a pharmaceutical composition of embodiment 132,

wherein said animal with type 1 myotonic dystrophy is treated.

Embodiment 163. A method of reducing DMPK expression comprising administering to an animal a compound according to any of embodiments 1 to 131 or a pharmaceutical composition of embodiment 132, wherein expression of DMPK is reduced.

Embodiment 164. A compound according to any of embodiments 1 to 131 or a pharmaceutical composition of embodiment 132, for use in treating DM1 in an animal.

Embodiment 165. A compound according to any of embodiments 1 to 131 or a pharmaceutical composition of embodiment 132, for use in reducing myotonia in an animal.

Embodiment 166. A compound according to any of embodiments 1 to 131 or a pharmaceutical composition of embodiment 132, for use in reducing MBLN dependent spliceopathy in an animal.

Detailed Description

It is to be understood that both the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive of the invention, as claimed. Herein, the use of the singular includes the plural unless specifically stated otherwise. Herein, the use of “or” means “and/or” unless stated otherwise. Furthermore, the use of the term “including” as well as other forms, such as “includes” and “included”, is not limiting. Also, terms such as "element" or "component" encompass both elements and components comprising one unit and elements and components that comprise more than one subunit, unless specifically stated otherwise.

The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described. All documents, or portions of documents, cited in this application, including, but not limited to, patents, patent applications, articles, books, and treatises, are hereby expressly incorporated-by-reference for the portions of the document discussed herein, as well as in their entirety.

Definitions

Unless specific definitions are provided, the nomenclature utilized in connection with, and the procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well known and commonly used in the art. Standard techniques can be used for chemical synthesis, and chemical analysis. Where permitted, all patents, applications, published applications and other publications, GENBANK Accession Numbers and associated sequence information obtainable through databases such as National Center for Biotechnology Information (NCBI) and other data referred to throughout in the disclosure herein are incorporated by reference for the portions of the document discussed herein, as well as in their entirety.

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

"2'-O-methoxyethyl" (also 2'-MOE and 2'-O$(CH_2)_2$-OCH_3) refers to an O-methoxy-ethyl modification of the 2' position of a furanosyl ring. A 2'-O-methoxyethyl modified sugar is a modified sugar.

"2'-O-methoxyethyl nucleotide" means a nucleotide comprising a 2'-O-methoxyethyl modified sugar moiety.

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

"About" means within ± 7% of a value. For example, if it is stated, "the compound affected at least about 70% inhibition of DMPK", it is implied that the DMPK levels are inhibited within a range of 63% and 77%.

"Active pharmaceutical agent" means the substance or substances in a pharmaceutical composition that provide a therapeutic benefit when administered to an animal. For example, in certain embodiments an antisense oligonucleotide targeted to DMPK is an active pharmaceutical agent.

"Active target region" or "target region" means a region to which one or more active antisense compounds is targeted. "Active antisense compounds" means antisense compounds that reduce target nucleic acid levels or protein levels.

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

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

"Agent" means an active substance that can provide a therapeutic benefit when administered to an animal. "First Agent" means a therapeutic compound of the invention. For example, a first agent can be an antisense oligonucleotide targeting DMPK. "Second agent" means a second therapeutic compound of the invention (e.g. a second antisense oligonucleotide targeting DMPK) and/or a non-DMPK therapeutic compound.

"Amelioration" refers to a lessening of at least one indicator, sign, or symptom of an associated disease, disorder, or condition. The severity of indicators can be determined by subjective or objective measures, which are known to those skilled in the art.

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

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

"Antisense compound" means an oligomeric compound that is capable of undergoing hybridization to a target nucleic acid through hydrogen bonding. Examples of antisense compounds include single-stranded and double-stranded compounds, such as, antisense oligonucleotides, siRNAs, shRNAs, snoRNAs, miRNAs, and satellite repeats.

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

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

"Bicyclic sugar" means a furanosyl ring modified by the bridging of two non-geminal carbon ring atoms. A bicyclic sugar is a modified sugar.

"Bicyclic nucleic acid" or "BNA" refers to a nucleoside or nucleotide wherein the furanose portion of the nucleoside or nucleotide includes a bridge connecting two carbon atoms on the furanose ring, thereby forming a bicyclic ring system.

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

"Chemically distinct region" refers to a region of an antisense compound that is in some way chemically different than another region of the same antisense compound. For example, a region having 2'-O-methoxyethyl nucleotides is chemically distinct from a region having nucleotides without 2'-O-methoxyethyl modifications.

"Chimeric antisense compound" means an antisense compound that has at least two chemically distinct regions.

"Co-administration" means administration of two or more agents to an individual. The two or more agents can be in a single pharmaceutical composition, or can be in separate pharmaceutical compositions. Each of the two or more agents can be administered through the same or different routes of administration. Co-administration encompasses parallel or sequential administration.

"Complementarity" means the capacity for pairing between nucleobases of a first nucleic acid and a second nucleic acid.

"Contiguous nucleobases" means nucleobases immediately adjacent to each other.

"CUGexp DMPK" means mutant DMPK RNA containing an expanded CUG repeat (CUGexp). The wild-type DMPK gene has 5-37 CTG repeats in the 3' untranslated region. In a "CUGexp DMPK" (such as in a myotonic dystrophy type I patient) this number is significantly expanded and is, for example, in the range of 50 to greater than 3,500 (Harper, Myotonic Dystrophy (Saunders, London, ed.3, 2001); Annu. Rev. Neurosci. 29: 259, 2006; EMBO J. 19: 4439, 2000; Curr Opin Neurol. 20: 572, 2007).

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

"DMPK" means any nucleic acid or protein of distrophia myotonica protein kinase. DMPK can be a mutant DMPK including CUGexp DMPK nucleic acid.

"DMPK expression" means the level of mRNA transcribed from the gene encoding DMPK or the level of protein translated from the mRNA. DMPK expression can be determined by art known methods such as a Northern or Western blot.

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

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

"Effective amount" or "therapeutically effective amount" means the amount of active pharmaceutical agent sufficient to effectuate a desired physiological outcome in an individual in need of the agent. The effective amount can vary among individuals depending on the health and physical condition of the individual to be treated, the taxonomic group of the individuals to be treated, the formulation of the composition, assessment of the individual's medical condition, and other relevant factors.

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

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

"Gap-widened" means a chimeric antisense compound having a gap segment of 12 or more contiguous 2'-deoxyribonucleosides positioned between and immediately adjacent to 5' and 3' wing segments having from one to six nucleosides.

"Hybridization" means the annealing of complementary nucleic acid molecules. In certain embodiments, complementary nucleic acid molecules include an antisense compound and a target nucleic acid.

"Identifying an animal with type 1 myotonic dystrophy" means identifying an animal having been diagnosed with a type 1 myotonic dystrophy, disorder or condition or identifying an animal predisposed to develop a type 1 myotonic dystrophy, disorder or condition. For example, individuals with a familial history can be predisposed to type 1 myotonic dystrophy, disorder or condition. Such identification can be accomplished by any method including evaluating an individual's medical history and standard clinical tests or assessments.

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

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

"Internucleoside linkage" refers to the chemical bond between nucleosides.

"Linked nucleosides" means adjacent nucleosides which are bonded or linked together by an internucleoside linkage.

"Mismatch" or "non-complementary nucleobase" refers to the case when a nucleobase of a first nucleic acid is not capable of pairing with the corresponding nucleobase of a second or target nucleic acid.

"Modified internucleoside linkage" refers to a substitution or any change from a naturally occurring internucleoside bond (i.e. a phosphodiester internucleoside bond).

"Modified nucleobase" refers to any nucleobase other than adenine, cytosine, guanine, thymidine, or uracil. An "unmodified nucleobase" means the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C), and uracil (U).

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

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

"Modified sugar" refers to a substitution or change from a natural sugar moiety. Modified sugars include substituted sugar moieities and surrogate sugar moieties..

"Motif" means the pattern of chemically distinct regions in an antisense compound.

"Myotonia" means an abnormally slow relaxation of a muscle after voluntary contraction or electrical stimulation.

"Nuclear ribonuclease" means a ribonuclease found in the nucleus. Nuclear ribonucleases include, but are not limited to, RNase H including RNase H1 and RNase H2, the double stranded RNase drosha and other double stranded RNases.

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

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

"Nucleic acid" refers to molecules composed of monomeric nucleotides. A nucleic acid includes ribonucleic acids (RNA), deoxyribonucleic acids (DNA), single-stranded nucleic acids, double-stranded nucleic acids, small interfering ribonucleic acids (siRNA), and microRNAs (miRNA). A nucleic acid can also comprise a combination of these elements in a single molecule.

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

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

“Nucleoside” means a nucleobase linked to a sugar. In certain embodiments, a nucleoside is linked to a phosphate group.

"Nucleoside mimetic" includes those structures used to replace the sugar or the sugar and the base and not necessarily the linkage at one or more positions of an oligomeric compound such as for example nucleoside mimetics having morpholino, cyclohexenyl, cyclohexyl, tetrahydropyranyl, bicyclo or tricyclo sugar mimetics e.g. non furanose sugar units.

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

"Nucleotide mimetic" includes those structures used to replace the nucleoside and the linkage at one or more positions of an oligomeric compound such as for example peptide nucleic acids or morpholinos (morpholinos linked by -N(H)-C(=O)-O- or other non-phosphodiester linkage).

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

“Oligonucleotide” means a polymer of linked nucleosides, wherein each nucleoside and each internucleoside linkage may be modified or unmodified, independent one from another.

“Parenteral administration” means administration through injection or infusion. Parenteral administration includes subcutaneous administration, intravenous administration, intramuscular administration, intraarterial administration, intraperitoneal administration, or intracranial administration, e.g. intrathecal or intracerebroventricular administration. Administration can be continuous, or chronic, or short or intermittent.

“Peptide” means a molecule formed by linking at least two amino acids by amide bonds. Peptide refers to polypeptides and proteins.

“Pharmaceutical composition” means a mixture of substances suitable for administering to an individual. For example, a pharmaceutical composition can comprise one or more active agents and a sterile aqueous solution.

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

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

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

“Preferentially reducing CUG exp DMPK RNA” refers to a preferential reduction of RNA transcripts from a CUGexp DMPK allele relative to RNA transcripts from a normal DMPK allele.

“Prevent” refers to delaying or forestalling the onset or development of a disease, disorder, or condition for a period of time from minutes to indefinitely. Prevent also means reducing risk of developing a disease, disorder, or condition.

“Prodrug” means a therapeutic agent that is prepared in an inactive form that is converted to an active form within the body or cells thereof by the action of endogenous enzymes or other chemicals or conditions.

“Side effects” means physiological responses attributable to a treatment other than the desired effects. In certain embodiments, side effects include injection site reactions, liver function test abnormalities, renal function abnormalities, liver toxicity, renal toxicity, central nervous system abnormalities, myopathies, and malaise. For example, increased aminotransferase levels in serum can indicate liver toxicity or liver function abnormality. For example, increased bilirubin can indicate liver toxicity or liver function abnormality.

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

“Specifically hybridizable” refers to an antisense compound having a sufficient degree of complementarity between an antisense oligonucleotide and a target nucleic acid to induce a desired effect, while exhibiting minimal or no effects on non-target nucleic acids under conditions in which specific binding is desired, i.e. under physiological conditions in the case of *in vivo* assays and therapeutic treatments.

“Spliceopathy” means a change in the alternative splicing of one or more RNAs that leads to the expression of altered splice products in a particular tissue.

“Subcutaneous administration” means administration just below the skin.

“Substituted sugar moiety” means a furanosyl other than a natural sugar of RNA or DNA.

“Sugar” or “Sugar moiety” means a natural sugar moiety or a modified sugar.

"Sugar surrogate" overlaps with the slightly broader term "nucleoside mimetic" but is intended to indicate replacement of the sugar unit (furanose ring) only A sugar surrogate is capable of replacing the naturally occurring sugar moiety of a nucleoside, such that the resulting nucleoside sub-units are capable of linking together and/or linking to other nucleosides to form an oligomeric compound which is capable of hybridizing to a complementary oligomeric compound. Such structures include rings comprising a different number of atoms than furanosyl (e.g., 4, 6, or 7-membered rings); replacement of the oxygen of a furanosyl with a non-oxygen atom (e.g., carbon, sulfur, or nitrogen); or both a change in the number of atoms and a replacement of the oxygen. Such structures may also comprise substitutions corresponding to those described for substituted sugar moieties (e.g., 6-membered carbocyclic bicyclic sugar surrogates optionally comprising additional substituents). Sugar surrogates also include more complex sugar replacements (e.g., the non-ring systems of peptide nucleic acid). Sugar surrogates include without limitation morpholinos, cyclohexenyls and cyclohexitols.

“Targeting” or “targeted” means the process of design and selection of an antisense compound that will specifically hybridize to a target nucleic acid and induce a desired effect.

“Target nucleic acid,” “target RNA,” and “target RNA transcript” all refer to a nucleic acid capable of being targeted by antisense compounds. In certain embodiments, a target nucleic acid comprises a region of a DMPK nucleic acid.

"Target segment" means the sequence of nucleotides of a target nucleic acid to which an antisense compound is targeted. "5' target site" refers to the 5'-most nucleotide of a target segment. "3' target site" refers to the 3'-most nucleotide of a target segment.

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

"Treat" refers to administering a pharmaceutical composition to effect an alteration or improvement of a disease, disorder, or condition.

"Type 1 myotonic dystrophy" or "DM1" means an autosomal dominant disorder caused by expansion of a non-coding CTG repeat in DMPK. This mutation leads to RNA dominance, a process in which expression of RNA containing an expanded CUG repeat (CUGexp) induced cell dysfunction. The CUGexp tract interacts with RNA binding proteins and causes the mutant transcript to be retained in nuclear foci. The toxicity of this RNA stems from sequestration of RNA binding proteins and activation of signaling pathways.

"Unmodified nucleotide" means a nucleotide composed of naturally occurring nucleobases, sugar moieties, and internucleoside linkages. In certain embodiments, an unmodified nucleotide is an RNA nucleotide (i.e. β-D-ribonucleosides) or a DNA nucleotide (i.e. β-D-deoxyribonucleoside).

Certain Embodiments

Certain embodiments provide methods, compounds, and compositions for inhibiting DMPK expression.

Certain embodiments provide a method of reducing DMPK expression in an animal comprising administering to the animal a compound comprising a modified oligonucleotide targeting DMPK.

Certain embodiments provide a method of preferentially reducing CUGexp DMPK RNA, reducing myotonia or reducing spliceopathy in an animal comprising administering to the animal a compound comprising a modified oligonucleotide targeted to DMPK, wherein the modified oligonucleotide preferentially reduces CUGexp DMPK RNA, reduces myotonia or reduces spliceopathy in the animal.

Certain embodiments provide a method of administering an antisense oligonucleotide to counteract RNA dominance by directing the cleavage of pathogenic transcripts.

Certain embodiments provide a method of reducing spliceopathy of *Serca1*. In certain embodiments, methods provided herein result in exon 22 inclusion. In certain embodiments, the corrective splicing occurs in the tibialis anterior, gastrocnemius, and quadriceps muscles.

Certain embodiments provide a method of reducing spliceopathy of *m-Titin*. In certain embodiments, methods provided herein result in exon 5 inclusion. In certain embodiments, the corrective splicing occurs in the tibialis anterior, gastrocnemius, and quadriceps muscles.

Certain embodiments provide a method of reducing spliceopathy of *Clcn1*. In certain embodiments, methods provided herein result in exon 7a inclusion. In certain embodiments, the corrective splicing occurs in the tibialis anterior, gastrocnemius, and quadriceps muscles.

Certain embodiments provide a method of reducing spliceopathy of *Zasp*. In certain embodiments, methods provided herein result in exon 11 inclusion. In certain embodiments, the corrective splicing occurs in the tibialis anterior, gastrocnemius, and quadriceps muscles.

Certain embodiments provide a method for treating an animal with type 1 myotonic dystrophy comprising: a) identifying said animal with type 1 myotonic dystrophy, and b) administering to said animal a therapeutically effective amount of a compound comprising a modified oligonucleotide targeted to DMPK. In certain embodiments, the therapeutically effective amount of the compound administered to the animal preferentially reduces CUGexp DMPK RNA, reduces myotonia or reduces spliceopathy in the animal.

Certain embodiments provide a method of achieving a preferential reduction of CUGexp DMPK RNA, including administering to the subject suspected of having type 1 myotonic dystrophy or having a CUGexp DMPK RNA a modified antisense oligonucleotide complementary to a non-repeat region of said CUGexp DMPK RNA. The modified antisense oligonucleotide, when bound to said CUGexp DMPK RNA, achieves a preferential reduction of the CUGexp DMPK RNA.

Certain embodiments provide a method of achieving a preferential reduction of CUGexp DMPK RNA, including selecting a subject having type 1 myotonic dystrophy or having a CUGexp DMPK RNA and administering to said subject a modified antisense oligonucleotide complementary to a non-repeat region of said CUGexp DMPK RNA. The modified antisense oligonucleotide, when bound to the CUGexp DMPK RNA, activates a ribonuclease or nuclear ribonuclease, thereby achieving a preferential reduction of the CUGexp DMPK RNA in the nucleus.

Certain embodiments provide a method of achieving a preferential reduction of CUGexp DMPK RNA, including selecting a subject having type 1 myotonic dystrophy or having a mutant or CUGexp DMPK RNA and systemically administering to said subject a modified antisense oligonucleotide complementary to a non-repeat region of said CUGexp DMPK RNA. The modified antisense oligonucleotide, when bound to the mutant or CUGexp DMPK RNA, achieves a preferential reduction of the mutant or CUGexp DMPK RNA.

Certain embodiments provide a method of reducing myotonia in a subject in need thereof. The method includes administering to the subject a modified antisense oligonucleotide complementary to a non-repeat region of a DMPK RNA, wherein the modified antisense oligonucleotide, when bound to the DMPK RNA, activates a ribonuclease or nuclear ribonuclease, thereby reducing myotonia. In certain embodiments, the subject has or is suspected of having type 1 myotonic dystrophy or having a mutant DMPK RNA or CUGexp DMPK RNA. In certain embodiments, the DMPK RNA is nuclear retained.

Certain embodiments provide a method of reducing spliceopathy in a subject in need thereof. The method includes administering to the subject a modified antisense oligonucleotide complementary to a non-repeat region of a DMPK RNA, wherein the modified antisense oligonucleotide, when bound to the DMPK RNA, activates a ribonuclease or nuclear ribonuclease, thereby reducing spliceopathy. In certain embodiments, the subject has or is suspected of having type 1 myotonic dystrophy or having a nuclear retained CUGexp DMPK RNA. In certain embodiments, the DMPK RNA is nuclear retained. In certain embodiments, the spliceopathy is MBNL dependent spliceopathy.

In certain embodiments, the modified antisense oligonucleotide of the methods is chimeric. In certain embodiments, the modified antisense oligonucleotide of the methods is a gapmer.

In certain embodiments of the methods provided herein, the administering is subcutaneous. In certain embodiments, the administering is intravenous.

In certain embodiments, the modified antisense oligonucleotide of the methods targets a non-coding sequence within the non-repeat region of a DMPK RNA. In certain embodiments, the oligonucleotide targets a coding region, an intron, a 5'UTR, or a 3'UTR of the mutant DMPK RNA.

In certain embodiments of the methods provided herein, the nuclear ribonuclease is RNase H1.

In certain embodiments of the methods, the DMPK RNA is reduced in muscle tissue. In certain embodiments, the mutant DMPK RNA CUGexp DMPK RNA is preferentially reduced.

In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. NM_001081560.1 (incorporated herein as SEQ ID NO: 1). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. NT_011109.15 truncated from nucleotides 18540696 to 18555106 (incorporated herein as SEQ ID NO: 2). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. NT_039413.7 truncated from nucleotides 16666001 to 16681000 (incorporated herein as SEQ ID NO: 3). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. NM_032418.1 (incorporated herein as SEQ ID NO: 4). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. AI007148.1 (incorporated herein as SEQ ID NO: 5). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. AI304033.1 (incorporated herein as SEQ ID NO: 6). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. BC024150.1 (incorporated herein as SEQ ID NO: 7). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. BC056615.1 (incorporated herein as SEQ ID NO: 8). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. BC075715.1 (incorporated herein as SEQ ID NO: 9). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. BU519245.1 (incorporated herein as SEQ ID NO: 10). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. CB247909.1 (incorporated herein as SEQ ID NO: 11). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. CX208906.1 (incorporated herein as SEQ ID NO: 12). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. CX732022.1 (incorporated herein as SEQ ID NO: 13). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. S60315.1 (incorporated herein as SEQ ID NO: 14). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. S60316.1 (incorporated herein as SEQ ID NO: 15). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. NM_001081562.1 (incorporated herein as SEQ ID NO: 16). In certain embodiments, the DMPK has the sequence as set forth in GenBank Accession No. NM_001100.3 (incorporated herein as SEQ ID NO: 17).

In certain embodiments, the modified oligonucleotide has a nucleobase sequence comprising at least 8 contiguous nucleobases of a nucleobase sequence recited in any one of SEQ ID NOs: 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33- 874. In certain embodiments, the modified oligonucleotide has a nucleobase sequence comprising at least 9, at least 10, or at least 11, contiguous nucleobases of a nucleobase sequence recited in any one of SEQ ID NOs: 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33- 874.

In certain embodiments, the modified oligonucleotide has a nucleobase sequence comprising at least 12 contiguous nucleobases of a nucleobase sequence recited in any one of SEQ ID NOs: 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33- 874. In certain embodiments, the modified oligonucleotide has a nucleobase sequence comprising at least 13, or at least 14, contiguous nucleobases of a nucleobase sequence recited in any one of SEQ ID NOs: 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33-874.

In certain embodiments, the modified oligonucleotide has a nucleobase sequence comprising at least 15 contiguous nucleobases of a nucleobase sequence recited in any one of SEQ ID NOs: 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33- 874. In certain embodiments, the modified oligonucleotide has a nucleobase sequence comprising at least 16 contiguous nucleobases of a nucleobase sequence recited in any one of SEQ ID NOs: 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33- 874.

In certain embodiments, the modified oligonucleotide has a nucleobase sequence comprising at least 17 contiguous nucleobases of a nucleobase sequence recited in any one of SEQ ID NOs: 24, 25, 27, or 28.

In certain embodiments, the modified oligonucleotide has a nucleobase sequence comprising at least 18 contiguous nucleobases of a nucleobase sequence recited in any one of SEQ ID NOs: 24 or 25. In certain embodiments, the modified oligonucleotide has a nucleobase sequence comprising at least 19 contiguous nucleobases of a nucleobase sequence recited in any one of SEQ ID NOs: 24 or 25.

In certain embodiments, the modified oligonucleotides provided herein are targeted to any one of the following regions of SEQ ID NO: 1: 1343-1368, 1317-1366, 2748-2791, 2155-2208, 2748-2791, 730-748, 528-547, 531-567, 636-697, 1311-1331, 1314-1339, 1446-1475, 1635-1670, 1610-1638, 1457-1486, 2773-1788, 931-948, 934-949, 937-952, 942-957, 937-957, 943-958, 937-953, 1346-1363, 1346-1361, 1347-1363, 2162-2179, 2492-2508, 2696-2717, and 2683-2703. In certain embodiments, the modified oligonucleotides provided herein are targeted to any one of the following regions of SEQ ID NO: 1: 2773-2788, 1343-1358, and 1344-1359.

In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 8 contiguous nucleobases complementary to a target region. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 8 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases 1343-1368, 1317-1366, 2748-2791, 2155-2208, 2748-2791, 730-748, 528-547, 531-567, 636-697, 1311-1331, 1314-1339, 1446-1475, 1635-1670, 1610-1638, 1457-1486, 2773-1788, 931-948, 934-949, 937-952, 942-957, 937-957, 943-958, 937-953, 1346-1363, 1346-1361, 1347-1363, 2162-2179, 2492-2508, 2696-2717, or 2683-2703 of SEQ ID NO: 1. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 8 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases 2773-2788, 1343-1358, or 1344-1359 of SEQ ID NO: 1.

In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 10 contiguous nucleobases complementary to a target region. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 10 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases 1343-1368, 1317-1366, 2748-2791, 2155-2208, 2748-2791, 730-748, 528-547, 531-567, 636-697, 1311-1331, 1314-1339, 1446-1475, 1635-1670, 1610-1638, 1457-1486, 2773-1788, 931-948, 934-949, 937-952, 942-957, 937-957, 943-958, 937-953, 1346-1363, 1346-1361, 1347-1363, 2162-2179, 2492-2508, 2696-2717, or 2683-2703 of SEQ ID NO: 1. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 10 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases 2773-2788, 1343-1358, or 1344-1359 of SEQ ID NO: 1.

In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 12 contiguous nucleobases complementary to a target region. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 12 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases 1343-1368, 1317-1366, 2748-2791, 2155-2208, 2748-2791, 730-748, 528-547, 531-567, 636-697, 1311-1331, 1314-1339, 1446-1475, 1635-1670, 1610-1638, 1457-1486, 2773-1788, 931-948, 934-949, 937-952, 942-957, 937-957, 943-958, 937-953, 1346-1363, 1346-1361, 1347-1363, 2162-2179, 2492-2508, 2696-2717, or 2683-2703 of SEQ ID NO: 1. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 12 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases 2773-2788, 1343-1358, or 1344-1359 of SEQ ID NO: 1.

In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 14 contiguous nucleobases complementary to a target region. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 14 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases 1343-1368, 1317-1366, 2748-2791, 2155-2208, 2748-2791, 730-748, 528-547, 531-567, 636-697, 1311-1331, 1314-1339, 1446-1475, 1635-1670, 1610-1638, 1457-1486, 2773-1788, 931-948, 934-949, 937-952, 942-957, 937-957, 943-958, 937-953, 1346-1363, 1346-1361, 1347-1363, 2162-2179, 2492-2508, 2696-2717, or 2683-2703 of SEQ ID NO: 1. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 14 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases 2773-2788, 1343-1358, or 1344-1359 of SEQ ID NO: 1.

In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 16 contiguous nucleobases complementary to a target region. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 16 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases 1343-1368, 1317-1366, 2748-2791, 2155-2208, 2748-2791, 730-748, 528-547, 531-567, 636-697, 1311-1331, 1314-1339, 1446-1475, 1635-1670, 1610-1638, 1457-1486, 2773-1788, 931-948, 934-949, 937-952, 942-957, 937-957, 943-958, 937-953, 1346-1363, 1346-1361, 1347-1363, 2162-2179, 2492-2508, 2696-2717, or 2683-2703 of SEQ ID NO: 1. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 16 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases 2773-2788, 1343-1358, or 1344-1359 of SEQ ID NO: 1.

In certain embodiments, the modified oligonucleotides provided herein are targeted to any one of the following regions of SEQ ID NO: 2: 10195-10294, 13553-13572, 13748-13767, 13455-13475, 13628-13657, 13735-13760, 13746-13905, 13836-13851, 13553-13568, 13563-13578, 13624-13639, 13686-13701, 13760-13775, 13763-13779, 13765-13780, 2580-2595, 6446-6461, 11099-11115, 11082-11099, 1974-1993, 4435-4456, 6035-6052, 6360-6385, 6445-6468, 6807-6824, 6789-6806, and 6596-6615. In certain embodiments, the modified oligonucleotides provided herein are targeted to any one of the following regions of SEQ ID NO: 2: 13836-13831, 8603-8618, and 8604-8619.

In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 8 contiguous nucleobases complementary to a target region. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 8 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases 10195-10294, 13553-13572, 13748-13767, 13455-13475, 13628-13657, 13735-13760, 13746-13905, 13836-13851, 13553-13568, 13563-13578, 13624-13639, 13686-13701, 13760-13775, 13763-13779, 13765-13780, 2580-2595, 6446-6461, 11099-11115, 11082-11099, 1974-1993, 4435-4456, 6035-6052, 6360-6385, 6445-6468, 6807-6824, 6789-6806, or 6596-6615 of SEQ ID NO: 2. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 8 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases13836-13831, 8603-8618, or 8604-8619 of SEQ ID NO: 2.

In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 10 contiguous nucleobases complementary to a target region. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 10 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases 10195-10294, 13553-13572, 13748-13767, 13455-13475, 13628-13657, 13735-13760, 13746-13905, 13836-13851, 13553-13568, 13563-13578, 13624-13639, 13686-13701, 13760-

13775, 13763-13779, 13765-13780, 2580-2595, 6446-6461, 11099-11115, 11082-11099, 1974-1993, 4435-4456, 6035-6052, 6360-6385, 6445-6468, 6807-6824, 6789-6806, or 6596-6615 of SEQ ID NO: 2. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 10 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases13836-13831, 8603-8618, or 8604-8619 of SEQ ID NO: 2.

In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 12 contiguous nucleobases complementary to a target region. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 12 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases 10195-10294, 13553-13572, 13748-13767, 13455-13475, 13628-13657, 13735-13760, 13746-13905, 13836-13851, 13553-13568, 13563-13578, 13624-13639, 13686-13701, 13760-13775, 13763-13779, 13765-13780, 2580-2595, 6446-6461, 11099-11115, 11082-11099, 1974-1993, 4435-4456, 6035-6052, 6360-6385, 6445-6468, 6807-6824, 6789-6806, or 6596-6615 of SEQ ID NO: 2. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 12 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases13836-13831, 8603-8618, or 8604-8619 of SEQ ID NO: 2.

In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 14 contiguous nucleobases complementary to a target region. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 14 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases 10195-10294, 13553-13572, 13748-13767, 13455-13475, 13628-13657, 13735-13760, 13746-13905, 13836-13851, 13553-13568, 13563-13578, 13624-13639, 13686-13701, 13760-13775, 13763-13779, 13765-13780, 2580-2595, 6446-6461, 11099-11115, 11082-11099, 1974-1993, 4435-4456, 6035-6052, 6360-6385, 6445-6468, 6807-6824, 6789-6806, or 6596-6615 of SEQ ID NO: 2. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 14 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases13836-13831, 8603-8618, or 8604-8619 of SEQ ID NO: 2.

In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 16 contiguous nucleobases complementary to a target region. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 16 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases 10195-10294, 13553-13572, 13748-13767, 13455-13475, 13628-13657, 13735-13760, 13746-13905, 13836-13851, 13553-13568, 13563-13578, 13624-13639, 13686-13701, 13760-13775, 13763-13779, 13765-13780, 2580-2595, 6446-6461, 11099-11115, 11082-11099, 1974-1993, 4435-4456, 6035-6052, 6360-6385, 6445-6468, 6807-6824, 6789-6806, or 6596-6615 of SEQ ID NO: 2. In certain embodiments, the modified oligonucleotides provided herein have a nucleobase sequence comprising a complementary region comprising at least 16 contiguous nucleobases complementary to a target region, wherein the target region is targeted to nucleobases13836-13831, 8603-8618, or 8604-8619 of SEQ ID NO: 2.

In certain embodiments, the animal is a human.

In certain embodiments, the compounds or compositions of the invention are designated as a first agent and the methods of the invention further comprise administering a second agent. In certain embodiments, the first agent and the second agent are co-administered. In certain embodiments the first agent and the second agent are co-administered sequentially or concomitantly.

In certain embodiments, administration comprises parenteral administration.

In certain embodiments, the compound is a single-stranded modified oligonucleotide. In certain embodiments, the nucleobase sequence of the modified oligonucleotide is at least 95% complementary to any one of SEQ ID NOs: 1-19 as measured over the entirety of said modified oligonucleotide. In certain embodiments, the nucleobase sequence of the modified oligonucleotide is 100% complementary to any one of SEQ ID NOs: 1-19 as measured over the entirety of said modified oligonucleotide. In certain embodiments, the compound is a single-stranded modified oligonucleotide. In certain embodiments, the nucleobase sequence of the modified oligonucleotide is at least 95% complementary to any one of SEQ ID NO: 1 as measured over the entirety of said modified oligonucleotide. In certain embodiments, the nucleobase sequence of the modified oligonucleotide is 100% complementary to any one of SEQ ID NO: 1 as measured over the entirety of said modified oligonucleotide.

In certain embodiments, the nucleobase sequence of the modified oligonucleotide is at least 90% complementary to any one of SEQ ID NO: 1 as measured over the entirety of said modified oligonucleotide. In certain embodiments, the nucleobase sequence of the modified oligonucleotide is 85% complementary to any one of SEQ ID NOs: 1 as measured over the entirety of said modified oligonucleotide.

In certain embodiments, the nucleobase sequence of the modified oligonucleotide is at least 90% complementary to any one of SEQ ID NO: 2 as measured over the entirety of said modified oligonucleotide. In certain embodiments, the nucleobase sequence of the modified oligonucleotide is 85% complementary to any one of SEQ ID NO: 2 as measured over the entirety of said modified oligonucleotide.

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

In certain embodiments, at least one nucleoside of said modified oligonucleotide comprises a modified sugar. In certain embodiments, at least one modified sugar is a bicyclic sugar. In certain embodiments, at least one modified sugar comprises a 2'-O-methoxyethyl or a 4'- $(CH_2)_n$-O-2' bridge, wherein n is 1 or 2.

In certain embodiments, at least one nucleoside of said modified oligonucleotide comprises a modified nucleobase. In certain embodiments, the modified nucleobase is a 5-methylcytosine.

In certain embodiments, the modified oligonucleotide comprises: a) a gap segment consisting of linked deoxynucleosides; b) a 5' wing segment consisting of linked nucleosides; and c) a 3' wing segment consisting of linked nucleosides. The gap segment is positioned between the 5' wing segment and the 3' wing segment and each nucleoside of each wing segment comprises a modified sugar.

In certain embodiments, the modified oligonucleotide comprises: a) a gap segment consisting of ten linked deoxynucleosides; b) a 5' wing segment consisting of five linked nucleosides; and c) a 3' wing segment consisting of five linked nucleosides. The gap segment is positioned between the 5' wing segment and the 3' wing segment, each nucleoside of each wing segment comprises a 2'-O-methoxyethyl sugar, each internucleoside linkage of said modified oligonucleotide is a phosphorothioate linkage, and each cytosine in said modified oligonucleotide is a 5'-methylcytosine.

In certain embodiments, the modified oligonucleotide consists of 20 linked nucleosides. In certain embodiments, the modified oligonucleotide consists of 19 linked nucleosides. In certain embodiments, the modified oligonucleotide consists of 18 linked nucleosides. In certain embodiments, the modified oligonucleotide consists of 17 linked nucleosides. In certain embodiments, the modified oligonucleotide consists of 16 linked nucleosides.

Certain embodiments provide a method of preferentially reducing CUGexp DMPK RNA, reducing myotonia or reducing spliceopathy in an animal comprising administering to the animal a compound comprising a modified oligonucleotide having a gap segment consisting of ten linked deoxynucleosides, a 5' wing segment consisting of five linked nucleosides and a 3' wing segment consisting of five linked nucleosides. The gap segment is positioned between the 5' wing segment and the 3' wing segment, each nucleoside of each wing segment comprises a 2'-O-methoxyethyl sugar, each internucleoside linkage of said modified oligonucleotide is a phosphorothioate linkage, each cytosine in said modified oligonucleotide is a 5'-methylcytosine.

In certain embodiments, the modified oligonucleotide comprises: a) a gap segment consisting of eight linked deoxynucleosides; b) a 5' wing segment consisting of four linked nucleosides and having a E-E-K-K 5'-wing motif; c) a 3' wing segment consisting of four linked nucleosides and having a K-K-E-E 3'-wing motif; and d) wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each E represents 2'-O-methoxyethyl sugar and each K represents a cEt sugar.

In certain embodiments, the modified oligonucleotide comprises: a) a gap segment consisting of seven linked deoxynucleosides; b) a 5' wing segment consisting of five linked nucleosides and having an E-E-E-K-K 5'-wing motif; c) a 3' wing segment consisting of five linked nucleosides and having a K-K-E-E-E 3'-wing motif; and d) wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each E represents 2'-O-methoxyethyl sugar and each K represents a cEt sugar.

In certain embodiments, the modified oligonucleotide comprises: a) a gap segment consisting of ten linked deoxynucleosides; b) a 5' wing segment consisting of five linked nucleosides; c) a 3' wing segment consisting of five linked nucleosides; and d) wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each nucleoside of each wing segment comprises a 2'-O-methoxyethyl sugar.

In certain embodiments, the modified oligonucleotide comprises: a) a gap segment consisting of ten linked deoxynucleosides; b) a 5' wing segment consisting of three linked nucleosides; c) a 3' wing segment consisting of three linked nucleosides; and d) wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each nucleoside of each wing segment comprises a cEt sugar.

Certain embodiments provide a method of preferentially reducing CUGexp DMPK RNA, reducing myotonia or reducing spliceopathy in an animal comprising administering to the animal a compound comprising a modified oligonucleotide having: a) a gap segment consisting of eight linked deoxynucleosides; b) a 5' wing segment consisting of four linked nucleosides and having a E-E-K-K 5'-wing motif; c) a 3' wing segment consisting of four linked nucleosides and having a K-K-E-E 3'-wing motif; and d) wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each E represents 2'-O-methoxyethyl sugar and each K represents a cEt sugar.

Certain embodiments provide a method of preferentially reducing CUGexp DMPK RNA, reducing myotonia or reducing spliceopathy in an animal comprising administering to the animal a compound comprising a modified oligonucleotide having: a) a gap segment consisting of seven linked deoxynucleosides; b) a 5' wing segment consisting of five linked nucleosides and having an E-E-E-K-K 5'-wing motif; c) a 3' wing segment consisting of five linked nucleosides and having a K-K-E-E-E 3'-wing motif; and d) wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each E represents 2'-O-methoxyethyl sugar and each K represents a cEt sugar.

Certain embodiments provide a method of preferentially reducing CUGexp DMPK RNA, reducing myotonia or reducing spliceopathy in an animal comprising administering to the animal a compound comprising a modified oligonucleotide having: a) a gap segment consisting of ten linked deoxynucleosides; b) a 5' wing segment consisting of five linked nucleosides; c) a 3' wing segment consisting of five linked nucleosides; and d) wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each nucleoside of each wing segment comprises a 2'-O-methoxyethyl sugar.

Certain embodiments provide a method of preferentially reducing CUGexp DMPK RNA, reducing myotonia or reducing spliceopathy in an animal comprising administering to the animal a compound comprising a modified oligonucleotide having: a) a gap segment consisting of ten linked deoxynucleosides; b) a 5' wing segment consisting of three linked nucleosides; c) a 3' wing segment consisting of three linked nucleosides; and d) wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each nucleoside of each wing segment comprises a cEt sugar.

Certain embodiments provide the use of any compound as described herein in the manufacture of a medicament for use in any of the therapeutic methods described herein. For example, certain embodiments provide the use of a compound as described herein in the manufacture of a medicament for treating, ameliorating, or preventing type 1 myotonic dystrophy. Certain embodiments provide the use of a compound as described herein in the manufacture of a medicament for inhibiting expression of DMPK and treating, preventing, delaying or ameliorating a DMPK related disease and or a symptom thereof. Certain embodiments provide the use of a compound as described herein in the manufacture of a medicament for reducing DMPK expression in an animal. Certain embodiments provide the use of a compound as described herein in the manufacture of a medicament for preferentially reducing CUGexp DMPK, reducing myotonia, or reducing spliceopathy in an animal. Certain embodiments provide the use of a compound as described herein in the manufacture of a medicament for treating an animal with type 1 myotonic dystrophy. Certain embodiments provide the use of a compound as described herein in the manufacture of a medicament for treating, preventing, delaying, or ameliorating symptoms and outcomes associated with development of DM1 including muscle stiffness, myotonia, disabling distal weakness, weakness in face and jaw muscles, difficulty in swallowing, drooping of the eyelids (ptosis), weakness of neck muscles, weakness in arm and leg muscles, persistent muscle pain, hypersomnia, muscle wasting, dysphagia, respiratory insufficiency, irregular heartbeat, heart muscle damage, apathy, insulin resistance, and cataracts. Certain embodiments provide the use of a compound as described herein in the manufacture of a medicament for counteracting RNA dominance by directing the cleavage of pathogenic transcripts.

Certain embodiments provide a kit for treating, preventing, or ameliorating type 1 myotonic dystrophy as described herein wherein the kit comprises: a) a compound as described herein; and optionally b) an additional agent or therapy as described herein. The kit can further include instructions or a label for using the kit to treat, prevent, or ameliorate type 1 myotonic dystrophy.

Certain embodiments provide any compound or composition as described herein, for use in any of the therapeutic methods described herein. For example, certain embodiments provide a compound or composition as described herein for inhibiting expression of DMPK and treating, preventing, delaying or ameliorating a DMPK related disease and or a symptom thereof. Certain embodiments provide a compound or composition as described herein for use in reducing DMPK expression in an animal. Certain embodiments provide a compound or composition as described herein for use in preferentially reducing CUGexp DMPK, reducing myotonia, or reducing spliceopathy in an animal. Certain embodiments provide a compound or composition as described herein for use in treating an animal with type 1 myotonic dystrophy. Certain embodiments provide a compound or composition as described herein for use in treating, preventing, delaying, or ameliorating symptoms and outcomes associated with development of DM1 including muscle stiffness, myotonia, disabling distal weakness, weakness in face and jaw muscles, difficulty in swallowing, drooping of the eyelids (ptosis), weakness of neck muscles, weakness in arm and leg muscles, persistent muscle pain, hypersomnia, muscle wasting, dysphagia, respiratory insufficiency, irregular heartbeat, heart muscle damage, apathy, insulin resistance, and cataracts. Certain embodiments provide a compound or composition as described herein for use in counteracting RNA dominance by directing the cleavage of pathogenic transcripts.Certain embodiments provide compounds comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides having a nucleobase sequence comprising at least 12 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33- 874.

Other compounds which can be used in the methods described herein are also provided.

For example, certain embodiments provide compounds comprising a modified oligonucleotide consisting of 10 to 80, 12 to 50, 12 to 30, 15 to 30, 18 to 24, 19 to 22, or 20 linked nucleosides having a nucleobase sequence comprising at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, or at least 19, contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33- 874.

Certain embodiments provide compounds comprising a modified oligonucleotide consisting of 10 to 80, 12 to 50, 12 to 30, 15 to 30, 18 to 24, 19 to 22, or 20, linked nucleosides having a nucleobase sequence comprising at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33- 874.

Certain embodiments provide compounds comprising a modified oligonucleotide consisting of 10 to 80, 12 to 50, 12 to 30, 15 to 30, or 15 to 17, linked nucleosides having a nucleobase sequence comprising a portion of at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, or at least 19, or more, contiguous nucleobases complementary to an equal length portion of nucleobases 1343-1368, 1317-1366, 2748-2791, 2155-2208, 2748-2791, 730-748, 528-547, 531-567, 636-697, 1311-1331, 1314-1339, 1446-1475, 1635-1670, 1610-1638, 1457-1486, 2773-1788, 931-948, 934-949, 937-952, 942-957, 937-957, 943-958, 937-953, 1346-1363, 1346-1361, 1347-1363, 2162-2179, 2492-2508, 2696-2717, or 2683-2703 of SEQ ID NO: 1.

Certain embodiments provide compounds comprising a modified oligonucleotide consisting of 10 to 80, 12 to 50, 12 to 30, 15 to 30, 18 to 24, 19 to 22, or 20, linked nucleosides having a nucleobase sequence comprising a portion of at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, or at least 19, or more, contiguous nucleobases complementary to an equal length portion of nucleobases 10195-10294, 13553-13572, 13748-13767, 13455-13475, 13628-13657, 13735-13760, 13746-13905, 13836-13851, 13553-13568, 13563-13578, 13624-13639, 13686-13701, 13760-13775, 13763-13779, 13765-13780, 2580-2595, 6446-6461, 11099-11115, 11082-11099, 1974-1993, 4435-4456, 6035-6052, 6360-6385, 6445-6468, 6807-6824, 6789-6806, or 6596-6615 of SEQ ID NO: 2.

In certain embodiments, the modified oligonucleotide is a single-stranded oligonucleotide.

In certain embodiments, the nucleobase sequence of the modified oligonucleotide is at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or 100%, complementary to any of SEQ ID NOs: 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33- 874.

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

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

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

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

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

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

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

In certain embodiments, the modified nucleobase is a 5-methylcytosine. In certain embodiments, each cytosine residue comprises a 5-methylcytosine.

In certain embodiments, the modified oligonucleotide consists of 16 linked nucleosides.

In certain embodiments, the modified oligonucleotide consists of 17 linked nucleosides.

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

Antisense Compounds

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

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

In certain embodiments, an antisense compound targeted to DMPK as described herein is 10 to 30 nucleotides in length. In other words, the antisense compounds are in some embodiments from 10 to 30 linked nucleobases. In other embodiments, the antisense compound comprises a modified oligonucleotide consisting of 8 to 80, 10 to 80, 12 to 30, 12 to 50, 15 to 30, 15 to 18, 15 to 17, 16 to 16, 18 to 24, 19 to 22, or 20 linked nucleobases. In certain such embodiments, the antisense compound comprises a modified oligonucleotide consisting of 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, or 80 linked nucleobases in length, or a range defined by any two of the above values. In certain embodiments, antisense compounds of any of these lengths contain at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, or at least 19, contiguous nucleobases of the nucleobase sequence of any of the exemplary antisense compounds described herein (e.g., at least 8 contiguous nucleobases of a nucleobase sequence recited in any one of SEQ ID NOs: 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33- 874..

In certain embodiments, the antisense compound comprises a shortened or truncated modified oligonucleotide. The shortened or truncated modified oligonucleotide can have a single nucleoside deleted from the 5' end (5' truncation), or alternatively from the 3' end (3' truncation). A shortened or truncated oligonucleotide can have two nucleosides deleted from the 5' end, or alternatively can have two subunits deleted from the 3' end. Alternatively, the deleted nucleosides can be dispersed throughout the modified oligonucleotide, for example, in an antisense compound having one nucleoside deleted from the 5' end and one nucleoside deleted from the 3' end.

When a single additional nucleoside is present in a lengthened oligonucleotide, the additional nucleoside can be located at the 5' or 3' end of the oligonucleotide. When two or more additional nucleosides are present, the added nucleosides can be adjacent to each other, for example, in an oligonucleotide having two nucleosides added to the 5' end (5' addition), or alternatively to the 3' end (3' addition), of the oligonucleotide. Alternatively, the added nucleoside can be dispersed throughout the antisense compound, for example, in an oligonucleotide having one nucleoside added to the 5' end and one subunit added to the 3' end.

It is possible to increase or decrease the length of an antisense compound, such as an antisense oligonucleotide, and/or introduce mismatch bases without eliminating activity. For example, in Woolf et al. (Proc. Natl. Acad. Sci. USA 89:7305-7309, 1992), a series of antisense oligonucleotides 13-25 nucleobases in length were tested for their ability to induce cleavage of a target RNA in an oocyte injection model. Antisense oligonucleotides 25 nucleobases in length with 8 or 11 mismatch bases near the ends of the antisense oligonucleotides were able to direct specific cleavage of the target mRNA, albeit to a lesser extent than the antisense oligonucleotides that contained no mismatches. Similarly, target specific cleavage was achieved using 13 nucleobase antisense oligonucleotides, including those with 1 or 3 mismatches.

Gautschi et al (J. Natl. Cancer Inst. 93:463-471, March 2001) demonstrated the ability of an oligonucleotide having 100% complementarity to the bcl-2 mRNA and having 3 mismatches to the bcl-xL mRNA to reduce the expression of both bcl-2 and bcl-xL *in vitro* and *in vivo*. Furthermore, this oligonucleotide demonstrated potent anti-tumor activity *in vivo*.

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

Target Nucleic Acids, Target Regions and Nucleotide Sequences

Nucleotide sequences that encode DMPK include, without limitation, the following sequences as set forth in GenBank Accession No. NM_001081560.1 (incorporated herein as SEQ ID NO: 1), GenBank Accession No. NT_011109.15 truncated from nucleotides 18540696 to 18555106 (incorporated herein as SEQ ID NO: 2), GenBank Accession No. NT_039413.7 truncated from nucleotides 16666001 to 16681000 (incorporated herein as SEQ ID NO: 3), GenBank Accession No. NM_032418.1 (incorporated herein as SEQ ID NO: 4), GenBank Accession No. AI007148.1 (incorporated herein as SEQ ID NO: 5), GenBank Accession No. AI304033.1 (incorporated herein as SEQ ID NO: 6), GenBank Accession No. BC024150.1 (incorporated herein as SEQ ID NO: 7), GenBank Accession No. BC056615.1 (incorporated herein as SEQ ID NO: 8), GenBank Accession No. BC075715.1 (incorporated herein as SEQ ID NO: 9), GenBank Accession No. BU519245.1 (incorporated herein as SEQ ID NO: 10), GenBank Accession No. CB247909.1 (incorporated herein as SEQ ID NO: 11), GenBank Accession No. CX208906.1 (incorporated herein as SEQ ID NO: 12), GenBank Accession No. CX732022.1 (incorporated herein as SEQ ID NO: 13), GenBank Accession No. S60315.1 (incorporated herein as SEQ ID NO: 14), GenBank Accession No. S60316.1 (incorporated herein as SEQ ID NO: 15), GenBank Accession No. NM_001081562.1 (incorporated herein as SEQ ID NO: 16), and GenBank Accession No. NM_001100.3 (incorporated herein as SEQ ID NO: 17). It is understood that the sequence set forth in each SEQ ID NO in the Examples contained herein is independent of any modification to a sugar moiety, an internucleoside linkage, or a nucleobase. As such, antisense compounds defined by a SEQ ID NO can comprise, independently, one or more modifications to a sugar moiety, an internucleoside linkage, or a nucleobase. Antisense compounds described by Isis Number (Isis No) indicate a combination of nucleobase sequence and motif.

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

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

A target region can contain one or more target segments. Multiple target segments within a target region can be overlapping. Alternatively, they can be non-overlapping. In certain embodiments, target segments within a target region are separated by no more than about 300 nucleotides. In certain embodiments, target segments within a target region are separated by a number of nucleotides that is, is about, is no more than, is no more than about, 250, 200, 150, 100, 90, 80, 70, 60, 50, 40, 30, 20, or 10 nucleotides on the target nucleic acid, or is a range defined by any two of the preceding values. In certain embodiments, target segments within a target region are separated by no more than, or no more than about, 5 nucleotides on the target nucleic acid. In certain embodiments, target segments are contiguous. Contemplated are target regions defined by a range having a starting nucleic acid that is any of the 5' target sites or 3' target sites listed herein.

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

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

There can be variation in activity (e.g., as defined by percent reduction of target nucleic acid levels) of the antisense compounds within an active target region. In certain embodiments, reductions in DMPK mRNA levels are indicative of inhibition of DMPK protein expression. Reductions in levels of a DMPK protein are also indicative of inhibition of target mRNA expression. Further, phenotypic changes, such as a reducing myotonia or reducing spliceopathy, can be indicative of inhibition of DMPK mRNA and/or protein expression.

Hybridization

In some embodiments, hybridization occurs between an antisense compound disclosed herein and a DMPK nucleic acid. The most common mechanism of hybridization involves hydrogen bonding (e.g., Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding) between complementary nucleobases of the nucleic acid molecules.

Hybridization can occur under varying conditions. Stringent conditions are sequence-dependent and are determined by the nature and composition of the nucleic acid molecules to be hybridized.

Methods of determining whether a sequence is specifically hybridizable to a target nucleic acid are well known in the art (Sambrooke and Russell, Molecular Cloning: A Laboratory Manual, 3rd Ed., 2001). In certain embodiments, the antisense compounds provided herein are specifically hybridizable with a DMPK nucleic acid.

Complementarity

An antisense compound and a target nucleic acid are complementary to each other when a sufficient number of nucleobases of the antisense compound can hydrogen bond with the corresponding nucleobases of the target nucleic acid, such that a desired effect will occur (e.g., antisense inhibition of a target nucleic acid, such as a DMPK nucleic acid).

An antisense compound can hybridize over one or more segments of a DMPK nucleic acid such that intervening or adjacent segments are not involved in the hybridization event (e.g., a loop structure, mismatch or hairpin structure).

In certain embodiments, the antisense compounds provided herein, or a specified portion thereof, are, or are at least, 70%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% complementary to a DMPK nucleic acid, a target region, target segment, or specified portion thereof. In certain embodiments, the antisense compounds are at least 70%, at least 80%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% complementary to a DMPK nucleic acid, a target region, target segment, or specified portion thereof, and contain at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, or at least 19, contiguous nucleobases of the nucleobase sequence of any of the exemplary antisense compounds described herein (e.g., at least 8 contiguous nucleobases of a nucleobase sequence recited in any one of SEQ ID NOs: 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33- 874). Percent complementarity of an antisense compound with a target nucleic acid can be determined using routine methods, and is measured over the entirety of the antisense compound.

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

In certain embodiments, the antisense compounds provided herein, or specified portions thereof, are fully complementary (i.e. 100% complementary) to a target nucleic acid, or specified portion thereof. For example, antisense compound can be fully complementary to a DMPK nucleic acid, or a target region, or a target segment or target sequence thereof. As used herein, “fully complementary” means each nucleobase of an antisense compound is capable of precise base pairing with the corresponding nucleobases of a target nucleic acid. For example, a 20 nucleobase antisense compound is fully complementary to a target sequence that is 400 nucleobases long, so long as there is a corresponding 20 nucleobase portion of the target nucleic acid that is fully complementary to the antisense compound. Fully complementary can also be used in reference to a specified portion of the first and /or the second nucleic acid. For example, a 20 nucleobase portion of a 30 nucleobase antisense compound can be “fully complementary” to a target sequence that is 400 nucleobases long. The 20 nucleobase portion of the 30 nucleobase oligonucleotide is fully complementary to the target sequence if the target sequence has a corresponding 20 nucleobase portion wherein each nucleobase is complementary to the 20 nucleobase portion of the antisense compound. At the same time, the entire 30 nucleobase antisense compound can be fully complementary to the target sequence, depending on whether the remaining 10 nucleobases of the antisense compound are also complementary to the target sequence.

The location of a non-complementary nucleobase can be at the 5’ end or 3’ end of the antisense compound. Alternatively, the non-complementary nucleobase or nucleobases can be at an internal position of the antisense compound. When two or more non-complementary nucleobases are present, they can be either contiguous (i.e. linked) or non-contiguous. In one embodiment, a non-complementary nucleobase is located in the wing segment of a gapmer antisense oligonucleotide.

In certain embodiments, antisense compounds that are, or are up to 10, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleobases in length comprise no more than 4, no more than 3, no more than 2, or no more than 1 non-complementary nucleobase(s) relative to a target nucleic acid, such as a DMPK nucleic acid, or specified portion thereof.

In certain embodiments, antisense compounds that are, or are up to 10, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleobases in length comprise no more than 6, no more than 5, no more than 4, no more than 3, no more than 2, or no more than 1 non-complementary nucleobase(s) relative to a target nucleic acid, such as a DMPK nucleic acid, or specified portion thereof.

The antisense compounds provided herein also include those which are complementary to a portion of a target nucleic acid. As used herein, “portion” refers to a defined number of contiguous (i.e. linked) nucleobases within a region or segment of a target nucleic acid. A “portion” can also refer to a defined number of contiguous nucleobases of an antisense compound. In certain embodiments, the antisense compounds, are complementary to at least an 8 nucleobase portion of a target segment. In certain embodiments, the antisense compounds are complementary to at least a 10 nucleobase portion of a target segment. In certain embodiments, the antisense compounds are complementary to at least a 15 nucleobase portion of a target segment. Also contemplated are antisense compounds that are complementary to at least an 8, at least a 9, at least a 10, at least an 11, at least a 12, at least a 13, at least a 14, at least a 15, at least a 16, at least a 17, at least an 18, at least a 19, at least a 20, or more nucleobase portion of a target segment, or a range defined by any two of these values.

Identity

The antisense compounds provided herein can also have a defined percent identity to a particular nucleotide sequence, SEQ ID NO, or compound represented by a specific Isis number, or portion thereof. As used herein, an antisense compound is identical to the sequence disclosed herein if it has the same nucleobase pairing ability. For example, a RNA which contains uracil in place of thymidine in a disclosed DNA sequence would be considered identical to the DNA sequence since both uracil and thymidine pair with adenine. Shortened and lengthened versions of the antisense compounds described herein as well as compounds having non-identical bases relative to the antisense compounds provided herein also are contemplated. The non-identical bases can be adjacent to each other or dispersed throughout the antisense compound. Percent identity of an antisense compound is calculated according to the number of bases that have identical base pairing relative to the sequence to which it is being compared.

In certain embodiments, the antisense compounds, or portions thereof, are at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least

98%, at least 99% or 100% identical to one or more of the exemplary antisense compounds or SEQ ID NOs, or a portion thereof, disclosed herein.

Modifications

A nucleoside is a base-sugar combination. The nucleobase (also known as base) portion of the nucleoside is normally a heterocyclic base moiety. Nucleotides are nucleosides that further include a phosphate group covalently linked to the sugar portion of the nucleoside. For those nucleosides that include a pentofuranosyl sugar, the phosphate group can be linked to the 2', 3' or 5' hydroxyl moiety of the sugar. Oligonucleotides are formed through the covalent linkage of adjacent nucleosides to one another, to form a linear polymeric oligonucleotide. Within the oligonucleotide structure, the phosphate groups are commonly referred to as forming the internucleoside linkages of the oligonucleotide.

Modifications to antisense compounds encompass substitutions or changes to internucleoside linkages, sugar moieties, or nucleobases. Modified antisense compounds are often preferred over native forms because of desirable properties such as, for example, enhanced cellular uptake, enhanced affinity for nucleic acid target, increased stability in the presence of nucleases, or increased inhibitory activity.

Chemically modified nucleosides can also be employed to increase the binding affinity of a shortened or truncated antisense oligonucleotide for its target nucleic acid. Consequently, comparable results can often be obtained with shorter antisense compounds that have such chemically modified nucleosides.

Modified Internucleoside Linkages

The naturally occurring internucleoside linkage of RNA and DNA is a 3' to 5' phosphodiester linkage. Antisense compounds having one or more modified, i.e. non-naturally occurring, internucleoside linkages are often selected over antisense compounds having naturally occurring internucleoside linkages because of desirable properties such as, for example, enhanced cellular uptake, enhanced affinity for target nucleic acids, and increased stability in the presence of nucleases.

Oligonucleotides having modified internucleoside linkages include internucleoside linkages that retain a phosphorus atom as well as internucleoside linkages that do not have a phosphorus atom. Representative phosphorus containing internucleoside linkages include, but are not limited to, phosphodiesters, phosphotriesters, methylphosphonates, phosphoramidate, and phosphorothioates. Methods of preparation of phosphorous-containing and non-phosphorous-containing linkages are well known.

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

Modified Sugar Moieties

Antisense compounds of the invention can optionally contain one or more nucleosides wherein the sugar group has been modified. Such sugar modified nucleosides may impart enhanced nuclease stability, increased binding affinity, or some other beneficial biological property to the antisense compounds. In certain embodiments, nucleosides comprise chemically modified ribofuranose ring moieties. Examples of chemically modified ribofuranose rings include without limitation, addition of substitutent groups (including 5' and 2' substituent groups, bridging of non-geminal ring atoms to form bicyclic nucleic acids (BNA), replacement of the ribosyl ring oxygen atom with S, N(R), or $C(R_1)(R_2)$ (R, R_1 and R_2 are each independently H, C_1-C_{12} alkyl or a protecting group) and combinations thereof. Examples of chemically modified sugars include 2'-F-5'-methyl substituted nucleoside (see PCT International Application WO 2008/101157 Published on 8/21/08 for other disclosed 5',2'-bis substituted nucleosides) or replacement of the ribosyl ring oxygen atom with S with further substitution at the 2'-position (see published U.S. Patent Application US2005-0130923, published on June 16, 2005) or alternatively 5'-substitution of a BNA (see PCT International Application WO 2007/134181 Published on 11/22/07 wherein LNA is substituted with for example a 5'-methyl or a 5'-vinyl group).

Examples of nucleosides having modified sugar moieties include without limitation nucleosides comprising 5'-vinyl, 5'-methyl (*R* or *S*), 4'-S, 2'-F, 2'-OCH_3, 2'-OCH_2CH_3, 2'-OCH_2CH_2F and 2'-$O(CH_2)_2OCH_3$ substituent groups. The substituent at the 2' position can also be selected from allyl, amino, azido, thio, O-allyl, O-C_1-C_{10} alkyl, OCF_3, OCH_2F, $O(CH_2)_2SCH_3$, $O(CH_2)_2$-O-$N(R_m)(R_n)$, O-CH_2-C(=O)-$N(R_m)(R_n)$, and O-CH_2-C(=O)-$N(R_l)$-$(CH_2)_2$-$N(R_m)(R_n)$, where each R_l, R_m and R_n is, independently, H or substituted or unsubstituted C_1-C_{10} alkyl.

Examples of bicyclic nucleic acids (BNAs) include without limitation nucleosides comprising a bridge between the 4' and the 2' ribosyl ring atoms. In certain embodiments, antisense compounds provided herein include one or more BNA nucleosides wherein the bridge comprises one of the formulas: 4'-(CH_2)-O-2' (LNA); 4'-(CH_2)-S-2'; 4'-(CH_2)$_2$-O-2' (ENA); 4'-CH(CH_3)-O-2' and 4'-CH(CH_2OCH_3)-O-2' (and analogs thereof see U.S. Patent 7,399,845, issued on July 15, 2008); 4'-C(CH_3)(CH_3)-O-2' (and analogs thereof see PCT/US2008/068922 published as WO/2009/006478, published January 8, 2009); 4'-CH_2-N(OCH_3)-2' (and analogs thereof see PCT/US2008/064591 published as WO/2008/150729, published December 11, 2008); 4'-CH_2-O-N(CH_3)-2' (see published U.S. Patent Application US2004-0171570, published September 2, 2004); 4'-CH_2-N(R)-O-2', wherein R is H, C_1-C_{12} alkyl, or a protecting group (see U.S. Patent 7,427,672, issued on September 23, 2008); 4'-CH_2-C(H)(CH_3)-2' (see Chattopadhyaya *et al., J. Org. Chem.,* 2009, *74*, 118-134); and 4'-CH_2-C(=CH_2)-2' (and analogs thereof see PCT/US2008/066154 published as WO 2008/154401, published on December 8, 2008).

Further bicyclic nucleosides have been reported in published literature (see for example: Srivastava et al., *J. Am. Chem. Soc.*, 2007, *129(26)* 8362-8379; Frieden *et al., Nucleic Acids Research,* 2003, *21*, 6365-6372; Elayadi *et al., Curr. Opinion Invens. Drugs,* 2001, *2*, 558-561; Braasch *et al., Chem. Biol.,* 2001, *8*, 1-7; Orum *et al., Curr. Opinion Mol. Ther.,* 2001, *3*, 239-243; Wahlestedt et al., *Proc. Natl. Acad. Sci. U. S. A.*, 2000, *97*, 5633-5638; Singh et al., *Chem. Commun.*, 1998, *4*, 455-456; Koshkin et al., *Tetrahedron*, 1998, *54*, 3607-3630; Kumar et al., *Bioorg. Med. Chem. Lett.*, 1998, *8*, 2219-2222; Singh et al., *J. Org. Chem.*, 1998, *63*, 10035-10039; U.S. Patents Nos.: 7,399,845; 7,053,207; 7,034,133; 6,794,499; 6,770,748; 6,670,461; 6,525,191; 6,268,490; U.S. Patent Publication Nos.: US2008-0039618; US2007-0287831; US2004-0171570; U.S. Patent Applications, Serial Nos.: 12/129,154; 61/099,844; 61/097,787; 61/086,231; 61/056,564; 61/026,998; 61/026,995; 60/989,574; International applications WO 2007/134181; WO 2005/021570; WO 2004/106356; WO 94/14226; and PCT International Applications Nos.: PCT/US2008/068922; PCT/US2008/066154; and PCT/US2008/064591). Each of the foregoing bicyclic nucleosides can be prepared having one or more stereochemical sugar configurations including for example α-L-ribofuranose and β-D-ribofuranose (see PCT international application PCT/DK98/00393, published on March 25, 1999 as WO 99/14226).

In certain embodiments, bicyclic nucleosides comprise a bridge between the 4' and the 2' carbon atoms of the pentofuranosyl sugar moiety including without limitation, bridges comprising 1 or from 1 to 4 linked groups independently selected from -[C(R_a)(R_b)]$_n$-, -C(R_a)=C(R_b)-, -C(R_a)=N-

, -C(=NR$_a$)-, -C(=O)-, -C(=S)-, -O-, -Si(R$_a$)$_2$-, -S(=O)$_x$-, and -N(R$_a$)-; wherein: x is 0, 1, or 2; n is 1, 2, 3, or 4; each R$_a$ and R$_b$ is, independently, H, a protecting group, hydroxyl, C$_1$-C$_{12}$ alkyl, substituted C$_1$-C$_{12}$ alkyl, C$_2$-C$_{12}$ alkenyl, substituted C$_2$-C$_{12}$ alkenyl, C$_2$-C$_{12}$ alkynyl, substituted C$_2$-C$_{12}$ alkynyl, C$_5$-C$_{20}$ aryl, substituted C$_5$-C$_{20}$ aryl, heterocycle radical, substituted heterocycle radical, heteroaryl, substituted heteroaryl, C$_5$-C$_7$ alicyclic radical, substituted C$_5$-C$_7$ alicyclic radical, halogen, OJ$_1$, NJ$_1$J$_2$, SJ$_1$, N$_3$, COOJ$_1$, acyl (C(=O)-H), substituted acyl, CN, sulfonyl (S(=O)$_2$-J$_1$), or sulfoxyl (S(=O)-J$_1$); and

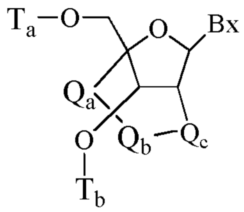
each J$_1$ and J$_2$ is, independently, H, C$_1$-C$_{12}$ alkyl, substituted C$_1$-C$_{12}$ alkyl, C$_2$-C$_{12}$ alkenyl, substituted C$_2$-C$_{12}$ alkenyl, C$_2$-C$_{12}$ alkynyl, substituted C$_2$-C$_{12}$ alkynyl, C$_5$-C$_{20}$ aryl, substituted C$_5$-C$_{20}$ aryl, acyl (C(=O)-H), substituted acyl, a heterocycle radical, a substituted heterocycle radical, C$_1$-C$_{12}$ aminoalkyl, substituted C$_1$-C$_{12}$ aminoalkyl or a protecting group.

In certain embodiments, the bridge of a bicyclic sugar moiety is , -[C(R$_a$)(R$_b$)]$_n$-, -[C(R$_a$)(R$_b$)]$_n$-O-, -C(R$_a$R$_b$)-N(R)-O- or –C(R$_a$R$_b$)-O-N(R)-. In certain embodiments, the bridge is 4'-CH$_2$-2', 4'-(CH$_2$)$_2$-2', 4'-(CH$_2$)$_3$-2', 4'-CH$_2$-O-2', 4'-(CH$_2$)$_2$-O-2', 4'-CH$_2$-O-N(R)-2' and 4'-CH$_2$-N(R)-O-2'- wherein each R is, independently, H, a protecting group or C$_1$-C$_{12}$ alkyl.

In certain embodiments, bicyclic nucleosides are further defined by isomeric configuration. For example, a nucleoside comprising a 4'-(CH$_2$)-O-2' bridge, may be in the α-L configuration or in the β-D configuration. Previously, α-L-methyleneoxy (4'-CH$_2$-O-2') BNA's have been incorporated into antisense oligonucleotides that showed antisense activity (Frieden *et al., Nucleic Acids Research,* 2003, *21*, 6365-6372).

In certain embodiments, bicyclic nucleosides include those having a 4' to 2' bridge wherein such bridges include without limitation, α-L-4'-(CH$_2$)-O-2', β-D-4'-CH$_2$-O-2', 4'-(CH$_2$)$_2$-O-2', 4'-CH$_2$-O-N(R)-2', 4'-CH$_2$-N(R)-O-2', 4'-CH(CH$_3$)-O-2', 4'-CH$_2$-S-2', 4'-CH$_2$-N(R)-2', 4'-CH$_2$-CH(CH$_3$)-2', and 4'-(CH$_2$)$_3$-2', wherein R is H, a protecting group or C$_1$-C$_{12}$ alkyl.

In certain embodiments, bicyclic nucleosides have the formula:



wherein:

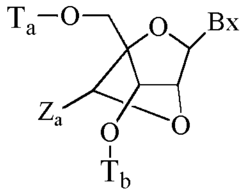
Bx is a heterocyclic base moiety;

$-Q_a-Q_b-Q_c-$ is $-CH_2-N(R_c)-CH_2-$, $-C(=O)-N(R_c)-CH_2-$, $-CH_2-O-N(R_c)-$, $-CH_2-N(R_c)-O-$ or $-N(R_c)-O-CH_2$;

R_c is C_1-C_{12} alkyl or an amino protecting group; and

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

In certain embodiments, bicyclic nucleosides have the formula:



wherein:

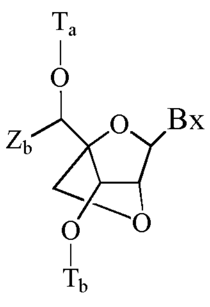
Bx is a heterocyclic base moiety;

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

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

In one embodiment, each of the substituted groups, is, independently, mono or poly substituted with substituent groups independently selected from halogen, oxo, hydroxyl, OJ_c, NJ_cJ_d, SJ_c, N_3, $OC(=X)J_c$, and $NJ_eC(=X)NJ_cJ_d$, wherein each J_c, J_d and J_e is, independently, H, C_1-C_6 alkyl, or substituted C_1-C_6 alkyl and X is O or NJ_c.

In certain embodiments, bicyclic nucleosides have the formula:



wherein:

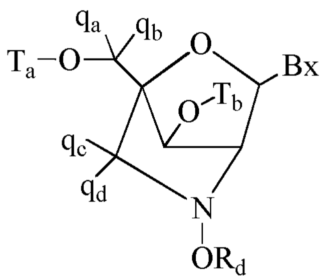
Bx is a heterocyclic base moiety;

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

Z_b is C_1-C_6 alkyl, C_2-C_6 alkenyl, C_2-C_6 alkynyl, substituted C_1-C_6 alkyl, substituted C_2-C_6

alkenyl, substituted C_2-C_6 alkynyl or substituted acyl (C(=O)-).

In certain embodiments, bicyclic nucleosides have the formula:



wherein:

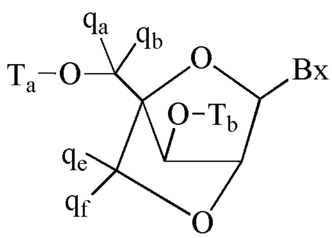
Bx is a heterocyclic base moiety;

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

R_d is C_1-C_6 alkyl, substituted C_1-C_6 alkyl, C_2-C_6 alkenyl, substituted C_2-C_6 alkenyl, C_2-C_6 alkynyl or substituted C_2-C_6 alkynyl;

each q_a, q_b, q_c and q_d is, independently, H, halogen, C_1-C_6 alkyl, substituted C_1-C_6 alkyl, C_2-C_6 alkenyl, substituted C_2-C_6 alkenyl, C_2-C_6 alkynyl or substituted C_2-C_6 alkynyl, C_1-C_6 alkoxyl, substituted C_1-C_6 alkoxyl, acyl, substituted acyl, C_1-C_6 aminoalkyl or substituted C_1-C_6 aminoalkyl;

In certain embodiments, bicyclic nucleosides have the formula:



wherein:

Bx is a heterocyclic base moiety;

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

q_a, q_b, q_e and q_f are each, independently, hydrogen, halogen, C_1-C_{12} alkyl, substituted C_1-C_{12} alkyl, C_2-C_{12} alkenyl, substituted C_2-C_{12} alkenyl, C_2-C_{12} alkynyl, substituted C_2-C_{12} alkynyl, C_1-C_{12} alkoxy, substituted C_1-C_{12} alkoxy, OJ_j, SJ_j, SOJ_j, SO_2J_j, NJ_jJ_k, N_3, CN, C(=O)OJ_j, C(=O)NJ_jJ_k, C(=O)J_j, O-C(=O)NJ_jJ_k, N(H)C(=NH)NJ_jJ_k, N(H)C(=O)NJ_jJ_k or N(H)C(=S)NJ_jJ_k;

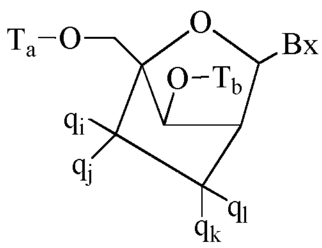
or q_e and q_f together are =C(q_g)(q_h);

q_g and q_h are each, independently, H, halogen, C_1-C_{12} alkyl or substituted C_1-C_{12} alkyl.

The synthesis and preparation of adenine, cytosine, guanine, 5-methyl-cytosine, thymine and uracil bicyclic nucleosides having a 4'-CH_2-O-2' bridge, along with their oligomerization, and nucleic acid recognition properties have been described (Koshkin et al., *Tetrahedron*, 1998, *54*, 3607-3630). The synthesis of bicyclic nucleosides has also been described in WO 98/39352 and WO 99/14226.

Analogs of various bicyclic nucleosides that have 4' to 2' bridging groups such as 4'-CH_2-O-2' and 4'-CH_2-S-2', have also been prepared (Kumar *et al., Bioorg. Med. Chem. Lett.*, 1998, *8*, 2219-2222). Preparation of oligodeoxyribonucleotide duplexes comprising bicyclic nucleosides for use as substrates for nucleic acid polymerases has also been described (Wengel et al., WO 99/14226). Furthermore, synthesis of 2'-amino-BNA, a novel conformationally restricted high-affinity oligonucleotide analog has been described in the art (Singh et al., *J. Org. Chem.*, 1998, *63*, 10035-10039). In addition, 2'-amino- and 2'-methylamino-BNA's have been prepared and the thermal stability of their duplexes with complementary RNA and DNA strands has been previously reported.

In certain embodiments, bicyclic nucleosides have the formula:



wherein:

Bx is a heterocyclic base moiety;

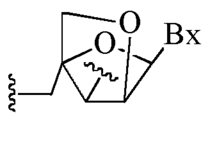
T_a and T_b are each, independently H, a hydroxyl protecting group, a conjugate group, a reactive phosphorus group, a phosphorus moiety or a covalent attachment to a support medium;

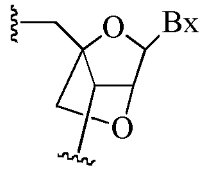
each q_i, q_j, q_k and q_l is, independently, H, halogen, C_1-C_{12} alkyl, substituted C_1-C_{12} alkyl, C_2-C_{12} alkenyl, substituted C_2-C_{12} alkenyl, C_2-C_{12} alkynyl, substituted C_2-C_{12} alkynyl, C_1-C_{12} alkoxyl, substituted C_1-C_{12} alkoxyl, OJ_j, SJ_j, SOJ_j, SO_2J_j, NJ_jJ_k, N_3, CN, C(=O)OJ_j, C(=O)NJ_jJ_k, C(=O)J_j, O-C(=O)NJ_jJ_k, N(H)C(=NH)NJ_jJ_k, N(H)C(=O)NJ_jJ_k or N(H)C(=S)NJ_jJ_k; and

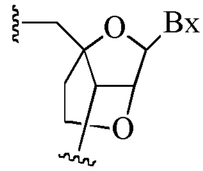
q_i and q_j or q_l and q_k together are =C(q_g)(q_h), wherein q_g and q_h are each, independently, H, halogen, C_1-C_{12} alkyl or substituted C_1-C_{12} alkyl.

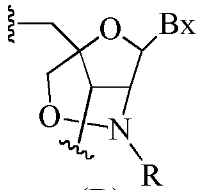
One carbocyclic bicyclic nucleoside having a 4'-$(CH_2)_3$-2' bridge and the alkenyl analog bridge 4'-CH=CH-CH_2-2' have been described (Frier *et al., Nucleic Acids Research*, 1997, *25*(*22*), 4429-4443 and Albaek *et al., J. Org. Chem*., 2006, *71*, 7731-7740). The synthesis and preparation of carbocyclic bicyclic nucleosides along with their oligomerization and biochemical studies have also been described (Srivastava *et al., J. Am. Chem. Soc.* 2007, *129(26)*, 8362-8379).

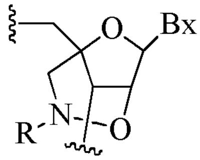
In certain embodiments, bicyclic nucleosides include, but are not limited to, (A) α-L-methyleneoxy (4'-CH_2-O-2') BNA , (B) β-D-methyleneoxy (4'-CH_2-O-2') BNA , (C) ethyleneoxy (4'-$(CH_2)_2$-O-2') BNA , (D) aminooxy (4'-CH_2-O-N(R)-2') BNA, (E) oxyamino (4'-CH_2-N(R)-O-2') BNA, (F) methyl(methyleneoxy) (4'-CH(CH_3)-O-2') BNA (also referred to as constrained ethyl or cEt), (G) methylene-thio (4'-CH_2-S-2') BNA, (H) methylene-amino (4'-CH_2-N(R)-2') BNA, (I) methyl carbocyclic (4'-CH_2-CH(CH_3)-2') BNA, (J) propylene carbocyclic (4'-$(CH_2)_3$-2') BNA, and (K) vinyl BNA as depicted below.

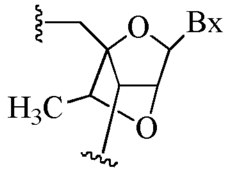

(A)

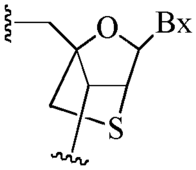

(B)

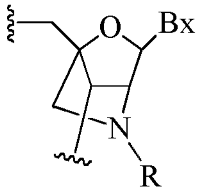

(C)

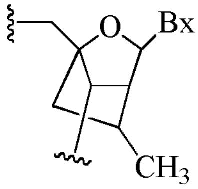

(D)

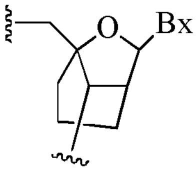

(E)

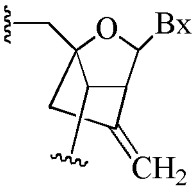

(F)


(G)


(H)

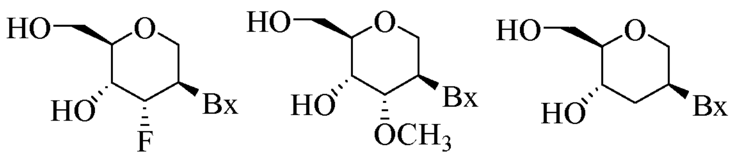

(I)


(J)

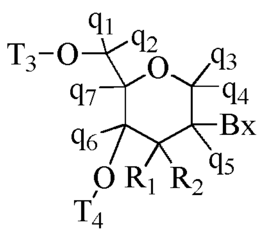

(K)

wherein Bx is the base moiety and R is, independently, H, a protecting group, C_1-C_6 alkyl or C_1-C_6 alkoxy.

In certain embodiments, nucleosides are modified by replacement of the ribosyl ring with a sugar surrogate. Such modification includes without limitation, replacement of the ribosyl ring with a surrogate ring system (sometimes referred to as DNA analogs) such as a morpholino ring, a cyclohexenyl ring, a cyclohexyl ring or a tetrahydropyranyl ring such as one having one of the formula:



In certain embodiments, sugar surrogates are selected having the formula:



wherein:

Bx is a heterocyclic base moiety;

T_3 and T_4 are each, independently, an internucleoside linking group linking the tetrahydropyran nucleoside analog to the oligomeric compound or one of T_3 and T_4 is an internucleoside linking group linking the tetrahydropyran nucleoside analog to an oligomeric compound or oligonucleotide and the other of T_3 and T_4 is H, a hydroxyl protecting group, a linked conjugate group or a 5' or 3'-terminal group;

q_1, q_2, q_3, q_4, q_5, q_6 and q_7 are each independently, H, C_1-C_6 alkyl, substituted C_1-C_6 alkyl, C_2-C_6 alkenyl, substituted C_2-C_6 alkenyl, C_2-C_6 alkynyl or substituted C_2-C_6 alkynyl; and

one of R_1 and R_2 is hydrogen and the other is selected from halogen, substituted or unsubstituted alkoxy, NJ_1J_2, SJ_1, N_3, $OC(=X)J_1$, $OC(=X)NJ_1J_2$, $NJ_3C(=X)NJ_1J_2$ and CN, wherein X is O, S or NJ_1 and each J_1, J_2 and J_3 is, independently, H or C_1-C_6 alkyl.

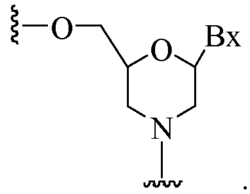
In certain embodiments, q_1, q_2, q_3, q_4, q_5, q_6 and q_7 are each H. In certain embodiments, at least one of q_1, q_2, q_3, q_4, q_5, q_6 and q_7 is other than H. In certain embodiments, at least one of q_1, q_2, q_3, q_4, q_5, q_6 and q_7 is methyl. In certain embodiments, THP nucleosides are provided wherein one of R_1 and R_2 is F. In certain embodiments, R_1 is fluoro and R_2 is H; R_1 is methoxy and R_2 is H, and

R_1 is methoxyethoxy and R_2 is H.

Such sugar surrogates include, but are not limited to, what is referred to in the art as hexitol nucleic acid (HNA), altritol nucleic acid (ANA), and mannitol nucleic acid (MNA) (*see* Leumann, C. J., *Bioorg. & Med. Chem.,* 2002, *10,* 841-854).

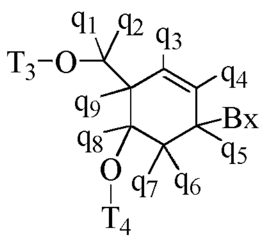
In certain embodiments, sugar surrogates comprise rings having more than 5 atoms and more than one heteroatom. For example nucleosides comprising morpholino sugar moieties and their use in oligomeric compounds has been reported (see for example: Braasch et al., Biochemistry, 2002, 41, 4503-4510; and U.S. Patents 5,698,685; 5,166,315; 5,185,444; and 5,034,506).

As used here, the term “morpholino” means a sugar surrogate having the following structure:


.

In certain embodiments, morpholinos may be modified, for example by adding or altering various substituent groups from the above morpholino structure. Such sugar surrogates are refered to herein as “modifed morpholinos.”

In certain embodiments, antisense compounds comprise one or more modified cyclohexenyl nucleosides, which is a nucleoside having a six-membered cyclohexenyl in place of the pentofuranosyl residue in naturally occurring nucleosides. Modified cyclohexenyl nucleosides include, but are not limited to those described in the art (see for example commonly owned, published PCT Application WO 2010/036696, published on April 10, 2010, Robeyns *et al., J. Am. Chem. Soc.,* 2008, *130(6)*, 1979-1984; Horváth *et al., Tetrahedron Letters,* 2007, *48*, 3621-3623; Nauwelaerts *et al., J. Am. Chem. Soc.*, 2007, *129(30)*, 9340-9348; Gu *et al.,*, *Nucleosides, Nucleotides & Nucleic Acids*, 2005, *24(5-7)*, 993-998; Nauwelaerts *et al., Nucleic Acids Research,* 2005, *33(8)*, 2452-2463; Robeyns et al., Acta Crystallographica, Section F: Structural Biology and Crystallization Communications, 2005, F61(6), 585-586; Gu et al., Tetrahedron, 2004, 60(9), 2111-2123; Gu et al., Oligonucleotides, 2003, 13(6), 479-489; Wang *et al., J. Org. Chem.,* 2003, *68*, 4499-4505; Verbeure et al., Nucleic Acids Research, 2001, 29(24), 4941-4947; Wang *et al., J. Org. Chem.,* 2001, *66*, 8478-82; Wang *et al.*, *Nucleosides, Nucleotides & Nucleic Acids*, 2001, *20(4-7)*, 785-788; Wang *et al., J. Am. Chem.,* 2000, 122, 8595-8602; Published PCT application, WO 06/047842; and Published PCT Application WO 01/049687; the text of each is incorporated by reference herein, in their entirety). Certain modified cyclohexenyl nucleosides have the formula:



wherein:

Bx is a heterocyclic base moiety;

T_3 and T_4 are each, independently, an internucleoside linking group linking the cyclohexenyl nucleoside analog to an antisense compound or one of T_3 and T_4 is an internucleoside linking group linking the tetrahydropyran nucleoside analog to an antisense compound and the other of T_3 and T_4 is H, a hydroxyl protecting group, a linked conjugate group, or a 5'-or 3'-terminal group; and

q_1, q_2, q_3, q_4, q_5, q_6, q_7, q_8 and q_9 are each, independently, H, C_1-C_6 alkyl, substituted C_1-C_6 alkyl, C_2-C_6 alkenyl, substituted C_2-C_6 alkenyl, C_2-C_6 alkynyl, substituted C_2-C_6 alkynyl or other sugar substituent group.

Many other bicyclic and tricyclic sugar surrogate ring systems are also known in the art that can be used to modify nucleosides for incorporation into antisense compounds (see for example review article: Leumann, Christian J., *Bioorg. & Med. Chem.*, 2002, *10*, 841-854). Such ring systems can undergo various additional substitutions to enhance activity.

Methods for the preparations of modified sugars are well known to those skilled in the art. Some representative U.S. patents that teach the preparation of such modified sugars include without limitation, U.S.: 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,670,633; 5,700,920; 5,792,847 and 6,600,032 and International Application PCT/US2005/019219, filed June 2, 2005 and published as WO 2005/121371 on December 22, 2005, and each of which is herein incorporated by reference in its entirety.

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

In certain embodiments, antisense compounds targeted to a DMPK nucleic acid comprise one or more nucleotides having modified sugar moieties. In certain embodiments, the modified sugar moiety is 2'-MOE. In certain embodiments, the 2'-MOE modified nucleotides are arranged in a gapmer motif.

Modified Nucleobases

Nucleobase (or base) modifications or substitutions are structurally distinguishable from, yet functionally interchangeable with, naturally occurring or synthetic unmodified nucleobases. Both natural and modified nucleobases are capable of participating in hydrogen bonding. Such nucleobase modifications can impart nuclease stability, binding affinity or some other beneficial biological property to antisense compounds. Modified nucleobases include synthetic and natural nucleobases such as, for example, 5-methylcytosine (5-me-C). Certain nucleobase substitutions, including 5-methylcytosine substitutions, are particularly useful for increasing the binding affinity of an antisense compound for a target nucleic acid. For example, 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2°C (Sanghvi, Y.S., Crooke, S.T. and Lebleu, B., eds., Antisense Research and Applications, CRC Press, Boca Raton, 1993, pp. 276-278).

Additional unmodified nucleobases include 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl ($-C{\equiv}C-CH_3$) uracil and cytosine and other alkynyl derivatives of pyrimidine bases, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 2-F-adenine, 2-amino-adenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine.

Heterocyclic base moieties can also include those in which the purine or pyrimidine base is replaced with other heterocycles, for example 7-deaza-adenine, 7-deazaguanosine, 2-aminopyridine and 2-pyridone. Nucleobases that are particularly useful for increasing the binding affinity of antisense compounds include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2 aminopropyladenine, 5-propynyluracil and 5-propynylcytosine.

In certain embodiments, antisense compounds targeted to a DMPK nucleic acid comprise one or more modified nucleobases. In certain embodiments, gap-widened antisense oligonucleotides targeted to a DMPK nucleic acid comprise one or more modified nucleobases. In certain embodiments, the modified nucleobase is 5-methylcytosine. In certain embodiments, each cytosine is a 5-methylcytosine.

Certain Antisense Compound Motifs

In certain embodiments, antisense compounds targeted to a DMPK nucleic acid have chemically modified subunits arranged in patterns, or motifs, to confer to the antisense compounds properties such as enhanced the inhibitory activity, increased binding affinity for a target nucleic acid, or resistance to degradation by *in vivo* nucleases.

Chimeric antisense compounds typically contain at least one region modified so as to confer increased resistance to nuclease degradation, increased cellular uptake, increased binding affinity for the target nucleic acid, and/or increased inhibitory activity. A second region of a chimeric antisense compound can optionally serve as a substrate for the cellular endonuclease RNase H, which cleaves the RNA strand of an RNA:DNA duplex.

Antisense compounds having a gapmer motif are considered chimeric antisense compounds. In a gapmer an internal region having a plurality of nucleotides that supports RNaseH cleavage is positioned between external regions having a plurality of nucleotides that are chemically distinct from the nucleosides of the internal region. In the case of an antisense oligonucleotide having a gapmer motif, the gap segment generally serves as the substrate for endonuclease cleavage, while the wing segments comprise modified nucleosides. In certain embodiments, the regions of a gapmer are differentiated by the types of sugar moieties comprising each distinct region. The types of sugar moieties that are used to differentiate the regions of a gapmer can in some embodiments include β-D-ribonucleosides, β-D-deoxyribonucleosides, 2'-modified nucleosides (such 2'-modified nucleosides can include 2'-MOE, and 2'-O-CH_3, among others), and bicyclic sugar modified nucleosides (such bicyclic sugar modified nucleosides can include those having a 4'-$(CH_2)_n$-O-2' bridge, where n=1 or n=2). The wing-gap-wing motif is frequently described as "X-Y-Z", where "X" represents the length of the 5' wing region, "Y" represents the length of the gap region, and "Z" represents the length of the 3' wing region. As used herein, a gapmer described as "X-Y-Z" has a configuration such that the gap segment is positioned immediately adjacent each of the 5' wing segment and the 3' wing segment. Thus, no intervening nucleotides exist between the 5' wing segment and gap segment, or the gap segment and the 3' wing segment. Any of the antisense compounds described herein can have a gapmer motif. In some embodiments, X and Z are the same, in other embodiments they are different. In a preferred embodiment, Y is between 8 and 15 nucleotides. X, Y or Z can be any of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30 or more nucleotides. Thus, gapmers include, but are not limited to, for example 5-10-5, 4-8-

4, 4-12-3, 4-12-4, 3-14-3, 2-13-5, 2-16-2, 1-18-1, 3-10-3, 2-10-2, 1-10-1, 2-8-2, 6-8-6, 5-8-5, 5-7-5, 1-8-1, or 2-6-2.

In certain embodiments, the antisense compound as a “wingmer” motif, having a wing-gap or gap-wing configuration, i.e. an X-Y or Y-Z configuration as described above for the gapmer configuration. Thus, wingmer configurations include, but are not limited to, for example 5-10, 8-4, 4-12, 12-4, 3-14, 16-2, 18-1, 10-3, 2-10, 1-10, 8-2, 2-13, or 5-13.

In certain embodiments, antisense compounds targeted to a DMPK nucleic acid possess a 5-10-5 gapmer motif. In certain embodiments, antisense compounds targeted to a DMPK nucleic acid possess a 5-7-5 gapmer motif. In certain embodiments, antisense compounds targeted to a DMPK nucleic acid possess a 3-10-3 gapmer motif. In certain embodiments, antisense compounds targeted to a DMPK nucleic acid possess a 4-8-4 gapmer motif.

In certain embodiments, an antisense compound targeted to a DMPK nucleic acid has a gap-widened motif.

In certain embodiments, antisense compounds of any of these gapmer or wingmer motifs contain at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, or at least 19, contiguous nucleobases of the nucleobase sequence of any of the exemplary antisense compounds described herein (e.g., at least 8 contiguous nucleobases of a nucleobase sequence recited in any one of SEQ ID NOs: 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33- 874.

In certain embodiments, the present invention provides oligomeric compounds comprising oligonucleotides. In certain embodiments, such oligonucleotides comprise one or more chemical modification. In certain embodiments, chemically modified oligonucleotides comprise one or more modified sugars. In certain embodiments, chemically modified oligonucleotides comprise one or more modified nucleobases. In certain embodiments, chemically modified oligonucleotides comprise one or more modified internucleoside linkages. In certain embodiments, the chemically modifications (sugar modifications, nucleobase modifications, and/or linkage modifications) define a pattern or motif. In certain embodiments, the patterns of chemical modifications of sugar moieties, internucleoside linkages, and nucleobases are each independent of one another. Thus, an oligonucleotide may be described by its sugar modification motif, internucleoside linkage motif and/or nucleobase modification motif (as used herein, nucleobase modification motif describes the chemical modifications to the nucleobases independent of the sequence of nucleobases).

Certain sugar motifs

In certain embodiments, oligonucleotides comprise one or more type of modified sugar moieties and/or naturally occurring sugar moieties arranged along an oligonucleotide or region thereof in a defined pattern or sugar modification motif. Such motifs may include any of the sugar modifications discussed herein and/or other known sugar modifications.

In certain embodiments, the oligonucleotides comprise or consist of a region having a gapmer sugar modification motif, which comprises two external regions or “wings” and an internal region or “gap.” The three regions of a gapmer motif (the 5’-wing, the gap, and the 3’-wing) form a contiguous sequence of nucleosides wherein at least some of the sugar moieties of the nucleosides of each of the wings differ from at least some of the sugar moieties of the nucleosides of the gap. Specifically, at least the sugar moieties of the nucleosides of each wing that are closest to the gap (the 3’-most nucleoside of the 5’-wing and the 5’-most nucleoside of the 3’-wing) differ from the sugar moiety of the neighboring gap nucleosides, thus defining the boundary between the wings and the gap. In certain embodiments, the sugar moieties within the gap are the same as one another. In certain embodiments, the gap includes one or more nucleoside having a sugar moiety that differs from the sugar moiety of one or more other nucleosides of the gap. In certain embodiments, the sugar modification motifs of the two wings are the same as one another (symmetric gapmer). In certain embodiments, the sugar modification motifs of the 5'-wing differs from the sugar modification motif of the 3'-wing (asymmetric gapmer).

Certain 5’-wings

In certain embodiments, the 5’- wing of a gapmer consists of 1 to 5 linked nucleosides. In certain embodiments, the 5’- wing of a gapmer consists of 2 to 5 linked nucleosides. In certain embodiments, the 5’-wing of a gapmer consists of 3 to 5 linked nucleosides. In certain embodiments, the 5’- wing of a gapmer consists of 4 or 5 linked nucleosides. In certain embodiments, the 5’- wing of a gapmer consists of 1 to 4 linked nucleosides. In certain embodiments, the 5’- wing of a gapmer consists of 1 to 3 linked nucleosides. In certain embodiments, the 5’- wing of a gapmer consists of 1 or 2 linked nucleosides. In certain embodiments, the 5’- wing of a gapmer consists of 2 to 4 linked nucleosides. In certain embodiments, the 5’-wing of a gapmer consists of 2 or 3 linked nucleosides. In certain embodiments, the 5’- wing of a gapmer consists of 3 or 4 linked nucleosides. In certain embodiments, the 5’- wing of a gapmer consists of 1 nucleoside. In certain embodiments, the 5’- wing of a gapmer consists of 2 linked nucleosides. In certain embodiments, the 5’- wing of a gapmer consists of 3linked nucleosides. In certain embodiments, the 5’- wing of a gapmer consists of 4 linked nucleosides. In certain embodiments, the 5’- wing of a gapmer consists of 5 linked nucleosides.

In certain embodiments, the 5’- wing of a gapmer comprises at least one bicyclic nucleoside. In certain embodiments, the 5’- wing of a gapmer comprises at least two bicyclic nucleosides. In certain embodiments, the 5’- wing of a gapmer comprises at least three bicyclic nucleosides. In certain embodiments, the 5'- wing of a gapmer comprises at least four bicyclic nucleosides. In certain embodiments, the 5'- wing of a gapmer comprises at least one constrained ethyl nucleoside. In certain embodiments, the 5'- wing of a gapmer comprises at least one LNA nucleoside. In certain embodiments, each nucleoside of the 5'- wing of a gapmer is a bicyclic nucleoside. In certain embodiments, each nucleoside of the 5'- wing of a gapmer is a constrained ethyl nucleoside. In certain embodiments, each nucleoside of the 5'- wing of a gapmer is a LNA nucleoside.

In certain embodiments, the 5'- wing of a gapmer comprises at least one non-bicyclic modified nucleoside. In certain embodiments, the 5'- wing of a gapmer comprises at least one 2'-substituted nucleoside. In certain embodiments, the 5'- wing of a gapmer comprises at least one 2'-MOE nucleoside. In certain embodiments, the 5'- wing of a gapmer comprises at least one 2'-OMe nucleoside. In certain embodiments, each nucleoside of the 5'- wing of a gapmer is a non-bicyclic modified nucleoside. In certain embodiments, each nucleoside of the 5'- wing of a gapmer is a 2'-substituted nucleoside. In certain embodiments, each nucleoside of the 5'- wing of a gapmer is a 2'-MOE nucleoside. In certain embodiments, each nucleoside of the 5'- wing of a gapmer is a 2'-OMe nucleoside.

In certain embodiments, the 5'-wing of a gapmer comprises at least one bicyclic nucleoside and at least one non-bicyclic modified nucleoside. In certain embodiments, the 5'-wing of a gapmer comprises at least one bicyclic nucleoside and at least one 2'-substituted nucleoside. In certain embodiments, the 5'-wing of a gapmer comprises at least one bicyclic nucleoside and at least one 2'-MOE nucleoside. In certain embodiments, the 5'-wing of a gapmer comprises at least one bicyclic nucleoside and at least one 2'-OMe nucleoside. In certain embodiments, the 5'-wing of a gapmer comprises at least one bicyclic nucleoside and at least one 2'-deoxynucleoside.

In certain embodiments, the 5'-wing of a gapmer comprises at least one constrained ethyl nucleoside and at least one non-bicyclic modified nucleoside. In certain embodiments, the 5'-wing of a gapmer comprises at least one constrained ethyl nucleoside and at least one 2'-substituted nucleoside. In certain embodiments, the 5'-wing of a gapmer comprises at least one constrained ethyl nucleoside and at least one 2'-MOE nucleoside. In certain embodiments, the 5'-wing of a gapmer comprises at least one constrained ethyl nucleoside and at least one 2'-OMe nucleoside. In certain embodiments, the 5'-wing of a gapmer comprises at least one constrained ethyl nucleoside and at least one 2'-deoxynucleoside.

In certain embodiments, the 5'-wing of a gapmer comprises at least one LNA nucleoside and at least one non-bicyclic modified nucleoside. In certain embodiments, the 5'-wing of a gapmer comprises at least one LNA nucleoside and at least one 2'-substituted nucleoside. In certain embodiments, the 5'-wing of a gapmer comprises at least one LNA nucleoside and at least one 2'-MOE nucleoside. In certain embodiments, the 5'-wing of a gapmer comprises at least one LNA nucleoside and at least one 2'-OMe nucleoside. In certain embodiments, the 5'-wing of a gapmer comprises at least one LNA nucleoside and at least one 2'-deoxynucleoside.

In certain embodiments, the 5'-wing of a gapmer comprises three constrained ethyl nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two bicyclic nucleosides and two non bicyclic modified nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two constrained ethyl nucleosides and two 2'-MOE nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two bicyclic nucleosides and two non bicyclic modified nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two constrained ethyl nucleosides and two 2'-MOE nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two constrained ethyl nucleosides and three 2'-MOE nucleosides.

In certain embodiments, the 5'-wing of a gapmer comprises three LNA nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two LNAnucleosides and two non bicyclic modified nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two LNA nucleosides and two 2'-MOE nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two LNA and two non bicyclic modified nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two LNA nucleosides and two 2'-MOE nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two LNA nucleosides and three 2'-MOE nucleosides.

In certain embodiments, the 5'-wing of a gapmer comprises three constrained ethyl nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two bicyclic nucleosides and two non bicyclic modified nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two constrained ethyl nucleosides and two 2'-OMe nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two bicyclic nucleosides and two non bicyclic modified nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two constrained ethyl nucleosides and two 2'-OMe nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two constrained ethyl nucleosides and three 2'-OMe nucleosides.

In certain embodiments, the 5'-wing of a gapmer comprises three LNA nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two LNAnucleosides and two non bicyclic modified nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two LNA nucleosides and two 2'-OMe nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two LNA and two non bicyclic modified nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two LNA nucleosides and two 2'-OMe nucleosides. In certain embodiments, the 5'-wing of a gapmer comprises two LNA nucleosides and three 2'-OMe nucleosides.

In certain embodiments, the 5'-wing of a gapmer has an AABB motif, wherein each A is selected from among a 2'-MOE nucleoside and a 2'OMe nucleoside. In certain embodiments, the 5'-wing of a gapmer has an AABB motif, wherein each B is selected from among a cEt, LNA, α-L-LNA, ENA and 2'-thio LNA nucleoside. In certain embodiments, the 5'-wing of a gapmer has an AABB motif, wherein each A represents a 2'-MOE nucleoside and each B represents a constrained ethyl nucleoside.

In certain embodiments, the 5'-wing of a gapmer has an AAABB motif, wherein each A is selected from among a 2'-MOE nucleoside and a 2'OMe nucleoside. In certain embodiments, the 5'-wing of a gapmer has an AABB motif, wherein each B is selected from among a cEt, LNA, α-L-LNA, ENA and 2'-thio LNA nucleoside. In certain embodiments, the 5'-wing of a gapmer has an AABB motif, wherein each A represents a 2'-MOE nucleoside and each B represents a constrained ethyl nucleoside.

Certain 3'-wings

In certain embodiments, the 3'- wing of a gapmer consists of 1 to 5 linked nucleosides. In certain embodiments, the 3'- wing of a gapmer consists of 2 to 5 linked nucleosides. In certain embodiments, the 3'- wing of a gapmer consists of 3 to 5 linked nucleosides. In certain embodiments, the 3'- wing of a gapmer consists of 4 or 5 linked nucleosides. In certain embodiments, the 3'- wing of a gapmer consists of 1 to 4 linked nucleosides. In certain embodiments, the 3'- wing of a gapmer consists of 1 to 3 linked nucleosides. In certain embodiments, the 3'- wing of a gapmer consists of 1 or 2 linked nucleosides. In certain embodiments, the 3'- wing of a gapmer consists of 2 to 4 linked nucleosides. In certain embodiments, the 3'- wing of a gapmer consists of 2 or 3 linked nucleosides. In certain embodiments, the 3'- wing of a gapmer consists of 3 or 4 linked nucleosides. In certain embodiments, the 3'- wing of a gapmer consists of 1 nucleoside. In certain embodiments, the 3'- wing of a gapmer consists of 2 linked nucleosides. In certain embodiments, the 3'- wing of a gapmer consists of 3linked nucleosides. In certain embodiments, the 3'- wing of a gapmer consists of 4 linked nucleosides. In certain embodiments, the 3'- wing of a gapmer consists of 5 linked nucleosides.

In certain embodiments, the 3'- wing of a gapmer comprises at least one bicyclic nucleoside. In certain embodiments, the 3'- wing of a gapmer comprises at least one constrained ethyl nucleoside. In certain embodiments, the 3'- wing of a gapmer comprises at least one LNA nucleoside. In certain embodiments, each nucleoside of the 3'- wing of a gapmer is a bicyclic nucleoside. In certain embodiments, each nucleoside of the 3'- wing of a gapmer is a constrained ethyl nucleoside. In certain embodiments, each nucleoside of the 3'- wing of a gapmer is a LNA nucleoside.

In certain embodiments, the 3'- wing of a gapmer comprises at least one non-bicyclic modified nucleoside. In certain embodiments, the 3'- wing of a gapmer comprises at least two non-bicyclic modified nucleosides. In certain embodiments, the 3'- wing of a gapmer comprises at least three non-bicyclic modified nucleosides. In certain embodiments, the 3'- wing of a gapmer comprises at least four non-bicyclic modified nucleosides. In certain embodiments, the 3'- wing of a gapmer comprises at least one 2'-substituted nucleoside. In certain embodiments, the 3'- wing of a gapmer comprises at least one 2'-MOE nucleoside. In certain embodiments, the 3'- wing of a gapmer comprises at least one 2'-OMe nucleoside. In certain embodiments, each nucleoside of the 3'- wing of a gapmer is a non-bicyclic modified nucleoside. In certain embodiments, each nucleoside of the 3'- wing of a gapmer is a 2'-substituted nucleoside. In certain embodiments, each nucleoside of the 3’- wing of a gapmer is a 2’-MOE nucleoside. In certain embodiments, each nucleoside of the 3’- wing of a gapmer is a 2’-OMe nucleoside.

In certain embodiments, the 3’-wing of a gapmer comprises at least one bicyclic nucleoside and at least one non-bicyclic modified nucleoside. In certain embodiments, the 3’-wing of a gapmer comprises at least one bicyclic nucleoside and at least one 2’-substituted nucleoside. In certain embodiments, the 3’-wing of a gapmer comprises at least one bicyclic nucleoside and at least one 2’-MOE nucleoside. In certain embodiments, the 3’-wing of a gapmer comprises at least one bicyclic nucleoside and at least one 2’-OMe nucleoside. In certain embodiments, the 3’-wing of a gapmer comprises at least one bicyclic nucleoside and at least one 2’-deoxynucleoside.

In certain embodiments, the 3’-wing of a gapmer comprises at least one constrained ethyl nucleoside and at least one non-bicyclic modified nucleoside. In certain embodiments, the 3’-wing of a gapmer comprises at least one constrained ethyl nucleoside and at least one 2’-substituted nucleoside. In certain embodiments, the 3’-wing of a gapmer comprises at least one constrained ethyl nucleoside and at least one 2’-MOE nucleoside. In certain embodiments, the 3’-wing of a gapmer comprises at least one constrained ethyl nucleoside and at least one 2’-OMe nucleoside. In certain embodiments, the 3’-wing of a gapmer comprises at least one constrained ethyl nucleoside and at least one 2’-deoxynucleoside.

In certain embodiments, the 3’-wing of a gapmer comprises at least one LNA nucleoside and at least one non-bicyclic modified nucleoside. In certain embodiments, the 3’-wing of a gapmer comprises at least one LNA nucleoside and at least one 2’-substituted nucleoside. In certain embodiments, the 3’-wing of a gapmer comprises at least one LNA nucleoside and at least one 2’-MOE nucleoside. In certain embodiments, the 3’-wing of a gapmer comprises at least one LNA nucleoside and at least one 2’-OMe nucleoside. In certain embodiments, the 3’-wing of a gapmer comprises at least one LNA nucleoside and at least one 2’-deoxynucleoside.

In certain embodiments, the 3’-wing of a gapmer comprises three constrained ethyl nucleosides. In certain embodiments, the 3’-wing of a gapmer comprises two bicyclic nucleosides and two non bicyclic modified nucleosides. In certain embodiments, the 3’-wing of a gapmer comprises two constrained ethyl nucleosides and two 2’-MOE nucleosides. In certain embodiments, the 3’-wing of a gapmer comprises two bicyclic nucleosides and two non bicyclic modified nucleosides. In certain embodiments, the 3’-wing of a gapmer comprises two constrained ethyl nucleosides and two 2’-MOE nucleosides. In certain embodiments, the 5’-wing of a gapmer comprises two constrained ethyl nucleosides and three 2’-MOE nucleosides.

In certain embodiments, the 3’-wing of a gapmer comprises three LNA nucleosides. In certain embodiments, the 3’-wing of a gapmer comprises two LNAnucleosides and two non bicyclic modified nucleosides. In certain embodiments, the 3’-wing of a gapmer comprises two LNA nucleosides and two 2’-MOE nucleosides. In certain embodiments, the 3’-wing of a gapmer comprises two LNA and two non bicyclic modified nucleosides. In certain embodiments, the 3’-wing of a gapmer comprises two LNA nucleosides and two 2'-MOE nucleosides. In certain embodiments, the 3'-wing of a gapmer comprises two LNA nucleosides and three 2'-MOE nucleosides.

In certain embodiments, the 3'-wing of a gapmer comprises three constrained ethyl nucleosides. In certain embodiments, the 3'-wing of a gapmer comprises two bicyclic nucleosides and two non bicyclic modified nucleosides. In certain embodiments, the 3'-wing of a gapmer comprises two constrained ethyl nucleosides and two 2'-OMe nucleosides. In certain embodiments, the 3'-wing of a gapmer comprises two bicyclic nucleosides and two non bicyclic modified nucleosides. In certain embodiments, the 3'-wing of a gapmer comprises two constrained ethyl nucleosides and two 2'-OMe nucleosides. In certain embodiments, the 3'-wing of a gapmer comprises two constrained ethyl nucleosides and three 2'-OMe nucleosides.

In certain embodiments, the 3'-wing of a gapmer comprises three LNA nucleosides. In certain embodiments, the 3'-wing of a gapmer comprises two LNAnucleosides and two non bicyclic modified nucleosides. In certain embodiments, the 3'-wing of a gapmer comprises two LNA nucleosides and two 2'-OMe nucleosides. In certain embodiments, the 3'-wing of a gapmer comprises two LNA and two non bicyclic modified nucleosides. In certain embodiments, the 3'-wing of a gapmer comprises two LNA nucleosides and two 2'-OMe nucleosides. In certain embodiments, the 3'-wing of a gapmer comprises two LNA nucleosides and three 2'-OMe nucleosides.

In certain embodiments, the 3'-wing of a gapmer has a BBAA motif, wherein each A is selected from among a 2'-MOE nucleoside and a 2'OMe nucleoside. In certain embodiments, the 3'-wing of a gapmer has an BBAA motif, wherein each B is selected from among a cEt, LNA, α-L-LNA, ENA and 2'-thio LNA nucleoside. In certain embodiments, the 3'-wing of a gapmer has a BBAA motif, wherein each A represents a 2'-MOE nucleoside and each B represents a constrained ethyl nucleoside.

In certain embodiments, the 3'-wing of a gapmer has a BBAAA motif, wherein each A is selected from among a 2'-MOE nucleoside and a 2'OMe nucleoside. In certain embodiments, the 3'-wing of a gapmer has a BBAA motif, wherein each B is selected from among a cEt, LNA, α-L-LNA, ENA and 2'-thio LNA nucleoside. In certain embodiments, the 3'-wing of a gapmer has a BBAA motif, wherein each A represents a 2'-MOE nucleoside and each B represents a constrained ethyl nucleoside.

Compositions and Methods for Formulating Pharmaceutical Compositions

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

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

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

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

Conjugated Antisense Compounds

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

Antisense compounds can also be modified to have one or more stabilizing groups that are generally attached to one or both termini of antisense compounds to enhance properties such as, for example, nuclease stability. Included in stabilizing groups are cap structures. These terminal modifications protect the antisense compound having terminal nucleic acid from exonuclease degradation, and can help in delivery and/or localization within a cell. The cap can be present at the 5'-terminus (5'-cap), or at the 3'-terminus (3'-cap), or can be present on both termini. Cap structures are well known in the art and include, for example, inverted deoxy abasic caps. Further 3' and 5'-stabilizing groups that can be used to cap one or both ends of an antisense compound to impart nuclease stability include those disclosed in WO 03/004602 published on January 16, 2003.

Cell culture and antisense compounds treatment

The effects of antisense compounds on the level, activity or expression of DMPK nucleic acids can be tested in vitro in a variety of cell types. Cell types used for such analyses are available from commercial vendors (e.g. American Type Culture Collection, Manassus, VA; Zen-Bio, Inc., Research Triangle Park, NC; Clonetics Corporation, Walkersville, MD) and cells are cultured according to the vendor's instructions using commercially available reagents (e.g. Invitrogen Life Technologies, Carlsbad, CA). Illustrative cell types include, but are not limited to, HepG2 cells, Hep3B cells, primary hepatocytes, A549 cells, GM04281 fibroblasts and LLC-MK2 cells.

In vitro testing of antisense oligonucleotides

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

In general, cells are treated with antisense oligonucleotides when the cells reach approximately 60-80% confluence in culture.

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

Another reagent used to introduce antisense oligonucleotides into cultured cells includes LIPOFECTAMINE 2000® (Invitrogen, Carlsbad, CA). Antisense oligonucleotide is mixed with LIPOFECTAMINE 2000® in OPTI-MEM® 1 reduced serum medium (Invitrogen, Carlsbad, CA) to achieve the desired concentration of antisense oligonucleotide and a LIPOFECTAMINE® concentration that typically ranges 2 to 12 ug/mL per 100 nM antisense oligonucleotide.

Another reagent used to introduce antisense oligonucleotides into cultured cells includes Cytofectin® (Invitrogen, Carlsbad, CA). Antisense oligonucleotide is mixed with Cytofectin® in

OPTI-MEM® 1 reduced serum medium (Invitrogen, Carlsbad, CA) to achieve the desired concentration of antisense oligonucleotide and a Cytofectin® concentration that typically ranges 2 to 12 ug/mL per 100 nM antisense oligonucleotide.

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

Cells are treated with antisense oligonucleotides by routine methods. Cells are typically harvested 16-24 hours after antisense oligonucleotide treatment, at which time RNA or protein levels of target nucleic acids are measured by methods known in the art and described herein. In general, when treatments are performed in multiple replicates, the data are presented as the average of the replicate treatments.

The concentration of antisense oligonucleotide used varies from cell line to cell line. Methods to determine the optimal antisense oligonucleotide concentration for a particular cell line are well known in the art. Antisense oligonucleotides are typically used at concentrations ranging from 1 nM to 300 nM when transfected with LIPOFECTAMINE2000®, Lipofectin or Cytofectin. Antisense oligonucleotides are used at higher concentrations ranging from 625 to 20,000 nM when transfected using electroporation.

RNA Isolation

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

Analysis of inhibition of target levels or expression

Inhibition of levels or expression of a DMPK nucleic acid can be assayed in a variety of ways known in the art. For example, target nucleic acid levels can be quantitated by, e.g., Northern blot analysis, competitive polymerase chain reaction (PCR), or quantitaive real-time PCR. RNA analysis can be performed on total cellular RNA or poly(A)+ mRNA. Methods of RNA isolation are well known in the art. Northern blot analysis is also routine in the art. Quantitative real-time PCR can be conveniently accomplished using the commercially available ABI PRISM® 7600, 7700, or 7900 Sequence Detection System, available from PE-Applied Biosystems, Foster City, CA and used according to manufacturer's instructions.

Quantitative Real-Time PCR Analysis of Target RNA Levels

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

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

Gene (or RNA) target quantities obtained by real time PCR are normalized using either the expression level of a gene whose expression is constant, such as cyclophilin A, or by quantifying total RNA using RIBOGREEN® (Invitrogen, Inc. Carlsbad, CA). Cyclophilin A expression is quantified by real time PCR, by being run simultaneously with the target, multiplexing, or separately. Total RNA is quantified using RIBOGREEN® RNA quantification reagent (Invitrogen, Inc. Eugene, OR). Methods of RNA quantification by RIBOGREEN® are taught in Jones, L.J., et al, (Analytical Biochemistry, 1998, 265, 368-374). A CYTOFLUOR® 4000 instrument (PE Applied Biosystems) is used to measure RIBOGREEN® fluorescence.

Probes and primers are designed to hybridize to a DMPK nucleic acid. Methods for designing real-time PCR probes and primers are well known in the art, and can include the use of software such as PRIMER EXPRESS® Software (Applied Biosystems, Foster City, CA).

Analysis of Protein Levels

Antisense inhibition of DMPK nucleic acids can be assessed by measuring DMPK protein levels. Protein levels of DMPK can be evaluated or quantitated in a variety of ways well known in the art, such as immunoprecipitation, Western blot analysis (immunoblotting), enzyme-linked immunosorbent assay (ELISA), quantitative protein assays, protein activity assays (for example, caspase activity assays), immunohistochemistry, immunocytochemistry or fluorescence-activated cell sorting (FACS). Antibodies directed to a target can be identified and obtained from a variety of sources, such as the MSRS catalog of antibodies (Aerie Corporation, Birmingham, MI), or can be prepared via conventional monoclonal or polyclonal antibody generation methods well known in the art.

In vivo testing of antisense compounds

Antisense compounds, for example, antisense oligonucleotides, are tested in animals to assess their ability to inhibit expression of DMPK and produce phenotypic changes. Testing can be performed in normal animals, or in experimental disease models, for example, the HSA^{LR} mouse model of myotonic dystrophy (DM1).

The HSA^{LR} mouse model is an established model for DM1 (Mankodi, A. et al. Science. 289: 1769, 2000). The mice carry a human skeletal actin (*hACTA1*) transgene with 220 CTG repeats inserted in the 3' UTR of the gene. The *hACTA1*-CUG^{exp} transcript accumulates in nuclear foci in skeletal muscles and results in myotonia similar to that in human DM1 (Mankodi, A. et al. Mol. Cell 10: 35, 2002; Lin, X. et al. Hum. Mol. Genet. 15: 2087, 2006). Hence, it is expected that amelioration of DM1 symptoms in the HSA^{LR} mouse by antisense inhibition of the *hACTA1* transgene would predict amelioration of similar symptoms in human patients by antisense inhibition of the DMPK transcript.

Expression of CUG^{exp} RNA in mice causes extensive remodeling of the muscle transcriptome, much of which is reproduced by ablation of MBNL1. Hence, it is expected that normalization of the transcriptome in HSA^{LR} mice would predict normalization of the human transcriptome in DM1 patients by antisense inhibition of the DMPK transcript.

For administration to animals, antisense oligonucleotides are formulated in a pharmaceutically acceptable diluent, such as phosphate-buffered saline. Administration includes parenteral routes of administration. Following a period of treatment with antisense oligonucleotides, RNA is isolated from tissue and changes in DMPK nucleic acid expression are measured. Changes in DMPK protein levels are also measured.

Splicing

Myotonic dystrophy (DM1) is caused by CTG repeat expansions in the 3' untranslated region of the DMPK gene (Brook, J.D. et al. Cell. 68: 799, 1992). This mutation leads to RNA dominance, a process in which expression of RNA containing an expanded CUG repeat (CUGexp) induces cell dysfunction (Osborne RJ and Thornton CA., *Human Molecular Genetics*., **2006**, *15*(2): R162-R169). Such CUGexp are retained in the nuclear foci of skeletal muscles (Davis, B.M. et al. Proc. Natl. Acad. Sci. U.S.A. 94:7388, 1997). The accumulation of CUGexp in the nuclear foci leads to the sequestration of poly(CUG)-binding proteins, such as, Muscleblind-like 1 (MBLN1) (Miller, J.W. et al. EMBO J. 19: 4439, 2000). MBLN1 is a splicing factor and regulates the splicing of genes such as Serca1, CIC-1, Titin, and Zasp. Therefore, sequestration of MBLN1 by CUGexp triggers misregulated alternative splicing of the exons of genes that MBLN1 normally controls (Lin, X. et al. Hum. Mol. Genet. 15: 2087, 2006). Correction of alternative splicing in an animal displaying such disregulation, such as, for example, in a DM1 patient and the HSALR mouse model, is a useful indicator for the efficacy of a treatment, including treatment with an antisense oligonucleotide.

Certain Antisense Mechanisms

Myotonic dystrophy (DM1) is caused by CTG repeat expansions in the 3' untranslated region of the DMPK gene. In certain embodiments, expansions in the 3' untranslated region of the DMPK gene results in the transcription of RNA containing an expanded CUG repeat, and RNA containing an expanded CUG repeat (CUGexp) is retained in the nuclear foci of skeletal muscles. In certain instances, the cellular machinery responsible for exporting mRNA from the nucleus into the cytoplasm does not export RNA containing an expanded CUG repeat from the nucleus or does so less efficiently. In certain embodiments, cells do not export DMPK CUGexp mRNA from the nucleus or such export is reduced. Accordingly, in certain embodiments, DMPK CUGexp mRNA accumulates in the nucleus. In certain embodiments, more copies of DMPK CUGexp mRNA are present in the nucleus of a cell than are copies of wild-type DMPK mRNA, which is exported normally. In such embodiments, antisense compounds that reduce target in the nucleus will preferentially reduce mutant DMPK CUGexp mRNA relative to wild type DMPK mRNA, due to their relative abundences in the nucleus, even if the antisense compound does not otherwise distinguish between mutant and wild type. Since RNase H dependent antisense compounds are active in the nucleus, such compounds are particularly well suited for such use.

In certain instances, wild-type DMPK pre-mRNA and mutant CUGexp DMPK pre-mRNA are expected to be processed into mRNA at similar rate. Accordingly, approximately the same amount of wild-type DMPK pre-mRNA and mutant CUGexp DMPK pre-mRNA are expected to be present in the nucleus of a cell. However, after proceesing, wild type DMPK mRNA is exported from the nucleus relatively quickly, and mutant CUGexp DMPK mRNA is exported slowly or not at all. In certan such embodiments, mutant CUGexp DMPK mRNA accumulates in the nucleus in greater amounts than wild-type DMPK mRNA. In certain such embodiments, an antisense oligonucleotide targeted to the mRNA, will preferentially reduce the expression of the mutant CUGexp DMPK mRNA compared to the wild-type DMPK mRNA because more copies of the mutant CUGexp DMPK mRNA are present in the nucleus of the cell. In certain embodiments, antisense compounds targeted to pre-mRNA and not mRNA (e.g., targeting an intron) are not expected to preferentially reduce mutant DMPK relative to wild type, because the nuclear abundance of the two pre-mRNAs is likely to be similar. In certain embodiments, antisense compounds described herein are not targeted to introns of DMPK pre-mRNA. In certain embodiments, antisense compounds described herein are targeted to exons or exon-exon junctions present in DMPK mRNA. In certain embodiments, use of an antisense oligonucleotide to target the mRNA is therefore preferred because an antisense oligonucleotide having one or more features described herein (i) has activity in the nucleus of a cell and (2) will preferentially reduce mutant CUGexp DMPK mRNA compared to wild-type DMPK mRNA.

Certain Biomarkers

DM1 severity in mouse models is determined, at least in part, by the level of CUG^{exp} transcript accumulation in the nucleus or nuclear foci. A useful physiological marker for DM1 severity is the development of high-frequency runs of involuntary action potentials (myotonia).

Certain Indications

In certain embodiments, provided herein are methods of treating an individual comprising administering one or more pharmaceutical compositions as described herein. In certain embodiments, the individual has type 1 myotonic dystrophy (DM1).

Accordingly, provided herein are methods for ameliorating a symptom associated with type 1 myotonic dystrophy in a subject in need thereof. In certain embodiments, provided is a method for reducing the rate of onset of a symptom associated with type 1 myotonic dystrophy. In certain embodiments, provided is a method for reducing the severity of a symptom associated with type 1 myotonic dystrophy. In certain embodiments, symptoms associated with DM1 include muscle stiffness, myotonia, disabling distal weakness, weakness in face and jaw muscles, difficulty in swallowing, drooping of the eyelids (ptosis), weakness of neck muscles, weakness in arm and leg muscles, persistent muscle pain, hypersomnia, muscle wasting, dysphagia, respiratory insufficiency, irregular heartbeat, heart muscle damage, apathy, insulin resistance, and cataracts. In children, the symptoms may also be developmental delays, learning problems, language and speech issues, and personality development issues.

In certain embodiments, the methods comprise administering to an individual in need thereof a therapeutically effective amount of a compound targeted to a DMPK nucleic acid.

In certain embodiments, administration of an antisense compound targeted to a DMPK nucleic acid results in reduction of DMPK expression by at least about 15%, by at least about 20%, by at least about 25%, by at least about 30%, by at least about 35%, by at least about 40%, by at least about 45%, by at least about 50%, by at least about 55%, by at least about 60%, by least about 65%, by least about 70%, by least about 75%, by least about 80%, by at least about 85%, by at least about 90%, by at least about 95% or by at least about 99%, or a range defined by any two of these values.

In certain embodiments, pharmaceutical compositions comprising an antisense compound targeted to DMPK are used for the preparation of a medicament for treating a patient suffering or susceptible to type 1 myotonic dystrophy.

In certain embodiments, the methods described herein include administering a compound comprising a modified oligonucleotide having a contiguous nucleobases portion as described herein of a sequence recited in SEQ ID NOs: 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33- 874.

Administration

In certain embodiments, the compounds and compositions as described herein are administered parenterally.

In certain embodiments, parenteral administration is by infusion. Infusion can be chronic or continuous or short or intermittent. In certain embodiments, infused pharmaceutical agents are delivered with a pump. In certain embodiments, parenteral administration is by injection (e.g., bolus injection). The injection can be delivered with a syringe.

Parenteral administration includes subcutaneous administration, intravenous administration, intramuscular administration, intraarterial administration, intraperitoneal administration, or intracranial administration, e.g., intrathecal or intracerebroventricular administration. Administration can be continuous, or chronic, or short, or intermittent.

In certain embodiments, the administering is subcutaneous, intravenous, intracerebral, intracerebroventricular, intrathecal or another administration that results in a systemic effect of the oligonucleotide (systemic administration is characterized by a systemic effect, i.e., an effect in more than one tissue) or delivery to the CNS or to the CSF.

The duration of action as measured by inhibition of alpha 1 actin and reduction of myotonia in the HSA^{LR} mouse model of DM1 is prolonged in muscle tissue including quadriceps, gastrocnemius, and the tibialis anterior (see Examples, below). Subcutaneous injections of antisense oligonucleotide for 4 weeks results in inhibition of alpha 1 actin by at least 70% in quadriceps, gastrocnemius, and the tibialis anterior in HSA^{LR} mice for at least 11 weeks (77 days) after termination of dosing. Subcutaneous injections of antisense oligonucleotide for 4 weeks results in elimination of myotonia in quadriceps, gastrocnemius, and the tibialis anterior in HSA^{LR} mice for at least 11 weeks (77 days) after termination of dosing.

In certain embodiments, delivery of a compound of composition, as described herein, results in at least 70% down-regulation of a target mRNA and/or target protein for at least 77 days. In certain embodiments, delivery of a compound or composition, as described herein, results in 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% down-regulation of a target mRNA and/or target protein for at least 30 days, at least 35 days, at least 40 days, at least 45 days, at least 50 days, at least 55 days, at least 60 days, at least 65 days, at least 70 days, at least 75 days, at least 76 days, at least 77 days, at least 78 days, at least 79 days, at least 80 days, at least 85 days, at least 90 days, at least 95 days, at least 100 days, at least 105 days, at least 110 days, at least 115 days, at least 120 days, at least 1 year.

In certain embodiments, an antisense oligonucleotide is delivered by injection or infusion once every 77 days. In certain embodiments, an antisense oligonucleotide is delivered by injection or infusion once every month, every two months, every three months, every 6 months, twice a year or once a year.

Certain Combination Therapies

In certain embodiments, a first agent comprising the modified oligonucleotide of the invention is co-administered with one or more secondary agents. In certain embodiments, such second agents are designed to treat the same type 1 myotonic dystrophy as the first agent described herein. In certain embodiments, such second agents are designed to treat a different disease, disorder, or condition as the first agent described herein. In certain embodiments, such second agents are designed to treat an undesired side effect of one or more pharmaceutical compositions as described herein. In certain embodiments, second agents are co-administered with the first agent to treat an undesired effect of the first agent. In certain embodiments, second agents are co-administered with the first agent to produce a combinational effect. In certain embodiments, second agents are co-administered with the first agent to produce a synergistic effect.

In certain embodiments, a first agent and one or more second agents are administered at the same time. In certain embodiments, the first agent and one or more second agents are administered at different times. In certain embodiments, the first agent and one or more second agents are prepared together in a single pharmaceutical formulation. In certain embodiments, the first agent and one or more second agents are prepared separately.

Certain Comparator Compounds

In certain embodiments, the compounds disclosed herein benefit from one or more improved *in vitro* and/or *in vivo* properties relative to an appropriate comparator compound.

In certain embodiments, ISIS 445569, a 5-10-5 MOE gapmer, having a sequence of (from 5' to 3') CGGAGCGGTTGTGAACTGGC (incorporated herein as SEQ ID NO: 24), wherein each internucleoside linkage is a phosphorothioate linkage, each cytosine is a 5-methylcytosine, and each of nucleosides 1-5 and 16-20 comprise a 2'-O-methoxyethyl moiety, which was previously described in WO 2012/012443, incorporated herein by reference, is a comparator compound.

ISIS 445569 is an appropriate representative comparator compound because ISIS 445569 demonstrates statistically significant reduction of human DMPK in vitro as measured using a plurality of primer probe sets (*see* e.g. Example 1 and Example 2 of WO 2012/012443). Additionally, ISIS 445569 demonstrates statistically significant dose-dependent inhibition of human DMPK in vitro in both human skeletal muscle cells and DM1 fibroblasts (*see* e.g. Example 4 and Example 5 of WO 2012/012443 and Example 28 of WO 2012/012467). ISIS 445569 also reduces human DMPK transcript expression in transgenic mice (Examples 23 and 24 of WO 2012/012443 and Examples 29 and 30 of WO 2012/012467). ISIS 445569 was a preferred human DMPK antisense compound in WO 2012/012443 and WO 2012/012467.

Certain Compounds

In certain embodiments, the compounds disclosed herein benefit from improved activity and/or improved tolerability relative to appropriate comparator compounds, such as ISIS 445569. For example, in certain embodiments, ISIS 598769, ISIS 598768, and/or ISIS 486178 have more activity and/or tolerability than appropriate comparator compounds, such as ISIS 445569.

In certain embodiments, the compounds disclosed herein are more potent than appropriate comparator compounds, such as ISIS 445569. For example, as provided in Example 10 (described herein), ISIS 598769 achieved an IC_{50} of 1.9 μM, ISIS 598768 achieved an IC_{50} of 1.2 μM, and ISIS 486178 achieved an IC_{50} of 0.7 μM in a 6 point dose response curve (61.7 nM, 185.2 nM, 555.6 nM, 1666.7 nM, 5000.0 nM, and 15000.0 nM) in cultured in HepG2 cells when transfected using electroporation, whereas ISIS 445569 achieved an IC_{50} of 2.3 μM. Thus, ISIS 598769, ISIS 598768, and ISIS 486178 are more potent than the comparator compound, ISIS 445569.

In certain embodiments, the compounds disclosed herein have greater activity than appropriate comparator compounds, such as ISIS 445569, at achieving dose-dependent inhibition of DMPK across multiple different muscle tissues. In another example, as provided in Example 16 (described herein), ISIS 598768 and ISIS 598769 achieved greater dose-dependent inhibition than the comparator compound ISIS 445569 across several different muscle tissues when administered subcutaneously to DMSXL transgenic mice twice a week for 4 weeks with 25 mg/kg/week, 50 mg/kg/wk, or 100 mg/kg/wk. In some muscle tissues, for example, in the tibialis anterior, both ISIS 598768 and ISIS 598769 achieved greater inhibition of DMPK at 25, 50 and 100 mg/kg/wk than ISIS 445569 achieved at 200 mg/kg/wk. In the quadriceps and gastrocnemius, both ISIS 598768 and ISIS 598769 achieved equal or greater inhibition of DMPK at 50 mg/kg/wk than ISIS 445569 achieved at 100 or 200 mg/kg/wk. Thus, ISIS 598768 and ISIS 598769 have greater activity than ISIS 445569 at achieving dose-dependent inhibition of DMPK across multiple different muscle tissues.

In certain embodiments, the compounds disclosed herein are more tolerable than appropriate comparator compounds, such as ISIS 445569, when administered to CD-1 mice. In another example, as provided in Example 17 (described herein), ISIS 598769, ISIS 598768, and ISIS 486178 exhibited more favorable tolerability markers than ISIS 445569 when administered to CD-1 mice. ISIS 598769, ISIS 598768, and ISIS 486178 were administered subcutaneously twice a week for 6 weeks at 50 mg/kg/wk. ISIS 445569 was administered subcutaneously twice a week for 6 weeks at 100mg/kg/wk. After treatment, ALT, AST, and BUN levels were lower in ISIS 486178 and ISIS 598768 treated mice than in ISIS 445569 treated mice. After treatment, ALT and AST levels were lower in ISIS 598769 treated mice than in ISIS 445569 treated mice. Therefore, ISIS 598769, ISIS 598768, and ISIS 486178 are more tolerable than the comparator compound, ISIS 445569 in CD-1 mice.

In certain embodiments, the compounds disclosed herein are more tolerable than appropriate comparator compounds, such as ISIS 445569, when administered to Sprague-Dawley rats. In another example, as provided in Example 18 (described herein), ISIS 598769, ISIS 598768, and ISIS 486178 exhibited more favorable tolerability markers than ISIS 445569 when administered to Sprague-Dawley rats. ISIS 598769, ISIS 598768, and ISIS 486178 were administered subcutaneously twice a week for 6 weeks at 50 mg/kg/wk. ISIS 445569 was administered subcutaneously twice a week for 6 weeks at 100mg/kg/wk. After treatment, ALT and AST levels were lower in ISIS 486178, ISIS 598769, and ISIS 598768 treated mice than in ISIS 445569 treated mice. Therefore ISIS 598769, ISIS 598768, and ISIS 486178 are more tolerable than the comparator compound, ISIS 445569 in Sprague-Dawley rats.

In certain embodiments, the compounds disclosed herein exhibit more favorable tolerability markers in cynomolgous monkeys than appropriate comparator compounds, such as ISIS 445569. In another example, as provided in Example 19 (described herein), ISIS 598769, ISIS 598768, and ISIS 486178 exhibited more favorable tolerability markers in cynomolgous monkeys including Alanine aminotransferase (ALT), aspartate aminotransferase (AST), lactate dehydrogenase (LDH), and creatine kinase (CK) assessment. In certain embodiments, ALT and AST levels are used as indicators of hepatotoxicity. For example, in certain embodiments, elevated ALT and AST levels indicate trauma to liver cells. In certain embodiments, elevated CK levels are associated with damage to cells in muscle tissue. In certain embodiments, elevated LDH levels are associated with cellular tissue damage.

In certain embodiments, the compounds disclosed herein are more tolerable than appropriate comparator compounds, such as ISIS 445569, when administered to cynomolgous monkeys. As provided in Example 19, groups of cynomolgous monkeys were treated with 40 mg/kg/wk of ISIS 598769, ISIS 598768, ISIS 486178, and ISIS 445569. Treatment with ISIS 445569 resulted in elevated ALT and AST levels at 93 days into treatment. Treatment with ISIS 598768, and ISIS 486178 resulted in lower ALT and AST levels at

58 and 93 days into treatment compared to ISIS 445569. Treatment with ISIS 598769, resulted in lower AST levels at 58 and 93 days into treatment and lower ALT levels at 93 days of treatment compared to ISIS 445569. Furthermore, the ALT and AST levels of monkeys receiving doses of ISIS 598769, ISIS 598768, and ISIS 486178 were consistent with the ALT and AST levels of monkeys given saline. Treatment with ISIS 445569 resulted in elevated LDH levels compared to the LDH levels measured in animals given ISIS 598769, ISIS 598768, and ISIS 486178 at 93 days into treatment. Additionally, treatment with ISIS 445569 resulted in elevated CK levels compared to the CK levels measured in animals given ISIS 598769, ISIS 598768, and ISIS 486178 at 93 days into treatment. Therefore, ISIS 598769, ISIS 598768, and ISIS 486178 are more tolerable than the comparator compound, ISIS 445569.

As the data discussed above demonstrate, ISIS 598769, ISIS 598768, and ISIS 486178 possess a wider range of well-tolerated doses at which ISIS 598769, ISIS 598768, and ISIS 486178 are active compared to the comparator compound, ISIS 445569. Additionally, the totality of the data presented in the examples herein and discussed above demonstrate that each of ISIS 598769, ISIS 598768, and ISIS 486178 possess a number of safety and activity advantages over the comparator compound, ISIS 445569. In other words, each of ISIS 598769, ISIS 598768, and ISIS 486178 are likely to be safer and more active drugs in humans than ISIS 445569.

In certain embodiments, ISIS 445569 is likely to be a safer and more active drug in humans for reducing CUGexp DMPK mRNA and\or treating conditions or symptoms associated with having myotonic dystrophy type 1 than the other compounds disclosed in WO 2012/012443 and/or WO 2012/012467.

In certain embodiments, ISIS 512497 has a better safety profile in primates and CD-1 mice than ISIS 445569. In certain embodiments, ISIS 512497 achieves greater knockdown of human DMPK nucleic acid in multiple muscle tissues when administered at the same dose and at lower doses than ISIS 445569.

In certain embodiments, ISIS 486178 has a better safety profile in mice, rats, and primates than ISIS 445569. In certain embodiments, ISIS 486178 achieves greater knockdown of human DMPK nucleic acid in one or more muscle tissues when administered at the same dose and at lower doses than ISIS 445569.

In certain embodiments, ISIS 570808 achieves much greater knockdown of human DMPK nucleic acid at least five different muscle tissues when administered at the same dose and at lower dose than ISIS 445569.

In certain embodiments, ISIS 594292 achieves greater knockdown of human DMPK nucleic acid in one or more muscle tissues when administered at the same dose as ISIS 445569. In certain embodiments, ISIS 486178 has a better safety profile in primates than ISIS 445569.

In certain embodiments, ISIS 569473 achieves greater knockdown of human DMPK nucleic acid in one or more muscle tissues when administered at the same dose as ISIS 445569. In certain embodiments, ISIS 569473 has a better safety profile in primates than ISIS 445569.

In certain embodiments, ISIS 594300 achieves greater knockdown of human DMPK nucleic acid in one or more muscle tissues when administered at the same dose as ISIS 445569. In certain embodiments, ISIS 594300 has a better safety profile in primates than ISIS 445569.

In certain embodiments, ISIS 598777 achieves greater knockdown of human DMPK nucleic acid in one or more muscle tissues when administered at the same dose as ISIS 445569. In certain embodiments, ISIS 598777 has a better safety profile in primates than ISIS 445569.

In certain embodiments, ISIS 598768 achieves greater knockdown of human DMPK nucleic acid in one or more muscle tissues when administered at the same dose as ISIS 445569. In certain embodiments, ISIS 598768 has a better safety profile in primates than ISIS 445569.

In certain embodiments, ISIS 598769 achieves greater knockdown of human DMPK nucleic acid in one or more muscle tissues when administered at the same dose as ISIS 445569. In certain embodiments, ISIS 598769 has a better safety profile in primates than ISIS 445569.

<u>Nonlimiting disclosure and incorporation by reference</u>

While certain compounds, compositions and methods described herein have been described with specificity in accordance with certain embodiments, the following examples serve only to illustrate the compounds described herein and are not intended to limit the same. Each of the references, GenBank accession numbers, and the like recited in the present application is incorporated herein by reference in its entirety.

Although the sequence listing accompanying this filing identifies each sequence as either “RNA” or “DNA” as required, in reality, those sequences may be modified with any combination of chemical modifications. One of skill in the art will readily appreciate that such designation as “RNA” or “DNA” to describe modified oligonucleotides is, in certain instances, arbitrary. For example, an oligonucleotide comprising a nucleoside comprising a 2’-OH sugar moiety and a thymine base could be described as a DNA having a modified sugar (2’-OH for the natural 2’-H of DNA) or as an RNA having a modified base (thymine (methylated uracil) for natural uracil of RNA).

Accordingly, nucleic acid sequences provided herein, including, but not limited to those in the sequence listing, are intended to encompass nucleic acids containing any combination of natural or modified RNA and/or DNA, including, but not limited to such nucleic acids having modified nucleobases. By way of further example and without limitation, an oligomeric compound having the nucleobase sequence "ATCGATCG" encompasses any oligomeric compounds having such nucleobase sequence, whether modified or unmodified, including, but not limited to, such compounds comprising RNA bases, such as those having sequence "AUCGAUCG" and those having some DNA bases and some RNA bases such as "AUCGATCG" and oligomeric compounds having other modified or naturally occurring bases, such as "AT^{me}CGAUCG," wherein ^{me}C indicates a cytosine base comprising a methyl group at the 5-position.

EXAMPLES

Non-limiting disclosure and incorporation by reference

While certain compounds, compositions and methods described herein have been described with specificity in accordance with certain embodiments, the following examples serve only to illustrate the compounds described herein and are not intended to limit the same. Each of the references recited in the present application is incorporated herein by reference in its entirety.

Example 1: Design of antisense oligonucleotides targeting human dystrophia myotonica protein kinase (hDMPK)

A series of antisense oligonucleotides (ASOs) were designed to target hDMPK. The newly designed ASOs were prepared using standard oligonucleotide synthesis well known in the art and are described in Tables 1 and 2, below. Subscripts "s" indicate phosphorothioate internucleoside linkages; subscripts "k" indicate 6'-*(S)*-CH_3 bicyclic nucleosides (cEt); subscripts "e" indicate 2'-O-methoxyethyl (MOE) modified nucleosides; and subscripts "d" indicate β-D-2'-deoxyribonucleosides. "^{m}C" indicates 5-methylcytosine nucleosides.

The antisense oligonucleotides are targeted to either SEQ ID NO: 1 (GENBANK Accession No. NM_001081560.1) and/or SEQ ID NO: 2 (the complement of GENBANK Accession No. NT_011109.15 truncated from nucleotides 18540696 to 18555106). "Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. "Stop site" indicates the 3'-most nucleoside to which the gapmer is targeted human gene sequence.

Table 1

Design of antisense oligonucleotides targeting hDMPK and targeted to SEQ ID NO 2

ISIS No.	Composition (5' to 3')	Motif	Length	Start Site	Stop Site	SEQ ID No.
486178	$A_{ks}{}^{m}C_{ks}A_{ks}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ks}G_{ks}G_{k}$	kkk-10-kkk	16	13836	13851	23
445569	${}^{m}C_{es}G_{es}G_{es}A_{es}G_{es}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}T_{ds}G_{ds}$	e5-d10-e5	20	13226	13245	24

	$T_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{es}T_{es}G_{es}G_{es}{}^{m}C_{e}$					
512497	$G_{es}{}^{m}C_{es}G_{es}{}^{m}C_{es}A_{es}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}T_{es}G_{es}T_{es}{}^{m}C_{es}{}^{m}C_{e}$	e5-d10-e5	20	8608	8627	25
598768	${}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{ks}G_{ks}A_{ds}A_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ks}{}^{m}C_{ks}A_{es}G_{e}$	eekk-d8-kkee	16	8603	8618	26
594300	${}^{m}C_{es}G_{es}G_{es}A_{ks}G_{ks}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ks}A_{ks}A_{es}{}^{m}C_{es}T_{e}$	eeekk-d7-kkeee	17	13229	13245	27
594292	$A_{es}{}^{m}C_{es}A_{es}A_{ks}T_{ks}A_{ds}A_{ds}A_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ks}A_{ks}G_{es}G_{es}A_{e}$	eeekk-d7-kkeee	17	13835	13851	28
569473	$G_{ks}A_{ks}{}^{m}C_{ks}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}G_{ks}G_{k}$	kkk-d10-kkk	16	5082	5097	29
598769	$T_{es}{}^{m}C_{es}{}^{m}C_{ks}{}^{m}C_{ks}G_{ds}A_{ds}A_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ks}A_{ks}{}^{m}C_{es}A_{e}$	eekk-d8-kkee	16	8604	8619	30
570808	$T_{ks}G_{ks}T_{ks}A_{ds}A_{ds}T_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}G_{ks}T_{k}$	kkk-d10-kkk	16	10201	10216	31
598777	$G_{es}T_{es}G_{ks}T_{ks}A_{ds}A_{ds}T_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{es}G_{e}$	eekk-d8-kkee	16	10202	10217	32

Table 2

Design of antisense oligonucleotides targeting hDMPK and targeted to SEQ ID NO 1

ISIS No.	Composition (5' to 3')	Motif	Length	Start Site	Stop Site
486178	$A_{ks}{}^{m}C_{ks}A_{ks}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ks}G_{ks}G_{k}$	kkk-10-kkk	16	2773	2788
445569	${}^{m}C_{es}G_{es}G_{es}A_{es}G_{es}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{es}T_{es}G_{es}G_{es}{}^{m}C_{e}$	e5-d10-e5	20	2163	2182
512497	$G_{es}{}^{m}C_{es}G_{es}{}^{m}C_{es}A_{es}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}T_{es}G_{es}T_{es}{}^{m}C_{es}{}^{m}C_{e}$	e5-d10-e5	20	1348	1367
598768	${}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{ks}G_{ks}A_{ds}A_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ks}{}^{m}C_{ks}A_{es}G_{e}$	eekk-d8-kkee	16	1343	1358
594300	${}^{m}C_{es}G_{es}G_{es}A_{ks}G_{ks}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ks}A_{ks}A_{es}{}^{m}C_{es}T_{e}$	eeekk-d7-kkeee	17	2166	2182
594292	$A_{es}{}^{m}C_{es}A_{es}A_{ks}T_{ks}A_{ds}A_{ds}A_{ds}T_{ds}$	eeekk-d7-kkeee	17	2772	2788

	$A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ks}A_{ks}G_{es}G_{es}A_{e}$				
569473	$G_{ks}A_{ks}{}^{m}C_{ks}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}T_{ds}$ ${}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}G_{ks}G_{k}$	kkk-d10-kkk	16	730	745
598769	$T_{es}{}^{m}C_{es}{}^{m}C_{ks}{}^{m}C_{ks}G_{ds}A_{ds}A_{ds}T_{ds}$ $G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ks}A_{ks}{}^{m}C_{es}A_{e}$	eekk-d8-kkee	16	1344	1359

Example 2: Antisense inhibition of human DMPK in human skeletal muscle cells (hSKMc)

Antisense oligonucleotides targeted to a human DMPK nucleic acid were tested for their effect on DMPK RNA transcript *in vitro*. Cultured hSKMc cells at a density of 20,000 cells per well were transfected using electroporation with 10,000 nM antisense oligonucleotide. After approximately 24 hours, RNA was isolated from the cells and DMPK transcript levels were measured by quantitative real-time PCR. DMPK RNA transcript levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent expression of DMPK, relative to untreated control cells.

The antisense oligonucleotides in Tables 3, 4, 5, and 6 are 5-10-5 gapmers, where the gap segment comprises ten 2'-deoxynucleosides and each wing segment comprises five 2'-MOE nucleosides. The internucleoside linkages throughout each gapmer are phosphorothioate (P=S) linkages. All cytsoine residues throughout each gapmer are 5-methylcytosines. 'Target start site' indicates the 5'-most nucleoside to which the antisense oligonucleotide is targeted in the human genomic gene sequence. 'Target stop site' indicates the 3'-most nucleoside to which the antisense oligonucleotide is targeted in the human genomic sequence. All the antisense oligonucleotides listed in Table 3, 4, or 5 target SEQ ID NO: 1 (GENBANK Accession No. NM_001081560.1). All the antisense oligonucleotides listed in Table 6 target SEQ ID NO: 2 (the complement of GENBANK Accession No. NT_011109.15 truncated from nucleotides 18540696 to 18555106).

Several of the antisense oligonucleotides in Tables 2, 3, 4, and 5 demonstrated significant inhibition of DMPK mRNA levels under the conditions specified above.

Table 3

Inhibition of human DMPK RNA transcript in hSKMc by 5-10-5 gapmers targeting SEQ ID NO: 1

ISIS No.	Sequence	% Target Expression	Start Site on Seq ID: 1	Stop Site on Seq ID: 1	SEQ ID NO.
UTC	N/A	100.0	N/A	N/A	33
444401	TTGCACTTTGCGAACCAACG	7.3	2490	2509	34

512326	CGACACCTCGCCCCTCTTCA	13.4	528	547	35
512327	ACGACACCTCGCCCCTCTTC	40.8	529	548	36
512328	CACGACACCTCGCCCCTCTT	27.8	530	549	37
512329	GCACGACACCTCGCCCCTCT	16.5	531	550	38
512330	AGCACGACACCTCGCCCCTC	17.9	532	551	39
512331	AAGCACGACACCTCGCCCCT	18.8	533	552	40
512332	GAAGCACGACACCTCGCCCC	23.3	534	553	41
512333	GGAAGCACGACACCTCGCCC	28.1	535	554	42
512334	CGGAAGCACGACACCTCGCC	16.3	536	555	43
512335	ACGGAAGCACGACACCTCGC	28.7	537	556	44
512336	CACGGAAGCACGACACCTCG	15.9	538	557	45
512337	TCACGGAAGCACGACACCTC	18.8	539	558	46
512338	CTCACGGAAGCACGACACCT	16.4	540	559	47
512339	CCTCACGGAAGCACGACACC	20.2	541	560	48
512340	TCCTCACGGAAGCACGACAC	19.3	542	561	49
512341	CTCCTCACGGAAGCACGACA	15.2	543	562	50
512342	TCTCCTCACGGAAGCACGAC	16.2	544	563	51
512343	CTCTCCTCACGGAAGCACGA	16.4	545	564	52
512344	CCTCTCCTCACGGAAGCACG	15.7	546	565	53
512345	CCCTCTCCTCACGGAAGCAC	14.7	547	566	54
512346	TCCCTCTCCTCACGGAAGCA	20.6	548	567	55
512347	GTCCCTCTCCTCACGGAAGC	32.6	549	568	56
512348	CGTCCCTCTCCTCACGGAAG	31.5	550	569	57
512349	GGTCCCCATTCACCAACACG	41.6	568	587	58
512350	CGGTCCCCATTCACCAACAC	31.6	569	588	59
512351	CCGGTCCCCATTCACCAACA	38.1	570	589	60
512352	GCCGGTCCCCATTCACCAAC	55.5	571	590	61
512353	CGCCGGTCCCCATTCACCAA	42.9	572	591	62
512354	CCGCCGGTCCCCATTCACCA	35.7	573	592	63
512355	ACCGCCGGTCCCCATTCACC	51.4	574	593	64
512356	CACCGCCGGTCCCCATTCAC	34.4	575	594	65
512357	CCACCGCCGGTCCCCATTCA	40.4	576	595	66
512358	TCCACCGCCGGTCCCCATTC	35.5	577	596	67
512359	ATCCACCGCCGGTCCCCATT	41.7	578	597	68
512360	GATCCACCGCCGGTCCCCAT	51.0	579	598	69
512361	TGATCCACCGCCGGTCCCCA	35.9	580	599	70
512362	GTGATCCACCGCCGGTCCCC	53.2	581	600	71
512363	CGTGATCCACCGCCGGTCCC	28.2	582	601	72
512364	TTCTCATCCTGGAAGGCGAA	34.6	611	630	73
512365	GTTCTCATCCTGGAAGGCGA	57.1	612	631	74

512366	AGTTCTCATCCTGGAAGGCG	72.1	613	632	75
512367	GTAGTTCTCATCCTGGAAGG	47.1	615	634	76
512368	GGTAGTTCTCATCCTGGAAG	56.0	616	635	77
512369	AGGTAGTTCTCATCCTGGAA	48.3	617	636	78
512370	CAGGTAGTTCTCATCCTGGA	20.2	618	637	79
512371	TACAGGTAGTTCTCATCCTG	44.0	620	639	80
512372	GTACAGGTAGTTCTCATCCT	64.1	621	640	81
512373	GGTACAGGTAGTTCTCATCC	54.2	622	641	82
512374	AGGTACAGGTAGTTCTCATC	65.6	623	642	83
512375	CCAGGTACAGGTAGTTCTCA	45.7	625	644	84
512376	ACCAGGTACAGGTAGTTCTC	60.4	626	645	85
512377	GACCAGGTACAGGTAGTTCT	62.2	627	646	86
512378	TGACCAGGTACAGGTAGTTC	64.9	628	647	87
512379	CATGACCAGGTACAGGTAGT	39.2	630	649	88
512380	CCATGACCAGGTACAGGTAG	27.7	631	650	89
512381	TCCATGACCAGGTACAGGTA	21.6	632	651	90
512382	CTCCATGACCAGGTACAGGT	25.7	633	652	91
512383	ACTCCATGACCAGGTACAGG	28.6	634	653	92
512384	TACTCCATGACCAGGTACAG	23.7	635	654	93
512385	ATACTCCATGACCAGGTACA	20.8	636	655	94
512386	AATACTCCATGACCAGGTAC	22.0	637	656	95
512387	TAATACTCCATGACCAGGTA	14.7	638	657	96
512388	CGTAATACTCCATGACCAGG	10.4	640	659	97
512389	AGCAGTGTCAGCAGGTCCCC	15.0	665	684	98
512390	CAGCAGTGTCAGCAGGTCCC	13.0	666	685	99
512391	TCAGCAGTGTCAGCAGGTCC	22.3	667	686	100
512392	CTCAGCAGTGTCAGCAGGTC	16.4	668	687	101
512393	GCTCAGCAGTGTCAGCAGGT	22.2	669	688	102
512394	TGCTCAGCAGTGTCAGCAGG	26.2	670	689	103
512395	TTGCTCAGCAGTGTCAGCAG	27.4	671	690	104
512396	CTTGCTCAGCAGTGTCAGCA	15.7	672	691	105
512397	ACTTGCTCAGCAGTGTCAGC	43.5	673	692	106
512398	AACTTGCTCAGCAGTGTCAG	26.9	674	693	107
512399	AAACTTGCTCAGCAGTGTCA	20.0	675	694	108
512400	CAAACTTGCTCAGCAGTGTC	23.1	676	695	109
512401	CCAAACTTGCTCAGCAGTGT	20.5	677	696	110
512402	CCCAAACTTGCTCAGCAGTG	13.5	678	697	33

Table 4

Inhibition of human DMPK RNA transcript in hSKMc by 5-10-5 gapmers targeting SEQ ID NO: 1

ISIS No.	Sequence	% Target Expression	Start Site on Seq ID: 1	Stop Site on Seq ID: 1	SEQ ID NO.
UTC	N/A	100	N/A	N/A	
444401	TTGCACTTTGCGAACCAACG	13.4	2490	2509	33
512480	GTGAGCCCGTCCTCCACCAA	29.8	1310	1329	111
512481	AGTGAGCCCGTCCTCCACCA	15.6	1311	1330	112
512482	CAGTGAGCCCGTCCTCCACC	10.7	1312	1331	113
512483	GCAGTGAGCCCGTCCTCCAC	33.3	1313	1332	114
512484	GGCAGTGAGCCCGTCCTCCA	9.6	1314	1333	115
512485	TGGCAGTGAGCCCGTCCTCC	8.8	1315	1334	116
512486	CATGGCAGTGAGCCCGTCCT	10.5	1317	1336	117
512487	CCATGGCAGTGAGCCCGTCC	10.1	1318	1337	118
512488	TCCATGGCAGTGAGCCCGTC	13.7	1319	1338	119
512489	CTCCATGGCAGTGAGCCCGT	16.9	1320	1339	120
512490	TCTCCATGGCAGTGAGCCCG	29.1	1321	1340	121
512491	GTCTCCATGGCAGTGAGCCC	41.3	1322	1341	122
512492	CCTTCCCGAATGTCCGACAG	8.8	1343	1362	123
512493	ACCTTCCCGAATGTCCGACA	12.1	1344	1363	124
512494	CACCTTCCCGAATGTCCGAC	6	1345	1364	125
512495	GCACCTTCCCGAATGTCCGA	8.5	1346	1365	126
512496	CGCACCTTCCCGAATGTCCG	5.6	1347	1366	127
512497	GCGCACCTTCCCGAATGTCC	7.7	1348	1367	25
512498	GGCGCACCTTCCCGAATGTC	15	1349	1368	128
512499	ACAAAAGGCAGGTGGACCCC	22.8	1373	1392	129
512500	CACAAAAGGCAGGTGGACCC	22	1374	1393	130
512501	CCACAAAAGGCAGGTGGACC	16.4	1375	1394	131
512502	CCCACAAAAGGCAGGTGGAC	15.8	1376	1395	132
512503	GCCCACAAAAGGCAGGTGGA	25.1	1377	1396	133
512504	AGCCCACAAAAGGCAGGTGG	24.7	1378	1397	134
512505	TAGCCCACAAAAGGCAGGTG	20.7	1379	1398	135
512506	GTAGCCCACAAAAGGCAGGT	20.7	1380	1399	136
512507	AGTAGCCCACAAAAGGCAGG	27.8	1381	1400	137
512508	GAGTAGCCCACAAAAGGCAG	43.9	1382	1401	138
512509	GGAGTAGCCCACAAAAGGCA	29.9	1383	1402	139
512510	AGGAGTAGCCCACAAAAGGC	31.9	1384	1403	140
512511	TAGGAGTAGCCCACAAAAGG	59.9	1385	1404	141
512512	GTAGGAGTAGCCCACAAAAG	40.1	1386	1405	142

512513	AGTAGGAGTAGCCCACAAAA	48.1	1387	1406	143
512514	GAGTAGGAGTAGCCCACAAA	53.3	1388	1407	144
512515	GGAGTAGGAGTAGCCCACAA	24.7	1389	1408	145
512516	AGGAGTAGGAGTAGCCCACA	22.1	1390	1409	146
512517	CAGGAGTAGGAGTAGCCCAC	15.4	1391	1410	147
512518	GCAGGAGTAGGAGTAGCCCA	32.8	1392	1411	148
512519	TGCAGGAGTAGGAGTAGCCC	37.6	1393	1412	149
512520	ATGCAGGAGTAGGAGTAGCC	47.4	1394	1413	150
512521	CATGCAGGAGTAGGAGTAGC	67.2	1395	1414	151
512522	CCATGCAGGAGTAGGAGTAG	58.8	1396	1415	152
512523	GCCATGCAGGAGTAGGAGTA	42.4	1397	1416	153
512524	GGCCATGCAGGAGTAGGAGT	34.1	1398	1417	154
512525	GGGCCATGCAGGAGTAGGAG	44.5	1399	1418	155
512526	AGGGCCATGCAGGAGTAGGA	42	1400	1419	156
512527	GAGGGCCATGCAGGAGTAGG	46.3	1401	1420	157
512528	CTGAGGGCCATGCAGGAGTA	25.3	1403	1422	158
512529	CCTGAGGGCCATGCAGGAGT	28.1	1404	1423	159
512530	CCCTGAGGGCCATGCAGGAG	22.8	1405	1424	160
512531	TCCCTGAGGGCCATGCAGGA	25.7	1406	1425	161
512532	GTCCCTGAGGGCCATGCAGG	17	1407	1426	162
512533	TGTCCCTGAGGGCCATGCAG	18.9	1408	1427	163
512534	CTGTCCCTGAGGGCCATGCA	27.3	1409	1428	164
512535	ACTGTCCCTGAGGGCCATGC	16.5	1410	1429	165
512536	CACTGTCCCTGAGGGCCATG	26	1411	1430	166
512537	TCACTGTCCCTGAGGGCCAT	22.7	1412	1431	167
512538	CTCACTGTCCCTGAGGGCCA	20.2	1413	1432	168
512539	CCTCACTGTCCCTGAGGGCC	19.3	1414	1433	169
512540	ACCTCACTGTCCCTGAGGGC	31	1415	1434	170
512541	GACCTCACTGTCCCTGAGGG	51.4	1416	1435	171
512542	GGACCTCACTGTCCCTGAGG	28	1417	1436	172
512543	GGGACCTCACTGTCCCTGAG	42.6	1418	1437	173
512544	CCTCCAGTTCCATGGGTGTG	16.7	1444	1463	174
512545	GCCTCCAGTTCCATGGGTGT	21.9	1445	1464	175
512546	GGCCTCCAGTTCCATGGGTG	19	1446	1465	176
512547	CGGCCTCCAGTTCCATGGGT	14.9	1447	1466	177
512548	TCGGCCTCCAGTTCCATGGG	23	1448	1467	178
512549	CTCGGCCTCCAGTTCCATGG	15.7	1449	1468	179
512550	GCTCGGCCTCCAGTTCCATG	16.2	1450	1469	180
512551	TGCTCGGCCTCCAGTTCCAT	17.7	1451	1470	181

512552	CTGCTCGGCCTCCAGTTCCA	18.4	1452	1471	182
512553	GCTGCTCGGCCTCCAGTTCC	22	1453	1472	183
512554	AGCTGCTCGGCCTCCAGTTC	32.4	1454	1473	184
512555	CAGCTGCTCGGCCTCCAGTT	15.7	1455	1474	185
512556	GCAGCTGCTCGGCCTCCAGT	16.3	1456	1475	186

Table 5

Inhibition of human DMPK RNA transcript in hSKMc by 5-10-5 gapmers targeting SEQ ID NO: 1

ISIS No.	Sequence	% Target Expression	Start Site on Seq ID: 1	Stop Site on Seq ID: 1	SEQ ID NO.
UTC	N/A	100.0	N/A	N/A	
444401	TTGCACTTTGCGAACCAACG	7.0	2490	2509	33
512557	AGCAGCTGCTCGGCCTCCAG	25.2	1457	1476	187
512558	AAGCAGCTGCTCGGCCTCCA	16.1	1458	1477	188
512559	CAAGCAGCTGCTCGGCCTCC	21.9	1459	1478	189
512560	TCAAGCAGCTGCTCGGCCTC	24.8	1460	1479	190
512561	CTCAAGCAGCTGCTCGGCCT	19.8	1461	1480	191
512562	GCTCAAGCAGCTGCTCGGCC	11.6	1462	1481	192
512563	GGCTCAAGCAGCTGCTCGGC	19.8	1463	1482	193
512564	TGGCTCAAGCAGCTGCTCGG	31.9	1464	1483	194
512565	GTGGCTCAAGCAGCTGCTCG	27.5	1465	1484	195
512566	TGTGGCTCAAGCAGCTGCTC	35.4	1466	1485	196
512567	GTGTGGCTCAAGCAGCTGCT	24.8	1467	1486	197
512568	CCACTTCAGCTGTTTCATCC	43.1	1525	1544	198
512569	TGCCACTTCAGCTGTTTCAT	35.0	1527	1546	199
512570	CTGCCACTTCAGCTGTTTCA	27.8	1528	1547	200
512571	ACTGCCACTTCAGCTGTTTC	78.9	1529	1548	201
512572	AACTGCCACTTCAGCTGTTT	36.4	1530	1549	202
512573	GAACTGCCACTTCAGCTGTT	30.3	1531	1550	203
512574	GGAACTGCCACTTCAGCTGT	66.7	1532	1551	204
512575	TGGAACTGCCACTTCAGCTG	22.6	1533	1552	205
512576	CTGGAACTGCCACTTCAGCT	22.9	1534	1553	206
512577	GCTGGAACTGCCACTTCAGC	59.5	1535	1554	207
512578	CGCTGGAACTGCCACTTCAG	24.9	1536	1555	208
512579	CCGCTGGAACTGCCACTTCA	42.5	1537	1556	209
512580	GCCGCTGGAACTGCCACTTC	20.0	1538	1557	210
512581	AGCCGCTGGAACTGCCACTT	19.4	1539	1558	211

512582	CTCAGCCTCTGCCGCAGGGA	22.1	1560	1579	212
512583	CCTCAGCCTCTGCCGCAGGG	33.7	1561	1580	213
512584	GGCCTCAGCCTCTGCCGCAG	24.6	1563	1582	214
512585	CGGCCTCAGCCTCTGCCGCA	55.1	1564	1583	215
512586	TCGGCCTCAGCCTCTGCCGC	60.8	1565	1584	216
512587	CTCGGCCTCAGCCTCTGCCG	31.8	1566	1585	217
512588	CCTCGGCCTCAGCCTCTGCC	16.4	1567	1586	218
512589	ACCTCGGCCTCAGCCTCTGC	31.1	1568	1587	219
512590	CACCTCGGCCTCAGCCTCTG	39.7	1569	1588	220
512591	TCACCTCGGCCTCAGCCTCT	24.8	1570	1589	221
512592	GTCACCTCGGCCTCAGCCTC	28.7	1571	1590	222
512593	CGTCACCTCGGCCTCAGCCT	20.3	1572	1591	223
512594	AGCACCTCCTCCTCCAGGGC	18.4	1610	1629	224
512595	GAGCACCTCCTCCTCCAGGG	19.9	1611	1630	225
512596	TGAGCACCTCCTCCTCCAGG	15.6	1612	1631	226
512597	GTGAGCACCTCCTCCTCCAG	22.3	1613	1632	227
512598	GGTGAGCACCTCCTCCTCCA	19.4	1614	1633	228
512599	GGGTGAGCACCTCCTCCTCC	17.3	1615	1634	229
512600	CGGGTGAGCACCTCCTCCTC	12.2	1616	1635	230
512601	CCGGGTGAGCACCTCCTCCT	15.9	1617	1636	231
512602	GCCGGGTGAGCACCTCCTCC	15.7	1618	1637	232
512603	TGCCGGGTGAGCACCTCCTC	15.1	1619	1638	233
512604	CTGCCGGGTGAGCACCTCCT	24.5	1620	1639	234
512605	TCTGCCGGGTGAGCACCTCC	33.8	1621	1640	235
512606	GCTCTGCCGGGTGAGCACCT	26.1	1623	1642	236
512607	GGCTCTGCCGGGTGAGCACC	50.4	1624	1643	237
512608	AGGCTCTGCCGGGTGAGCAC	42.9	1625	1644	238
512609	CAGGCTCTGCCGGGTGAGCA	39.2	1626	1645	239
512610	TCAGGCTCTGCCGGGTGAGC	20.2	1627	1646	240
512611	GCTCAGGCTCTGCCGGGTGA	22.5	1629	1648	241
512612	CGGCTCAGGCTCTGCCGGGT	27.0	1631	1650	242
512613	CCGGCTCAGGCTCTGCCGGG	68.8	1632	1651	243
512614	CCCGGCTCAGGCTCTGCCGG	58.8	1633	1652	244
512615	TCCCGGCTCAGGCTCTGCCG	24.8	1634	1653	245
512616	CTCCCGGCTCAGGCTCTGCC	10.4	1635	1654	246
512617	TCTCCCGGCTCAGGCTCTGC	12.8	1636	1655	247
512618	ATCTCCCGGCTCAGGCTCTG	13.3	1637	1656	248
512619	CATCTCCCGGCTCAGGCTCT	7.7	1638	1657	249
512620	CCATCTCCCGGCTCAGGCTC	2.8	1639	1658	250
512621	TCCATCTCCCGGCTCAGGCT	2.6	1640	1659	251

512622	CTCCATCTCCCGGCTCAGGC	1.5	1641	1660	252
512623	CCTCCATCTCCCGGCTCAGG	1.4	1642	1661	253
512624	GCCTCCATCTCCCGGCTCAG	2.0	1643	1662	254
512625	GGCCTCCATCTCCCGGCTCA	8.3	1644	1663	255
512626	TGGCCTCCATCTCCCGGCTC	9.4	1645	1664	256
512627	ATGGCCTCCATCTCCCGGCT	6.3	1646	1665	257
512628	GATGGCCTCCATCTCCCGGC	2.7	1647	1666	258
512629	GGATGGCCTCCATCTCCCGG	1.3	1648	1667	259
512630	CGGATGGCCTCCATCTCCCG	1.5	1649	1668	260
512631	GCGGATGGCCTCCATCTCCC	2.4	1650	1669	261
512632	TGCGGATGGCCTCCATCTCC	2.2	1651	1670	262
512633	GTTCCGAGCCTCTGCCTCGC	29.2	1701	1720	263

Table 6

Inhibition of human DMPK RNA transcript in hSKMc by 5-10-5 gapmers targeting SEQ ID NO: 2

ISIS No.	Sequence	% Target Expression	Start Site on Seq ID: 2	Stop Site on Seq ID: 2	SEQ ID NO.
UTC	N/A	100.0	N/A	N/A	
444401	TTGCACTTTGCGAACCAACG	7.0	13553	13572	33
444436	GTCGGAGGACGAGGTCAATA	9.7	13748	13767	264
512634	AGGGCCTCAGCCTGGCCGAA	31.7	13452	13471	265
512635	CAGGGCCTCAGCCTGGCCGA	39.5	13453	13472	266
512636	GTCAGGGCCTCAGCCTGGCC	20.5	13455	13474	267
512637	CGTCAGGGCCTCAGCCTGGC	23.3	13456	13475	268
512638	AGCAAATTTCCCGAGTAAGC	14.7	13628	13647	269
512639	AAGCAAATTTCCCGAGTAAG	21.2	13629	13648	270
512640	AAAAGCAAATTTCCCGAGTA	23.0	13631	13650	271
512641	CAAAAGCAAATTTCCCGAGT	19.7	13632	13651	272
512642	GCAAAAGCAAATTTCCCGAG	26.6	13633	13652	273
512643	GGCAAAAGCAAATTTCCCGA	12.8	13634	13653	274
512644	TGGCAAAAGCAAATTTCCCG	12.2	13635	13654	275
512645	TTTGGCAAAAGCAAATTTCC	24.2	13637	13656	276
512646	GTTTGGCAAAAGCAAATTTC	25.5	13638	13657	277
512647	GGGTTTGGCAAAAGCAAATT	43.0	13640	13659	278
512648	CGGGTTTGGCAAAAGCAAAT	27.2	13641	13660	279
512649	AAGCGGGTTTGGCAAAAGCA	27.0	13644	13663	280
512650	AATATCCAAACCGCCGAAGC	45.7	13728	13747	281

512651	AAATATCCAAACCGCCGAAG	56.6	13729	13748	282
512652	ATAAATATCCAAACCGCCGA	39.0	13731	13750	283
512653	AATAAATATCCAAACCGCCG	34.7	13732	13751	284
512654	TCAATAAATATCCAAACCGC	34.7	13734	13753	285
512655	GTCAATAAATATCCAAACCG	19.1	13735	13754	286
512656	GGTCAATAAATATCCAAACC	24.3	13736	13755	287
512657	AGGTCAATAAATATCCAAAC	23.5	13737	13756	288
512658	GAGGTCAATAAATATCCAAA	24.2	13738	13757	289
512659	ACGAGGTCAATAAATATCCA	28.3	13740	13759	290
512660	GACGAGGTCAATAAATATCC	17.8	13741	13760	291
512661	AGGACGAGGTCAATAAATAT	45.7	13743	13762	292
512662	GAGGACGAGGTCAATAAATA	27.6	13744	13763	293
512663	CGGAGGACGAGGTCAATAAA	15.8	13746	13765	294
512664	TCGGAGGACGAGGTCAATAA	10.8	13747	13766	295
512665	AGTCGGAGGACGAGGTCAAT	15.4	13749	13768	296
512666	GAGTCGGAGGACGAGGTCAA	18.8	13750	13769	297
512667	GCGAGTCGGAGGACGAGGTC	26.0	13752	13771	298
512668	AGCGAGTCGGAGGACGAGGT	21.7	13753	13772	299
512669	CAGCGAGTCGGAGGACGAGG	13.7	13754	13773	300
512670	TCAGCGAGTCGGAGGACGAG	16.5	13755	13774	301
512671	GTCAGCGAGTCGGAGGACGA	17.4	13756	13775	302
512672	CTGTCAGCGAGTCGGAGGAC	25.2	13758	13777	303
512673	CCTGTCAGCGAGTCGGAGGA	18.4	13759	13778	304
512674	AGCCTGTCAGCGAGTCGGAG	16.8	13761	13780	305
512675	GTCTCAGTGCATCCAAAACG	11.8	13807	13826	306
512676	GGTCTCAGTGCATCCAAAAC	17.7	13808	13827	307
512677	GGGTCTCAGTGCATCCAAAA	11.2	13809	13828	308
512678	GGAGGGCCTTTTATTCGCGA	17.8	13884	13903	309
512679	TGGAGGGCCTTTTATTCGCG	13.2	13885	13904	310
512680	ATGGAGGGCCTTTTATTCGC	19.3	13886	13905	311
512681	GATGGAGGGCCTTTTATTCG	30.5	13887	13906	312
512682	AGATGGAGGGCCTTTTATTC	50.8	13888	13907	313
512683	CAGATGGAGGGCCTTTTATT	46.1	13889	13908	314
512684	GCAGATGGAGGGCCTTTTAT	50.4	13890	13909	315
512685	CCCTCAGGCTCTCTGCTTTA	34.7	655	674	316
512686	GCCCTCAGGCTCTCTGCTTT	47.9	656	675	317
512687	AGCCCTCAGGCTCTCTGCTT	47.4	657	676	318
512688	TAGCCCTCAGGCTCTCTGCT	54.1	658	677	319
512689	TTAGCCCTCAGGCTCTCTGC	48.0	659	678	320
512690	TTTAGCCCTCAGGCTCTCTG	50.7	660	679	321

512691	ATTTAGCCCTCAGGCTCTCT	47.3	661	680	322
512692	AATTTAGCCCTCAGGCTCTC	44.8	662	681	323
512693	AAATTTAGCCCTCAGGCTCT	39.2	663	682	324
512694	TAAATTTAGCCCTCAGGCTC	48.0	664	683	325
512695	TTAAATTTAGCCCTCAGGCT	54.9	665	684	326
512696	GTTAAATTTAGCCCTCAGGC	48.1	666	685	327
512697	AGTTAAATTTAGCCCTCAGG	39.3	667	686	328
512698	CAGTTAAATTTAGCCCTCAG	47.5	668	687	329
512699	ACAGTTAAATTTAGCCCTCA	68.2	669	688	330
512700	GACAGTTAAATTTAGCCCTC	59.2	670	689	331
512701	GGACAGTTAAATTTAGCCCT	63.7	671	690	332
512702	CGGACAGTTAAATTTAGCCC	50.7	672	691	333
512703	TCGGACAGTTAAATTTAGCC	39.6	673	692	334
512704	CTCGGACAGTTAAATTTAGC	36.5	674	693	335
512705	ACTCGGACAGTTAAATTTAG	59.1	675	694	336
512706	GACTCGGACAGTTAAATTTA	50.0	676	695	337
512707	CGACTCGGACAGTTAAATTT	63.0	677	696	338
512708	CCGACTCGGACAGTTAAATT	34.3	678	697	339
512709	TCCGACTCGGACAGTTAAAT	39.5	679	698	340

Example 3: Design of antisense oligonucleotides targeting human dystrophia myotonica protein kinase (hDMPK)

A series of antisense oligonucleotides (ASOs) were designed to target hDMPK. The newly designed ASOs were prepared using standard oligonucleotide synthesis well known in the art and are described in Table 7, below. Subscripts "s" indicate phosphorothioate internucleoside linkages; subscripts "k" indicate 6'-*(S)*-CH_3 bicyclic nucleosides (cEt); subscripts "e" indicate 2'-O-methoxyethyl (MOE) modified nucleosides; and subscripts "d" indicate β-D-2'-deoxyribonucleosides. "^{m}C" indicates 5-methylcytosine nucleosides.

The antisense oligonucleotides targeted to a human DMPK nucleic acid were tested for their effect on DMPK RNA transcript *in vitro*. Cultured HepG2 cells at a density of 20,000 cells per well were transfected using electroporation with 4,500 nM antisense oligonucleotide. After approximately 24 hours, RNA was isolated from the cells and DMPK transcript levels were measured by quantitative real-time PCR. DMPK RNA transcript levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent expression of DMPK, relative to untreated control cells.

'Target start site' indicates the 5'-most nucleoside to which the antisense oligonucleotide is targeted in the human genomic gene sequence. 'Target stop site' indicates the 3'-most nucleoside to which the antisense oligonucleotide is targeted in the human genomic sequence. All the antisense oligonucleotides listed in Table 7 target SEQ ID NO: 1 (GENBANK Accession No. NM_001081560.1).

Several of the antisense oligonucleotides demonstrated significant inhibition of DMPK mRNA levels under the conditions specified above.

Table 7

Inhibition of human DMPK RNA transcript in HepG2 cells targeting SEQ ID NO: 1

ISIS No.	Sequence	% Target Expression	Start Site on Seq ID: 1	Stop Site on Seq ID: 1	Seq ID No.
UTC	N/A	100	N/A	N/A	
533424	$T_{es}{}^{m}C_{es}T_{es}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}A_{ds}G_{ks}{}^{m}C_{ks}A_{k}$	34.4	548	563	341
533425	${}^{m}C_{es}T_{es}{}^{m}C_{es}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	32.1	549	564	342
533426	${}^{m}C_{es}{}^{m}C_{es}T_{es}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ks}A_{ks}G_{k}$	52.1	550	565	343
533427	$A_{es}A_{es}A_{es}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ks}G_{ks}T_{k}$	36.8	679	694	344
533428	${}^{m}C_{es}A_{es}A_{es}A_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ks}A_{ks}G_{k}$	59.9	680	695	345
533429	${}^{m}C_{es}{}^{m}C_{es}A_{es}A_{ds}A_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ks}{}^{m}C_{ks}A_{k}$	39.3	681	696	346
533430	${}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{es}A_{ds}A_{ds}A_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	37.6	682	697	347
533431	${}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}A_{ks}G_{k}$	39.6	683	698	348
533432	$T_{es}{}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}A_{k}$	52.1	684	699	349
533433	$G_{es}T_{es}T_{es}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ks}T_{ks}G_{k}$	53.9	782	797	350
533434	$G_{es}G_{es}T_{es}T_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}G_{ks}T_{k}$	38.1	783	798	351
533435	$G_{es}G_{es}G_{es}T_{ds}T_{ds}T_{ds}G_{ds}A_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}G_{k}$	43.7	784	799	352
533436	$A_{es}{}^{m}C_{es}A_{es}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}A_{ds}T_{ks}{}^{m}C_{ks}T_{k}$	29.5	927	942	353
533437	${}^{m}C_{es}A_{es}{}^{m}C_{es}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}A_{ks}T_{ks}{}^{m}C_{k}$	48.6	928	943	354
533438	${}^{m}C_{es}{}^{m}C_{es}A_{es}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ks}A_{ks}T_{k}$	46.9	929	944	355
533439	${}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{es}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ks}G_{ks}A_{k}$	43.6	930	945	356
533440	$G_{es}{}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ks}G_{ks}G_{k}$	26.9	931	946	357
533441	${}^{m}C_{es}G_{es}{}^{m}C_{es}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ks}A_{ks}G_{k}$	31.3	932	947	358
533442	${}^{m}C_{es}{}^{m}C_{es}G_{es}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ks}{}^{m}C_{ks}A_{k}$	20.5	933	948	359
533443	$A_{es}{}^{m}C_{es}{}^{m}C_{es}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}G_{ks}{}^{m}C_{k}$	13.7	934	949	360

533444	${}^{m}C_{es}A_{es}{}^{m}C_{es}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}G_{k}$	29.4	935	950	361
533445	${}^{m}C_{es}{}^{m}C_{es}A_{es}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ks}{}^{m}C_{ks}T_{k}$	32	936	951	362
533446	${}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{es}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	8.3	937	952	363
533447	$G_{es}{}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	18.3	938	953	364
533448	${}^{m}C_{es}{}^{m}C_{es}A_{es}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	19.4	942	957	365
533449	${}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{es}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	24.2	943	958	366
533450	$T_{es}{}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	39.2	944	959	367
533451	$T_{es}G_{es}{}^{m}C_{es}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	44.2	950	965	368
533452	${}^{m}C_{es}T_{es}G_{es}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	55.6	951	966	369
533453	$G_{es}{}^{m}C_{es}T_{es}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ks}G_{ks}{}^{m}C_{k}$	71.2	952	967	370
533454	$G_{es}G_{es}T_{es}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}G_{ds}A_{ks}A_{ks}A_{k}$	39.6	1276	1291	371
533455	${}^{m}C_{es}G_{es}G_{es}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}G_{ks}A_{ks}A_{k}$	52.9	1277	1292	372
533456	$T_{es}{}^{m}C_{es}G_{es}G_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ks}G_{ks}A_{k}$	27	1278	1293	373
533457	$A_{es}G_{es}T_{es}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	51.5	1315	1330	374
533458	${}^{m}C_{es}A_{es}G_{es}T_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	55.1	1316	1331	375
533459	$G_{es}{}^{m}C_{es}A_{es}G_{ds}T_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}T_{k}$	33.7	1317	1332	376
533460	$T_{es}{}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ks}{}^{m}C_{ks}A_{k}$	28.7	1344	1359	377
533461	$T_{es}T_{es}{}^{m}C_{es}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ks}A_{ks}{}^{m}C_{k}$	36.2	1345	1360	378
533462	${}^{m}C_{es}T_{es}T_{es}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}G_{ks}A_{k}$	23	1346	1361	379
533463	${}^{m}C_{es}{}^{m}C_{es}T_{es}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}G_{k}$	11.5	1347	1362	380
533464	$A_{es}{}^{m}C_{es}{}^{m}C_{es}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}T_{ds}G_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	19.9	1348	1363	381
533465	${}^{m}C_{es}A_{es}{}^{m}C_{es}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}T_{ds}G_{ks}T_{ks}{}^{m}C_{k}$	30.2	1349	1364	382
533466	$G_{es}{}^{m}C_{es}A_{es}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}T_{ks}G_{ks}T_{k}$	30.2	1350	1365	383
533467	${}^{m}C_{es}G_{es}{}^{m}C_{es}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ks}T_{ks}G_{k}$	35.5	1351	1366	384
533468	$A_{es}T_{es}{}^{m}C_{es}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}A_{ks}{}^{m}C_{ks}T_{k}$	47.4	1746	1761	385
533469	${}^{m}C_{es}A_{es}T_{es}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ks}A_{ks}{}^{m}C_{k}$	51.2	1747	1762	386
533470	${}^{m}C_{es}{}^{m}C_{es}A_{es}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ks}A_{ks}A_{k}$	35.5	1748	1763	387
533471	$G_{es}{}^{m}C_{es}T_{es}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ks}{}^{m}C_{ks}A_{k}$	65.6	1770	1785	388
533472	$A_{es}G_{es}G_{es}T_{ds}G_{ds}G_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}T_{ds}G_{ds}G_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	51.8	1816	1831	389
533473	$G_{es}G_{es}G_{es}A_{ds}A_{ds}G_{ds}G_{ds}T_{ds}G_{ds}G_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}G_{ks}T_{k}$	44.9	1820	1835	390
533474	$A_{es}{}^{m}C_{es}A_{es}G_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}G_{ds}A_{ds}A_{ks}A_{ks}G_{k}$	80.8	1955	1970	391
533475	${}^{m}C_{es}A_{es}G_{es}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}G_{ds}A_{ds}G_{ks}T_{ks}T_{k}$	95.5	2034	2049	392
533476	$G_{es}G_{es}{}^{m}C_{es}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}G_{ds}G_{ds}{}^{m}C_{ks}G_{ks}{}^{m}C_{k}$	55.7	2050	2065	393
533477	$G_{es}G_{es}{}^{m}C_{es}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ks}G_{ks}G_{k}$	45.8	2053	2068	394

533478	${}^{m}C_{es}G_{es}{}^{m}C_{es}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}G_{ks}G_{k}$	83.7	2057	2072	395
533479	$G_{es}A_{es}G_{es}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	79.8	2060	2075	396
533480	$G_{es}G_{es}T_{es}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ks}G_{ks}G_{k}$	49.4	2068	2083	397
533481	$A_{es}G_{es}T_{es}T_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}G_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}A_{ks}G_{ks}G_{k}$	37	2076	2091	398
533482	${}^{m}C_{es}A_{es}G_{es}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}G_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ks}A_{ks}G_{k}$	28.5	2077	2092	399
533483	$A_{es}{}^{m}C_{es}A_{es}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}G_{ds}G_{ds}T_{ds}T_{ks}{}^{m}C_{ks}A_{k}$	42	2078	2093	400
533484	$G_{es}A_{es}{}^{m}C_{es}A_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}G_{ds}G_{ds}T_{ks}T_{ks}{}^{m}C_{k}$	37.4	2079	2094	401
533485	$A_{es}G_{es}A_{es}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}G_{ds}G_{ks}T_{ks}T_{k}$	66.5	2080	2095	402
533486	$A_{es}A_{es}G_{es}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}G_{ks}G_{ks}T_{k}$	62.4	2081	2096	403
533487	$G_{es}A_{es}A_{es}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ks}G_{ks}G_{k}$	56.9	2082	2097	404
533488	${}^{m}C_{es}G_{es}A_{es}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}A_{ks}G_{ks}G_{k}$	36.8	2083	2098	405
533489	$T_{es}{}^{m}C_{es}G_{es}A_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ks}A_{ks}G_{k}$	49.6	2084	2099	406
533490	$G_{es}T_{es}{}^{m}C_{es}G_{ds}A_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ks}T_{ks}A_{k}$	40.4	2085	2100	407
533491	$A_{es}G_{es}T_{es}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}T_{ks}{}^{m}C_{ks}T_{k}$	37.4	2086	2101	408
533492	$G_{es}A_{es}G_{es}T_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ks}T_{ks}{}^{m}C_{k}$	36.6	2087	2102	409
533493	$G_{es}G_{es}A_{es}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ks}T_{ks}T_{k}$	33.2	2088	2103	410
533494	${}^{m}C_{es}G_{es}G_{es}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ks}G_{ks}T_{k}$	45.3	2089	2104	411
533495	${}^{m}C_{es}{}^{m}C_{es}G_{es}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ks}A_{ks}G_{k}$	45.9	2090	2105	412
533496	${}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{es}G_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}G_{ds}A_{ks}{}^{m}C_{ks}A_{k}$	51.3	2091	2106	413
533497	${}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}G_{ks}A_{ks}{}^{m}C_{k}$	49.2	2092	2107	414
533498	$G_{es}{}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ks}G_{ks}A_{k}$	52.3	2093	2108	415
533499	$G_{es}G_{es}{}^{m}C_{es}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}A_{ks}A_{ks}G_{k}$	54.9	2094	2109	416
533500	$G_{es}G_{es}G_{es}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ks}A_{ks}A_{k}$	46.7	2095	2110	417
533809	$A_{es}{}^{m}C_{es}A_{es}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ks}G_{ks}G_{k}$	51.4	2773	2788	418

Example 4: Design of antisense oligonucleotides targeting human dystrophia myotonica protein kinase (hDMPK)

Dose Response HepG2

A series of antisense oligonucleotides (ASOs) were designed to target hDMPK. The newly designed ASOs were prepared using standard oligonucleotide synthesis well known in the art and are described in Table 8, below. Subscripts “s” indicate phosphorothioate internucleoside linkages; subscripts “k” indicate 6’-*(S)*-CH_3 bicyclic nucleosides (cEt); subscripts “e” indicate 2’-O-methoxyethyl (MOE) modified nucleosides; and subscripts “d” indicate β-D-2’-deoxyribonucleosides. “${}^{m}C$” indicates 5-methylcytosine nucleosides.

The antisense oligonucleotides are targeted to SEQ ID NO: 1 (GENBANK Accession No. NM_001081560.1). "Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. "Stop site" indicates the 3'-most nucleoside to which the gapmer is targeted human gene sequence.

Table 8

Design of antisense oligonucleotides targeting hDMPK

ISIS No.	Composition (5' to 3')	Start Site	Stop Site	SEQ ID NO
533440	$G_{es}{}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ks}G_{ks}G_{k}$	931	946	357
533442	${}^{m}C_{es}{}^{m}C_{es}G_{es}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ks}{}^{m}C_{ks}A_{k}$	933	948	359
533443	$A_{es}{}^{m}C_{es}{}^{m}C_{es}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}G_{ks}{}^{m}C_{k}$	934	949	360
533446	${}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{es}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	937	952	363
533447	$G_{es}{}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	938	953	364
533448	${}^{m}C_{es}{}^{m}C_{es}A_{es}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	942	957	365
533449	${}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{es}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	943	958	366
533462	${}^{m}C_{es}T_{es}T_{es}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}G_{ks}A_{k}$	1346	1361	379
533463	${}^{m}C_{es}{}^{m}C_{es}T_{es}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}G_{k}$	1347	1362	380
533464	$A_{es}{}^{m}C_{es}{}^{m}C_{es}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}T_{ds}G_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	1348	1363	381
533529	${}^{m}C_{es}G_{es}G_{es}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ks}{}^{m}C_{ks}A_{k}$	2162	2177	23
533530	$A_{es}G_{es}{}^{m}C_{es}G_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{ds}T_{ks}G_{ks}G_{k}$	2164	2179	419
533599	$G_{es}{}^{m}C_{es}A_{es}{}^{m}C_{ds}T_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}A_{k}$	2492	2507	420
533600	$T_{es}G_{es}{}^{m}C_{es}A_{ds}{}^{m}C_{ds}T_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	2493	2508	421

Example 5: Dose Response HepG2

Antisense oligonucleotides targeted to a human DMPK nucleic acid were tested for their effect on human DMPK RNA transcript *in vitro*. Cultured HepG2 cells at a density of 20,000 cells per well were transfected using electroporation with 625 nM, 1250 nM, 2500 nM, 5000 nM, and 10000.0 nM concentrations of each antisense oligonucleotide. After approximately 24 hours, RNA was isolated from the cells and DMPK RNA transcript levels were measured by quantitative real-time PCR using primer probe set RTS3164 (forward sequence AGCCTGAGCCGGGAGATG, designated herein as SEQ ID NO: 20; reverse sequence GCGTAGTTGACTGGCGAAGTT, designated herein as SEQ ID NO: 21; probe sequence AGGCCATCCGCACGGACAACCX, designated herein as SEQ ID NO: 22). Human DMPK RNA transcript levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented in the table below as percent expression of human DMPK, relative to untreated control (UTC) cells. The tested antisense oligonucleotide sequences demonstrated dose-dependent inhibition of human DMPK mRNA levels under the conditions specified above.

Table 9

Inhibition of human DMPK RNA transcript in HepG2 cells targeting SEQ ID NO: 1

ISIS No.	Dose (nM)	% Target Expression	Start Site on Seq ID: 1	Stop Site on Seq ID: 1
UTC	N/A	100	N/A	N/A
486178	625.0	39.4	2773	2788
486178	1250.0	31.2	2773	2788
486178	2500.0	20.6	2773	2788
486178	5000.0	13	2773	2788
486178	10000.0	11.5	2773	2788
533440	625.0	55.4	931	946
533440	1250.0	40.4	931	946
533440	2500.0	25.4	931	946
533440	5000.0	22.6	931	946
533440	10000.0	10.3	931	946
533442	625.0	55.2	933	948
533442	1250.0	33.1	933	948
533442	2500.0	29	933	948
533442	5000.0	16.9	933	948
533442	10000.0	7.2	933	948
533443	625.0	44.8	934	949

533443	1250.0	29.4	934	949
533443	2500.0	19.9	934	949
533443	5000.0	10.8	934	949
533443	10000.0	7	934	949
533446	625.0	50.9	937	952
533446	1250.0	35.5	937	952
533446	2500.0	30.4	937	952
533446	5000.0	14.6	937	952
533446	10000.0	14	937	952
533447	625.0	53.3	938	953
533447	1250.0	31.7	938	953
533447	2500.0	16.8	938	953
533447	5000.0	11.7	938	953
533447	10000.0	4.4	938	953
533448	625.0	58.8	942	957
533448	1250.0	36.9	942	957
533448	2500.0	24.8	942	957
533448	5000.0	11.5	942	957
533448	10000.0	10.1	942	957
533449	625.0	61.1	943	958
533449	1250.0	42.8	943	958
533449	2500.0	30.4	943	958
533449	5000.0	20.2	943	958
533449	10000.0	10.1	943	958
533462	625.0	50.7	1346	1361
533462	1250.0	32.3	1346	1361
533462	2500.0	29.2	1346	1361
533462	5000.0	12.5	1346	1361
533462	10000.0	5.8	1346	1361
533463	625.0	39.1	1347	1362
533463	1250.0	23.7	1347	1362

533463	2500.0	12.6	1347	1362
533463	5000.0	9.3	1347	1362
533463	10000.0	3.2	1347	1362
533464	625.0	48.8	1348	1363
533464	1250.0	36.4	1348	1363
533464	2500.0	24.5	1348	1363
533464	5000.0	11.7	1348	1363
533464	10000.0	5	1348	1363
533529	625.0	35.8	2162	2177
533529	1250.0	26.4	2162	2177
533529	2500.0	18.3	2162	2177
533529	5000.0	14.8	2162	2177
533529	10000.0	14.7	2162	2177
533530	625.0	47.4	2164	2179
533530	1250.0	22.1	2164	2179
533530	2500.0	21.5	2164	2179
533530	5000.0	14.4	2164	2179
533530	10000.0	8	2164	2179
533599	625.0	31.3	2492	2507
533599	1250.0	21.9	2492	2507
533599	2500.0	13.1	2492	2507
533599	5000.0	8.8	2492	2507
533599	10000.0	7.3	2492	2507
533600	625.0	33.8	2493	2508
533600	1250.0	20.9	2493	2508
533600	2500.0	16.5	2493	2508
533600	5000.0	10.4	2493	2508
533600	10000.0	12.1	2493	2508

Example 6: Design of antisense oligonucleotides targeting human dystrophia myotonica protein kinase (hDMPK)

A series of antisense oligonucleotides (ASOs) were designed to target hDMPK. The newly designed ASOs were prepared using standard oligonucleotide synthesis well known in the art and are described in Table 10, below. Subscripts “s” indicate phosphorothioate internucleoside linkages; subscripts “k” indicate 6’-*(S)*-CH_3 bicyclic nucleosides (cEt); subscripts “e” indicate 2’-O-methoxyethyl (MOE) modified nucleosides; and subscripts “d” indicate β-D-2’-deoxyribonucleosides. “^{m}C” indicates 5-methylcytosine nucleosides.

The antisense oligonucleotides are targeted to SEQ ID NO: 2 (the complement of GENBANK Accession No. NT_011109.15 truncated from nucleotides 18540696 to 18555106). “Start site” indicates the 5’-most nucleoside to which the gapmer is targeted in the human gene sequence. “Stop site” indicates the 3’-most nucleoside to which the gapmer is targeted human gene sequence.

Table 10

Design of antisense oligonucleotides targeting hDMPK

ISIS No.	Sequence	Start Site on Seq ID: 2	Stop Site on Seq ID: 2	Seq ID No.
UTC	N/A	N/A	N/A	
486178	$A_{ks}{}^{m}C_{ks}A_{ks}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ks}G_{ks}G_{k}$	13836	13851	23
533597	$A_{es}{}^{m}C_{es}T_{es}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ks}{}^{m}C_{ks}G_{k}$	13553	13568	422
533603	$A_{es}A_{es}A_{es}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}T_{ks}T_{ks}G_{k}$	13563	13578	423
533617	$T_{es}{}^{m}C_{es}{}^{m}C_{es}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}T_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ks}G_{ks}{}^{m}C_{k}$	13624	13639	424
533649	$G_{es}{}^{m}C_{es}A_{es}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}A_{ds}A_{ds}G_{ds}T_{ds}G_{ds}A_{ds}G_{ks}G_{ks}A_{k}$	13686	13701	425
533694	$G_{es}T_{es}{}^{m}C_{es}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ks}G_{ks}G_{k}$	13760	13775	426
533697	${}^{m}C_{es}{}^{m}C_{es}T_{es}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ks}G_{ks}G_{k}$	13763	13778	427
533698	$G_{es}{}^{m}C_{es}{}^{m}C_{es}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}T_{ks}{}^{m}C_{ks}G_{k}$	13764	13779	428
533699	$A_{es}G_{es}{}^{m}C_{es}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ks}T_{ks}{}^{m}C_{k}$	13765	13780	429
533711	$G_{es}G_{es}G_{es}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	13813	13828	430
533721	$A_{es}G_{es}G_{es}T_{ds}T_{ds}T_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}G_{ks}G_{ks}{}^{m}C_{k}$	2580	2595	431
533722	$A_{es}A_{es}G_{es}G_{ds}T_{ds}T_{ds}T_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ks}G_{ks}G_{k}$	2581	2596	432
533751	$G_{es}G_{es}T_{es}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}G_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	6446	6461	433
533786	$G_{es}T_{es}G_{es}G_{ds}T_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ks}{}^{m}C_{ks}T_{k}$	11099	11114	434
533787	${}^{m}C_{es}G_{es}T_{es}G_{ds}G_{ds}T_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}T_{ks}G_{ks}{}^{m}C_{k}$	11100	11115	435

Example 7: Dose Response for ASOs targeted to a human DMPK RNA transcript in HepG2 cells

Antisense oligonucleotides targeted to a human DMPK nucleic acid were tested for their effect on human DMPK RNA transcript *in vitro*. Cultured HepG2 cells at a density of 20,000 cells per well were transfected using electroporation with 625 nM, 1250 nM, 2500 nM, 5000 nM, and 10000.0 nM concentrations of each antisense oligonucleotide. After approximately 24 hours, RNA was isolated from the cells and DMPK RNA transcript levels were measured by quantitative real-time PCR using primer probe set RTS3164 (forward sequence AGCCTGAGCCGGGAGATG, designated herein as SEQ ID NO: 20; reverse sequence GCGTAGTTGACTGGCGAAGTT, designated herein as SEQ ID NO: 21; probe sequence AGGCCATCCGCACGGACAACCX, designated herein as SEQ ID NO: 22). Human DMPK RNA transcript levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent expression of human DMPK, relative to untreated control (UTC) cells and are shown in the table below. The tested antisense oligonucleotide sequences demonstrated dose-dependent inhibition of human DMPK mRNA levels under the conditions specified above.

Table 11

Inhibition of human DMPK RNA transcript in HepG2 cells targeting SEQ ID NO: 1

ISIS No.	Dose (nM)	% Target Expression	Start Site on Seq ID: 2	Stop Site on Seq ID: 2
UTC	NA	100	N/A	N/A
486178	625.000	39.4	13836	13851
486178	1250.000	27.3	13836	13851
486178	2500.000	14	13836	13851
486178	5000.000	16.3	13836	13851
486178	10000.000	8.3	13836	13851
533597	625.000	42.4	13553	13568
533597	1250.000	30.3	13553	13568
533597	2500.000	15.3	13553	13568
533597	5000.000	10	13553	13568
533597	10000.000	10.6	13553	13568

533603	625.000	48.2	13563	13578
533603	1250.000	31.1	13563	13578
533603	2500.000	22.4	13563	13578
533603	5000.000	15.6	13563	13578
533603	10000.000	9.9	13563	13578
533617	625.000	38.4	13624	13639
533617	1250.000	26.3	13624	13639
533617	2500.000	21.6	13624	13639
533617	5000.000	15.8	13624	13639
533617	10000.000	14.6	13624	13639
533649	625.000	52.2	13686	13701
533649	1250.000	27.8	13686	13701
533649	2500.000	24.6	13686	13701
533649	5000.000	20.5	13686	13701
533649	10000.000	14.5	13686	13701
533694	625.000	53.3	13760	13775
533694	1250.000	29.4	13760	13775
533694	2500.000	23.6	13760	13775
533694	5000.000	18.7	13760	13775
533694	10000.000	13.5	13760	13775
533697	625.000	30.6	13763	13778
533697	1250.000	14.9	13763	13778
533697	2500.000	13.8	13763	13778
533697	5000.000	9.7	13763	13778
533697	10000.000	7.1	13763	13778
533698	625.000	23.4	13764	13779
533698	1250.000	15.5	13764	13779
533698	2500.000	13.8	13764	13779
533698	5000.000	12.4	13764	13779
533698	10000.000	10.2	13764	13779
533699	625.000	38.2	13765	13780

533699	1250.000	26.9	13765	13780
533699	2500.000	17.6	13765	13780
533699	5000.000	12.9	13765	13780
533699	10000.000	9.3	13765	13780
533711	625.000	35.1	13813	13828
533711	1250.000	34.6	13813	13828
533711	2500.000	22.4	13813	13828
533711	5000.000	22	13813	13828
533711	10000.000	13	13813	13828
533721	625.000	36.3	2580	2595
533721	1250.000	29.8	2580	2595
533721	2500.000	23.2	2580	2595
533721	5000.000	17.8	2580	2595
533721	10000.000	17.2	2580	2595
533722	625.000	48.5	2581	2596
533722	1250.000	28.6	2581	2596
533722	2500.000	21.9	2581	2596
533722	5000.000	28.1	2581	2596
533722	10000.000	13.8	2581	2596
533751	625.000	37.7	6446	6461
533751	1250.000	21.6	6446	6461
533751	2500.000	12.6	6446	6461
533751	5000.000	9.7	6446	6461
533751	10000.000	8.5	6446	6461
533786	625.000	53.6	11099	11114
533786	1250.000	26.6	11099	11114
533786	2500.000	14.7	11099	11114
533786	5000.000	9.6	11099	11114
533786	10000.000	5.5	11099	11114
533787	625.000	43.8	11100	11115
533787	1250.000	27.7	11100	11115

533787	2500.000	16.3	11100	11115
533787	5000.000	7	11100	11115
533787	10000.000	4.5	11100	11115

Example 8: ASOs designed to target a human DMPK RNA transcript

A series of antisense oligonucleotides (ASOs) were designed to target hDMPK. The newly designed ASOs were prepared using standard oligonucleotide synthesis well known in the art and are described in Table 12, below. Subscripts “s” indicate phosphorothioate internucleoside linkages; subscripts “k” indicate 6’-*(S)*-CH_3 bicyclic nucleosides (cEt); subscripts “e” indicate 2’-O-methoxyethyl (MOE) modified nucleosides; and subscripts “d” indicate β-D-2’-deoxyribonucleosides. “^{m}C” indicates 5-methylcytosine nucleosides.

The antisense oligonucleotides targeted to a human DMPK nucleic acid were tested for their effect on DMPK RNA transcript *in vitro*. Cultured hSKMC cells at a density of 20,000 cells per well were transfected using electroporation with 800 nM antisense oligonucleotide. After approximately 24 hours, RNA was isolated from the cells and DMPK transcript levels were measured by quantitative real-time PCR. DMPK RNA transcript levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent expression of DMPK, relative to untreated control cells.

‘Target start site’ indicates the 5’-most nucleoside to which the antisense oligonucleotide is targeted in the human genomic gene sequence. ‘Target stop site’ indicates the 3’-most nucleoside to which the antisense oligonucleotide is targeted in the human genomic sequence. All the antisense oligonucleotides listed in Table 12 target SEQ ID NO: 1 (GENBANK Accession No. NM_001081560.1).

Several of the antisense oligonucleotides demonstrated significant inhibition of DMPK mRNA levels under the conditions specified above.

Table 12

Inhibition of human DMPK RNA transcript in HepG2 cells using ASOs targeting SEQ ID NO: 1

ISIS No.	Sequence	% Target Expression	Start Site on Seq ID: 1	Stop Site on Seq ID: 1	Seq ID No.
UTC	N/A	100	N/A	N/A	
444401	$T_{es}T_{es}G_{es}{}^{m}C_{es}A_{es}{}^{m}C_{ds}T_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{es}A_{es}A_{es}{}^{m}C_{es}G_{e}$	25.2	2490	2509	33
444436	$G_{es}T_{es}{}^{m}C_{es}G_{es}G_{es}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{es}A_{es}A_{es}T_{es}A_{e}$	30.8	2685	2704	264
486072	$A_{ks}A_{ks}G_{ks}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}G_{ks}G_{ks}T_{k}$	36.8	2081	2096	403
486073	${}^{m}C_{ks}G_{ks}A_{ks}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}A_{ks}G_{ks}G_{k}$	22.4	2083	2098	405
486075	$G_{ks}T_{ks}{}^{m}C_{ks}G_{ds}A_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ks}T_{ks}A_{k}$	41.3	2085	2100	407
486076	$A_{ks}G_{ks}T_{ks}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}T_{ks}{}^{m}C_{ks}T_{k}$	22.4	2086	2101	408
486077	$G_{ks}A_{ks}G_{ks}T_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ks}T_{ks}{}^{m}C_{k}$	35.2	2087	2102	409
486078	${}^{m}C_{ks}G_{ks}G_{ks}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ks}G_{ks}T_{k}$	12.4	2089	2104	411
486079	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}G_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}G_{ds}A_{ks}{}^{m}C_{ks}A_{k}$	36.5	2091	2106	413
486080	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}G_{ks}A_{ks}{}^{m}C_{k}$	19.9	2092	2107	414
486085	$G_{ks}A_{ks}A_{ks}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}G_{ds}G_{ks}T_{ks}G_{k}$	30.1	2155	2170	436
486086	$T_{ks}G_{ks}T_{ks}G_{ds}A_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ks}{}^{m}C_{ks}G_{k}$	17.2	2158	2173	437
486087	$G_{ks}G_{ks}T_{ks}T_{ds}G_{ds}T_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ks}A_{ks}G_{k}$	11.5	2161	2176	438
486088	$G_{ks}A_{ks}G_{ks}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{ks}T_{ks}G_{k}$	21.7	2165	2180	439
486094	$A_{ks}{}^{m}C_{ks}T_{ks}G_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}G_{ks}G_{ks}A_{k}$	30.2	2193	2208	440
486096	$A_{ks}G_{ks}G_{ks}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ks}G_{ks}{}^{m}C_{k}$	43.5	2196	2211	441
486097	$T_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}A_{ds}G_{ks}{}^{m}C_{ks}T_{k}$	54.5	2200	2215	442
486098	$A_{ks}T_{ks}{}^{m}C_{ks}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	77.3	2201	2216	443
486099	$G_{ks}G_{ks}A_{ks}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ks}G_{ks}A_{k}$	24.8	2203	2218	444
486101	${}^{m}C_{ks}A_{ks}G_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}A_{ks}G_{ks}A_{k}$	31.6	2386	2401	445
486102	${}^{m}C_{ks}T_{ks}{}^{m}C_{ks}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ks}A_{ks}A_{k}$	35.1	2388	2403	446
486104	$G_{ks}T_{ks}{}^{m}C_{ks}A_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ks}{}^{m}C_{ks}T_{k}$	26.9	2396	2411	447
486105	${}^{m}C_{ks}G_{ks}T_{ks}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	48.4	2397	2412	448
486110	$T_{ks}T_{ks}T_{ks}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ks}A_{ks}{}^{m}C_{k}$	31.6	2495	2510	449
486111	$G_{ks}A_{ks}A_{ks}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ks}T_{ks}T_{k}$	31.9	2501	2516	450
486112	$A_{ks}A_{ks}T_{ks}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}T_{ds}A_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	47.4	2565	2580	451
486115	$G_{ks}{}^{m}C_{ks}A_{ks}A_{ds}A_{ds}T_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ks}T_{ks}A_{k}$	20.8	2568	2583	452
486116	$A_{ks}G_{ks}{}^{m}C_{ks}A_{ds}A_{ds}A_{ds}T_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ks}G_{ks}T_{k}$	23.9	2569	2584	453
486117	$A_{ks}A_{ks}G_{ks}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}T_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ks}A_{ks}G_{k}$	22	2570	2585	454
486118	$A_{ks}A_{ks}A_{ks}G_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}T_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}G_{ks}A_{k}$	26.7	2571	2586	455

486119	$A_{ks}A_{ks}A_{ks}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}T_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}G_{k}$	33.5	2572	2587	456
486120	$G_{ks}{}^{m}C_{ks}A_{ks}A_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}T_{ds}T_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	51.4	2574	2589	457
486121	$G_{ks}G_{ks}{}^{m}C_{ks}A_{ds}A_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}T_{ds}T_{ks}T_{ks}{}^{m}C_{k}$	60.8	2575	2590	458
486123	$T_{ks}T_{ks}G_{ks}G_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ks}T_{ks}T_{k}$	39.8	2577	2592	459
486125	$G_{ks}T_{ks}T_{ks}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ks}A_{ks}A_{k}$	32.7	2579	2594	460
486126	$G_{ks}G_{ks}T_{ks}T_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ks}A_{ks}A_{k}$	19.2	2580	2595	461
486127	$G_{ks}G_{ks}G_{ks}T_{ds}T_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}A_{ds}G_{ks}{}^{m}C_{ks}A_{k}$	36.1	2581	2596	462
486128	$G_{ks}{}^{m}C_{ks}G_{ks}G_{ds}G_{ds}T_{ds}T_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ks}A_{ks}G_{k}$	39.1	2583	2598	463
486129	$A_{ks}G_{ks}{}^{m}C_{ks}G_{ds}G_{ds}G_{ds}T_{ds}T_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}A_{ks}A_{ks}A_{k}$	31.4	2584	2599	464
486130	$A_{ks}A_{ks}G_{ks}{}^{m}C_{ds}G_{ds}G_{ds}G_{ds}T_{ds}T_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ks}A_{ks}A_{k}$	35.7	2585	2600	465
486133	${}^{m}C_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ks}{}^{m}C_{ks}A_{k}$	45.9	2631	2646	466
486134	$G_{ks}{}^{m}C_{ks}T_{ks}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ks}G_{ks}{}^{m}C_{k}$	29.5	2632	2647	467
486135	$G_{ks}G_{ks}{}^{m}C_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ks}{}^{m}C_{ks}G_{k}$	51.4	2633	2648	468
486142	$T_{ks}A_{ks}A_{ks}A_{ds}T_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ks}G_{ks}{}^{m}C_{k}$	64.4	2671	2686	469
486147	$G_{ks}T_{ks}{}^{m}C_{ks}A_{ds}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}T_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}A_{k}$	16.1	2676	2691	470
486148	$A_{ks}G_{ks}G_{ks}T_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}T_{ds}A_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	18.3	2678	2693	471
486149	${}^{m}C_{ks}G_{ks}A_{ks}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}T_{ks}A_{ks}T_{k}$	37.9	2680	2695	472
486150	$A_{ks}{}^{m}C_{ks}G_{ks}A_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}A_{ds}A_{ds}A_{ks}T_{ks}A_{k}$	45.3	2681	2696	473
486151	$G_{ks}A_{ks}{}^{m}C_{ks}G_{ds}A_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}A_{ds}A_{ks}A_{ks}T_{k}$	52.2	2682	2697	474
486152	$G_{ks}G_{ks}A_{ks}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}A_{ks}A_{ks}A_{k}$	19.8	2683	2698	475
486153	$A_{ks}G_{ks}G_{ks}A_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ks}A_{ks}A_{k}$	19.9	2684	2699	476
486154	$G_{ks}A_{ks}G_{ks}G_{ds}A_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}A_{ks}T_{ks}A_{k}$	19.6	2685	2700	477
486155	$G_{ks}G_{ks}A_{ks}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ks}A_{ks}T_{k}$	38.3	2686	2701	478
486156	${}^{m}C_{ks}G_{ks}G_{ks}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ks}A_{ks}A_{k}$	14.1	2687	2702	479
486157	$T_{ks}{}^{m}C_{ks}G_{ks}G_{ds}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}G_{ds}T_{ks}{}^{m}C_{ks}A_{k}$	23.2	2688	2703	480
486158	$G_{ks}T_{ks}{}^{m}C_{ks}G_{ds}G_{ds}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}G_{ks}T_{ks}{}^{m}C_{k}$	34.5	2689	2704	481
486159	$A_{ks}G_{ks}T_{ks}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ks}G_{ks}T_{k}$	23.7	2690	2705	482
486160	$G_{ks}A_{ks}G_{ks}T_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}G_{ds}A_{ks}G_{ks}G_{k}$	14.3	2691	2706	483
486161	${}^{m}C_{ks}G_{ks}A_{ks}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}G_{ks}A_{ks}G_{k}$	29	2692	2707	484
486162	$A_{ks}G_{ks}{}^{m}C_{ks}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}G_{ds}G_{ds}A_{ks}{}^{m}C_{ks}G_{k}$	20.6	2694	2709	485
486163	${}^{m}C_{ks}A_{ks}G_{ks}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}G_{ds}G_{ks}A_{ks}{}^{m}C_{k}$	29	2695	2710	486
486164	$T_{ks}{}^{m}C_{ks}A_{ks}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}G_{ks}G_{ks}A_{k}$	17	2696	2711	487
486165	$G_{ks}T_{ks}{}^{m}C_{ks}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ks}G_{ks}G_{k}$	14.2	2697	2712	426
486166	$T_{ks}G_{ks}T_{ks}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}G_{ks}A_{ks}G_{k}$	25.1	2698	2713	488

486167	$^{m}C_{ks}T_{ks}G_{ks}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ks}G_{ks}A_{k}$	15	2699	2714	489
486168	$^{m}C_{ks}{}^{m}C_{ks}T_{ks}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ks}G_{ks}G_{k}$	12.4	2700	2715	427
486169	$G_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}T_{ks}{}^{m}C_{ks}G_{k}$	24.5	2701	2716	428
486170	$A_{ks}G_{ks}{}^{m}C_{ks}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ks}T_{ks}{}^{m}C_{k}$	16.3	2702	2717	429
486171	$^{m}C_{ks}A_{ks}G_{ks}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}A_{ks}{}^{m}C_{ks}G_{k}$	31.8	2744	2759	490
486172	$T_{ks}{}^{m}C_{ks}A_{ks}G_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ks}A_{ks}{}^{m}C_{k}$	23.1	2745	2760	491
486173	$^{m}C_{ks}T_{ks}{}^{m}C_{ks}A_{ds}G_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ks}A_{ks}A_{k}$	23	2746	2761	492
486174	$T_{ks}{}^{m}C_{ks}T_{ks}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}A_{ks}A_{k}$	50.9	2747	2762	493
486175	$G_{ks}T_{ks}{}^{m}C_{ks}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}A_{k}$	17.2	2748	2763	494
486176	$G_{ks}G_{ks}G_{ks}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	37.6	2750	2765	430
486177	$^{m}C_{ks}A_{ks}A_{ks}T_{ds}A_{ds}A_{ds}A_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ks}G_{ks}A_{k}$	40	2772	2787	495
486178	$A_{ks}{}^{m}C_{ks}A_{ks}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ks}G_{ks}G_{k}$	11.3	2773	2788	23
486179	$A_{ks}G_{ks}A_{ks}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ks}G_{ks}A_{k}$	13.5	2775	2790	496
486180	$^{m}C_{ks}A_{ks}G_{ks}A_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}T_{ds}A_{ds}{}^{m}C_{ks}{}^{m}C_{ks}G_{k}$	18.6	2776	2791	497

Example 9: ASOs designed to target a human DMPK RNA transcript

A series of antisense oligonucleotides (ASOs) were designed to target hDMPK. The newly designed ASOs were prepared using standard oligonucleotide synthesis well known in the art and are described in Table 13 to 18, below. Subscripts “s” indicate phosphorothioate internucleoside linkages; subscripts “k” indicate 6’-*(S)*-CH_3 bicyclic nucleosides (cEt); subscripts “e” indicate 2’-O-methoxyethyl (MOE) modified nucleosides; and subscripts “d” indicate β-D-2’-deoxyribonucleosides. “^{m}C” indicates 5-methylcytosine nucleosides.

The antisense oligonucleotides targeted to a human DMPK nucleic acid were tested for their effect on DMPK RNA transcript *in vitro*. Cultured HepG2 cells at a density of 20,000 cells per well were transfected using electroporation with 4,500 nM antisense oligonucleotide. After approximately 24 hours, RNA was isolated from the cells and DMPK transcript levels were measured by quantitative real-time PCR. DMPK RNA transcript levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent expression of DMPK, relative to untreated control cells, with “% Target Expression” representing the percent expression of DMPK relative to untreated control cells

All the antisense oligonucleotides listed in Table 13 target SEQ ID NO: 1 (GENBANK Accession No. NM_001081560.1). All the antisense oligonucleotides listed in Table 14 to 18 target SEQ ID NO: 2 (the complement of GENBANK Accession No. NT_011109.15 truncated from nucleotides 18540696 to 18555106). 'Target start site' indicates the 5'-most nucleoside to which the antisense oligonucleotide is targeted in the human genomic gene sequence. 'Target stop site' indicates the 3'-most nucleoside to which the antisense oligonucleotide is targeted in the human genomic sequence.

Table13

Inhibition of human DMPK RNA transcript in HepG2 cells targeting SEQ ID NO: 1

ISIS No.	Sequence	% Target Expression	Start Site on Seq ID: 1	Stop Site on Seq ID: 1	Seq ID No.
UTC	N/A	100	N/A	N/A	
445569	${}^{m}C_{es}G_{es}G_{es}A_{es}G_{es}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{es}T_{es}G_{es}G_{es}{}^{m}C_{e}$	36.7	2163	2182	24
486178	$A_{ks}{}^{m}C_{ks}A_{ks}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ks}G_{ks}G_{k}$	21.3	2773	2788	23
569403	${}^{m}C_{ks}A_{ks}{}^{m}C_{ks}G_{ds}G_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}G_{ds}A_{ds}{}^{m}C_{ks}A_{ks}{}^{m}C_{k}$	18.8	542	557	498
569404	$T_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}G_{ds}A_{ks}{}^{m}C_{ks}A_{k}$	25.2	543	558	499
569405	${}^{m}C_{ks}T_{ks}{}^{m}C_{ks}A_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}G_{ks}A_{ks}{}^{m}C_{k}$	21.2	544	559	500
569406	${}^{m}C_{ks}{}^{m}C_{ks}T_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ks}A_{ks}G_{k}$	27.9	550	565	343
569407	$G_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ks}G_{ks}G_{k}$	30.9	553	568	501
569408	${}^{m}C_{ks}G_{ks}T_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ks}{}^{m}C_{ks}G_{k}$	32.8	554	569	502
569409	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}A_{ds}T_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}{}^{m}C_{ds}A_{ks}{}^{m}C_{ks}G_{k}$	33	568	583	503
569410	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}{}^{m}C_{ks}A_{ks}{}^{m}C_{k}$	42.1	569	584	504
569411	$T_{ks}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ks}{}^{m}C_{ks}A_{k}$	68.6	570	585	505
569412	$G_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}A_{ks}{}^{m}C_{k}$	60.7	571	586	506
569413	$G_{ks}G_{ks}T_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}A_{k}$	65.1	572	587	507
569414	${}^{m}C_{ks}G_{ks}G_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	54.4	573	588	508
569415	${}^{m}C_{ks}{}^{m}C_{ks}G_{ks}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ds}A_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	51.3	574	589	509
569416	$G_{ks}{}^{m}C_{ks}{}^{m}C_{ks}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ks}A_{ks}{}^{m}C_{k}$	57.9	575	590	510
569417	${}^{m}C_{ks}G_{ks}{}^{m}C_{ks}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ks}{}^{m}C_{ks}A_{k}$	43.2	576	591	511
569418	${}^{m}C_{ks}{}^{m}C_{ks}G_{ks}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ks}T_{ks}{}^{m}C_{k}$	79.3	577	592	512
569419	$A_{ks}{}^{m}C_{ks}{}^{m}C_{ks}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}T_{ks}T_{k}$	36	578	593	513
569420	${}^{m}C_{ks}A_{ks}{}^{m}C_{ks}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}T_{k}$	36.2	579	594	514

569421	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	34.7	580	595	515
569422	$T_{ks}{}^{m}C_{ks}{}^{m}C_{ks}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	40	581	596	516
569423	$A_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	31.6	582	597	517
569424	$G_{ks}A_{ks}T_{ks}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	56	583	598	518
569425	$T_{ks}G_{ks}A_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ks}T_{ks}{}^{m}C_{k}$	53.9	584	599	519
569426	$G_{ks}T_{ks}G_{ks}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ks}G_{ks}T_{k}$	54.1	585	600	520
569427	${}^{m}C_{ks}G_{ks}T_{ks}G_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ks}G_{ks}G_{k}$	34.8	586	601	521
569428	${}^{m}C_{ks}A_{ks}T_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}A_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}G_{ks}A_{ks}A_{k}$	71	611	626	522
569429	$T_{ks}{}^{m}C_{ks}A_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}A_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ks}G_{ks}A_{k}$	51.1	612	627	523
569430	$A_{ks}G_{ks}T_{ks}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ks}A_{ks}A_{k}$	69.2	617	632	524
569431	$T_{ks}A_{ks}G_{ks}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ks}G_{ks}A_{k}$	48.6	618	633	525
569432	$G_{ks}T_{ks}A_{ks}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}G_{ks}G_{k}$	29.6	619	634	526
569433	${}^{m}C_{ks}A_{ks}G_{ks}G_{ds}T_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}T_{ds}A_{ds}G_{ds}T_{ks}T_{ks}{}^{m}C_{k}$	36.5	628	643	527
569434	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}G_{ds}G_{ds}T_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}T_{ds}A_{ds}G_{ks}T_{ks}T_{k}$	51	629	644	528
569435	$G_{ks}A_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}T_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}T_{ks}A_{ks}G_{k}$	49.9	631	646	529
569436	${}^{m}C_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}T_{ks}A_{ks}{}^{m}C_{k}$	41	637	652	530
569437	$A_{ks}{}^{m}C_{ks}T_{ks}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ks}T_{ks}A_{k}$	32.9	638	653	531
569438	$T_{ks}A_{ks}{}^{m}C_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ks}G_{ks}T_{k}$	25.7	639	654	532
569439	$A_{ks}T_{ks}A_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}G_{ks}G_{k}$	9.4	640	655	533
569440	$A_{ks}A_{ks}T_{ks}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}G_{k}$	21.2	641	656	534
569441	$T_{ks}A_{ks}A_{ks}T_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	30.8	642	657	535
569442	$G_{ks}T_{ks}A_{ks}A_{ds}T_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}G_{ds}A_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	29.8	643	658	536
569443	${}^{m}C_{ks}G_{ks}T_{ks}A_{ds}A_{ds}T_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}G_{ks}A_{ks}{}^{m}C_{k}$	25.3	644	659	537
569444	${}^{m}C_{ks}T_{ks}T_{ks}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}G_{ks}T_{ks}{}^{m}C_{k}$	19.3	676	691	538
569445	$A_{ks}{}^{m}C_{ks}T_{ks}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ks}G_{ks}T_{k}$	35	677	692	539
569446	$A_{ks}A_{ks}{}^{m}C_{ks}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ks}T_{ks}G_{k}$	30	678	693	540
569447	$A_{ks}A_{ks}A_{ks}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ks}G_{ks}T_{k}$	32.2	679	694	344
569448	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}A_{ds}A_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ks}{}^{m}C_{ks}A_{k}$	30.1	681	696	346
569449	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}A_{ds}A_{ds}A_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	18.4	682	697	347
569450	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}A_{ks}G_{k}$	44.8	683	698	348
569451	$G_{ks}{}^{m}C_{ks}T_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ks}{}^{m}C_{ks}T_{k}$	47	686	701	541
569452	${}^{m}C_{ks}G_{ks}{}^{m}C_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}{}^{m}C_{ds}T_{ds}T_{ks}G_{ks}{}^{m}C_{k}$	35.4	687	702	542
569453	${}^{m}C_{ks}{}^{m}C_{ks}G_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}{}^{m}C_{ds}T_{ks}T_{ks}G_{k}$	46.6	688	703	543
569454	$T_{ks}{}^{m}C_{ks}{}^{m}C_{ks}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}{}^{m}C_{ks}T_{ks}T_{k}$	29.4	689	704	544

569455	$A_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ks}{}^{m}C_{ks}T_{k}$	36.9	690	705	545
569456	$A_{ks}A_{ks}T_{ks}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ks}A_{ks}{}^{m}C_{k}$	32.9	691	706	546
569457	$G_{ks}A_{ks}A_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}A_{ks}A_{k}$	41.7	692	707	547
569458	$G_{ks}G_{ks}A_{ks}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}A_{k}$	36.4	693	708	548
569459	${}^{m}C_{ks}G_{ks}G_{ks}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	30	694	709	549
569460	${}^{m}C_{ks}{}^{m}C_{ks}G_{ks}G_{ds}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	26.5	695	710	550
569461	$G_{ks}{}^{m}C_{ks}{}^{m}C_{ks}G_{ds}G_{ds}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	36.5	696	711	551
569462	$A_{ks}G_{ks}A_{ks}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	26	713	728	552
569463	$T_{ks}A_{ks}G_{ks}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ks}{}^{m}C_{ks}T_{k}$	40.3	714	729	553
569464	$G_{ks}T_{ks}A_{ks}G_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}T_{ks}{}^{m}C_{k}$	28.9	715	730	554
569465	$G_{ks}G_{ks}T_{ks}A_{ds}G_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}T_{k}$	35.7	716	731	555
569466	$A_{ks}G_{ks}G_{ks}T_{ds}A_{ds}G_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	31.1	717	732	556
569467	${}^{m}C_{ks}A_{ks}G_{ks}G_{ds}T_{ds}A_{ds}G_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}G_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	14.8	718	733	557
569468	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}G_{ds}G_{ds}T_{ds}A_{ds}G_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ks}G_{ks}{}^{m}C_{k}$	32.1	719	734	558
569469	$G_{ks}{}^{m}C_{ks}{}^{m}C_{ks}A_{ds}G_{ds}G_{ds}T_{ds}A_{ds}G_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ks}{}^{m}C_{ks}G_{k}$	54.5	720	735	559
569470	${}^{m}C_{ks}G_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}T_{ds}A_{ds}G_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ks}G_{ks}{}^{m}C_{k}$	50.5	721	736	560
569471	${}^{m}C_{ks}{}^{m}C_{ks}G_{ks}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}T_{ds}A_{ds}G_{ds}A_{ds}A_{ds}G_{ks}{}^{m}C_{ks}G_{k}$	56.6	722	737	561
569472	$T_{ks}{}^{m}C_{ks}{}^{m}C_{ks}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}T_{ds}A_{ds}G_{ds}A_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	44.1	723	738	562
569473	$G_{ks}A_{ks}{}^{m}C_{ks}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}G_{ks}G_{k}$	14.2	730	745	29
569474	$T_{ks}G_{ks}A_{ks}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}G_{k}$	25.9	731	746	563
569475	$A_{ks}T_{ks}G_{ks}A_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	28.7	732	747	564
569476	${}^{m}C_{ks}A_{ks}T_{ks}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	27.4	733	748	565
569477	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}G_{ks}{}^{m}C_{k}$	52.4	734	749	566
569478	$G_{ks}{}^{m}C_{ks}{}^{m}C_{ks}A_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}G_{k}$	50.5	735	750	567
569479	$G_{ks}G_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	48.4	736	751	568

Table 14

Inhibition of human DMPK RNA transcript in HepG2 cells targeting SEQ ID NO: 2

ISIS No.	Sequence	% Target Expression	Start Site on Seq ID: 2	Stop Site on Seq ID: 2	Seq ID No.
UTC	N/A	100	N/A	N/A	
445569	${}^{m}C_{es}G_{es}G_{es}A_{es}G_{es}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{es}T_{es}G_{es}G_{es}{}^{m}C_{e}$	31.4	13226	13245	24

486178	$A_{ks}{}^{m}C_{ks}A_{ks}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ks}G_{ks}G_{k}$	25.3	13836	13851	23
570801	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}T_{ks}A_{ks}G_{k}$	22.7	10165	10180	569
570802	$A_{ks}A_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}T_{ks}T_{k}$	22.6	10167	10182	570
570803	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}G_{ds}T_{ds}A_{ds}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ks}T_{ks}G_{k}$	37.4	10190	10205	571
570804	$G_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}A_{ds}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	24.9	10192	10207	572
570805	$G_{ks}T_{ks}T_{ks}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}A_{ds}A_{ds}T_{ds}A_{ks}A_{ks}A_{k}$	23.8	10195	10210	573
570806	$A_{ks}T_{ks}G_{ks}T_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}A_{ds}A_{ks}T_{ks}A_{k}$	21.9	10197	10212	574
570807	$T_{ks}A_{ks}A_{ks}T_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ks}A_{ks}A_{k}$	20	10199	10214	575
570808	$T_{ks}G_{ks}T_{ks}A_{ds}A_{ds}T_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}G_{ks}T_{k}$	11.5	10201	10216	31
570809	$T_{ks}T_{ks}{}^{m}C_{ks}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}{}^{m}C_{k}$	34.7	10279	10294	576
570810	$G_{ks}G_{ks}T_{ks}T_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	76.4	10281	10296	577
570811	$T_{ks}G_{ks}G_{ks}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ks}A_{ks}{}^{m}C_{k}$	72.4	10283	10298	578
570812	$G_{ks}A_{ks}T_{ks}G_{ds}G_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}G_{k}$	49	10285	10300	579
570813	$A_{ks}G_{ks}G_{ks}A_{ds}T_{ds}G_{ds}G_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	80.8	10287	10302	580
570814	$A_{ks}G_{ks}A_{ks}G_{ds}G_{ds}A_{ds}T_{ds}G_{ds}G_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}A_{ks}A_{ks}T_{k}$	43.3	10289	10304	581
570815	$A_{ks}T_{ks}A_{ks}G_{ds}A_{ds}G_{ds}G_{ds}A_{ds}T_{ds}G_{ds}G_{ds}G_{ds}T_{ds}T_{ks}{}^{m}C_{ks}A_{k}$	63.2	10291	10306	582
570816	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}G_{ds}A_{ds}A_{ks}{}^{m}C_{ks}A_{k}$	38.8	10349	10364	583
570817	$G_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}G_{ks}A_{ks}A_{k}$	91	10351	10366	584
570818	${}^{m}C_{ks}A_{ks}G_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}G_{ks}G_{ks}G_{k}$	64.8	10353	10368	585
570819	$A_{ks}G_{ks}{}^{m}C_{ks}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ks}T_{ks}G_{k}$	28.5	10355	10370	586
570820	$A_{ks}{}^{m}C_{ks}T_{ks}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}G_{ds}A_{ks}A_{ks}G_{k}$	62.9	10417	10432	587
570821	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}G_{ks}G_{ks}G_{k}$	79.9	10420	10435	588
570822	$A_{ks}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ks}T_{ks}G_{k}$	47.5	10422	10437	589
570823	$A_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ks}T_{ks}G_{k}$	78.1	10424	10439	590
570824	$G_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	82.5	10426	10441	591
570825	$T_{ks}{}^{m}C_{ks}A_{ks}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	52.6	10429	10444	592
570826	$G_{ks}T_{ks}G_{ks}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}A_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}T_{ks}G_{ks}G_{k}$	30.9	10474	10489	593
570827	$G_{ks}A_{ks}T_{ks}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}A_{ds}A_{ds}G_{ks}A_{ks}{}^{m}C_{k}$	25.5	10477	10492	594
570828	${}^{m}C_{ks}A_{ks}G_{ks}A_{ds}T_{ds}G_{ds}T_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}A_{ks}A_{ks}G_{k}$	18.6	10479	10494	595
570829	${}^{m}C_{ks}{}^{m}C_{ks}T_{ks}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}T_{ds}G_{ds}T_{ds}G_{ks}G_{ks}T_{k}$	44.5	10485	10500	596
570830	${}^{m}C_{ks}A_{ks}{}^{m}C_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}T_{ds}G_{ks}T_{ks}G_{k}$	67.4	10487	10502	597
570831	$G_{ks}G_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ks}A_{ks}T_{k}$	56.3	10490	10505	598
570832	$T_{ks}G_{ks}{}^{m}C_{ks}T_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	42.4	10501	10516	599
570833	$A_{ks}{}^{m}C_{ks}T_{ks}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ks}G_{ks}{}^{m}C_{k}$	16	10503	10518	600

570834	$A_{ks}G_{ks}A_{ks}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}T_{ks}G_{k}$	47.5	10505	10520	601
570835	$G_{ks}G_{ks}A_{ks}G_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	37.2	10507	10522	602
570836	$T_{ks}G_{ks}{}^{m}C_{ks}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}T_{ks}{}^{m}C_{ks}T_{k}$	63.1	10556	10571	603
570837	${}^{m}C_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ks}T_{ks}G_{k}$	60.7	10579	10594	604
570838	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}G_{ds}T_{ks}T_{ks}{}^{m}C_{k}$	42.9	10609	10624	605
570839	$G_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ks}G_{ks}T_{k}$	64.3	10611	10626	606
570840	$G_{ks}G_{ks}G_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}T_{k}$	68.5	10613	10628	607
570841	$A_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}G_{ds}A_{ks}{}^{m}C_{ks}T_{k}$	14.9	10631	10646	608
570842	$T_{ks}A_{ks}A_{ks}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ks}G_{ks}G_{k}$	51.7	10634	10649	609
570843	$G_{ks}A_{ks}A_{ks}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}T_{k}$	46.3	10684	10699	610
570844	$T_{ks}A_{ks}G_{ks}G_{ds}A_{ds}A_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	52.3	10687	10702	611
570845	${}^{m}C_{ks}T_{ks}T_{ks}A_{ds}G_{ds}G_{ds}A_{ds}A_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}G_{k}$	53.8	10689	10704	612
570846	$T_{ks}G_{ks}{}^{m}C_{ks}T_{ds}T_{ds}A_{ds}G_{ds}G_{ds}A_{ds}A_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	47.8	10691	10706	613
570847	$T_{ks}{}^{m}C_{ks}T_{ks}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}A_{ds}G_{ds}G_{ds}A_{ds}A_{ds}A_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	43.9	10693	10708	614
570848	${}^{m}C_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}A_{ds}G_{ds}G_{ks}A_{ks}A_{k}$	67.9	10697	10712	615
570849	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}A_{ks}G_{ks}G_{k}$	50.8	10699	10714	616
570850	${}^{m}C_{ks}T_{ks}G_{ks}A_{ds}T_{ds}T_{ds}T_{ds}G_{ds}A_{ds}G_{ds}G_{ds}A_{ds}A_{ds}G_{ks}G_{ks}G_{k}$	41.1	10759	10774	617
570851	$T_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}G_{ds}A_{ds}T_{ds}T_{ds}T_{ds}G_{ds}A_{ds}G_{ds}G_{ds}A_{ks}A_{ks}G_{k}$	87.4	10761	10776	618
570852	${}^{m}C_{ks}{}^{m}C_{ks}T_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}T_{ds}T_{ds}T_{ds}G_{ds}A_{ds}G_{ks}G_{ks}A_{k}$	75.8	10763	10778	619
570853	$G_{ks}A_{ks}{}^{m}C_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}T_{ds}T_{ds}T_{ds}G_{ks}A_{ks}G_{k}$	87.4	10765	10780	620
570854	$A_{ks}A_{ks}G_{ks}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}T_{ds}T_{ks}T_{ks}G_{k}$	60.3	10767	10782	621
570855	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ks}T_{ks}T_{k}$	61.4	10769	10784	622
570856	${}^{m}C_{ks}T_{ks}G_{ks}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	40.4	10775	10790	623
570857	$A_{ks}G_{ks}{}^{m}C_{ks}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}G_{ds}A_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	48.5	10777	10792	624
570858	$G_{ks}{}^{m}C_{ks}A_{ks}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ks}G_{ks}A_{k}$	87.7	10779	10794	625
570859	${}^{m}C_{ks}T_{ks}G_{ks}G_{ds}T_{ds}G_{ds}G_{ds}A_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}G_{ks}A_{k}$	92.6	10816	10831	626
570860	${}^{m}C_{ks}T_{ks}{}^{m}C_{ks}T_{ds}G_{ds}G_{ds}T_{ds}G_{ds}G_{ds}A_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	86.6	10818	10833	627
570861	$T_{ks}T_{ks}{}^{m}C_{ks}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}T_{ds}G_{ds}G_{ds}A_{ds}G_{ds}A_{ks}A_{ks}{}^{m}C_{k}$	82.6	10820	10835	628
570862	$G_{ks}A_{ks}T_{ks}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}T_{ds}G_{ds}G_{ds}A_{ks}G_{ks}A_{k}$	76.1	10822	10837	629
570863	$A_{ks}{}^{m}C_{ks}T_{ks}T_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}T_{ds}T_{ds}{}^{m}C_{ds}A_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	80.6	10981	10996	630
570864	${}^{m}C_{ks}G_{ks}G_{ks}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	58.7	11002	11017	631
570865	$G_{ks}A_{ks}{}^{m}C_{ks}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	61.5	11004	11019	632
570866	${}^{m}C_{ks}T_{ks}G_{ks}A_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	47.6	11006	11021	633
570867	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}T_{k}$	69.5	11008	11023	634

570868	$A_{ks}A_{ks}G_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}T_{ks}T_{ks}{}^{m}C_{k}$	54	11036	11051	635
570869	$G_{ks}G_{ks}A_{ks}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}T_{ks}T_{k}$	37.5	11038	11053	636
570870	${}^{m}C_{ks}G_{ks}G_{ks}G_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ks}{}^{m}C_{ks}T_{k}$	70.7	11040	11055	637
570871	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}G_{ds}G_{ds}G_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}A_{ks}{}^{m}C_{k}$	71.2	11042	11057	638
570872	${}^{m}C_{ks}A_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ds}G_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	51.6	11044	11059	639
570873	$G_{ks}{}^{m}C_{ks}{}^{m}C_{ks}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ds}G_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	45.8	11046	11061	640
570874	$A_{ks}{}^{m}C_{ks}G_{ks}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ds}G_{ds}A_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	31.8	11048	11063	641
570875	${}^{m}C_{ks}T_{ks}G_{ks}T_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}A_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	14.3	11082	11097	642
570876	$T_{ks}T_{ks}{}^{m}C_{ks}T_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}A_{ds}A_{ds}G_{ks}T_{ks}{}^{m}C_{k}$	18	11084	11099	643
570877	$G_{ks}{}^{m}C_{ks}T_{ks}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}A_{ks}A_{ks}G_{k}$	44	11086	11101	644

Table 15

Inhibition of human DMPK RNA transcript in HepG2 cells targeting SEQ ID NO: 2

ISIS No.	Sequence	% Target Expression	Start Site on Seq ID: 2	Stop Site on Seq ID: 2	Seq ID No.
UTC	N/A	100	N/A	N/A	
445569	${}^{m}C_{es}G_{es}G_{es}A_{es}G_{es}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{es}T_{es}G_{es}G_{es}{}^{m}C_{e}$	55	13226	13245	24
486178	$A_{ks}{}^{m}C_{ks}A_{ks}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ks}G_{ks}G_{k}$	33.9	13836	13851	23
570647	$G_{ks}{}^{m}C_{ks}T_{ks}T_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}T_{k}$	80.3	5718	5733	645
570648	$A_{ks}G_{ks}G_{ks}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	92.3	5720	5735	646
570649	${}^{m}C_{ks}G_{ks}A_{ks}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}{}^{m}C_{k}$	100.7	5722	5737	647
570650	$A_{ks}G_{ks}{}^{m}C_{ks}G_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	75.8	5724	5739	648
570651	$A_{ks}G_{ks}A_{ks}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}G_{ks}G_{ks}{}^{m}C_{k}$	99.8	5726	5741	649
570652	$G_{ks}{}^{m}C_{ks}A_{ks}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ks}G_{ks}G_{k}$	135.4	5728	5743	650
570653	$G_{ks}A_{ks}G_{ks}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ks}T_{ks}T_{k}$	111.5	5730	5745	651
570654	$A_{ks}A_{ks}A_{ks}G_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ks}A_{ks}G_{k}$	87.5	5734	5749	652
570655	${}^{m}C_{ks}A_{ks}A_{ks}A_{ds}A_{ds}G_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}G_{ks}{}^{m}C_{ks}G_{k}$	94.5	5736	5751	653
570656	$T_{ks}G_{ks}G_{ks}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}A_{ds}G_{ds}G_{ds}A_{ds}G_{ks}{}^{m}C_{ks}A_{k}$	75.4	5741	5756	654
570657	${}^{m}C_{ks}{}^{m}C_{ks}T_{ks}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}A_{ds}G_{ds}G_{ks}A_{ks}G_{k}$	87.3	5743	5758	655
570658	${}^{m}C_{ks}A_{ks}{}^{m}C_{ks}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}A_{ks}G_{ks}G_{k}$	93.2	5745	5760	656
570659	${}^{m}C_{ks}G_{ks}{}^{m}C_{ks}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ks}A_{ks}A_{k}$	70	5747	5762	657
570660	$G_{ks}A_{ks}{}^{m}C_{ks}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	46.4	5750	5765	658

570661	$A_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}T_{ds}G_{ds}T_{ds}A_{ds}G_{ds}T_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ks}G_{ks}A_{k}$	44	5951	5966	659
570662	$T_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}T_{ds}A_{ds}G_{ds}T_{ds}G_{ds}G_{ks}A_{ks}{}^{m}C_{k}$	76.8	5953	5968	660
570663	$G_{ks}{}^{m}C_{ks}T_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}T_{ds}A_{ds}G_{ds}T_{ks}G_{ks}G_{k}$	69.5	5955	5970	661
570664	$G_{ks}G_{ks}A_{ks}G_{ds}A_{ds}G_{ds}G_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}T_{ks}A_{ks}G_{k}$	88.2	6015	6030	662
570665	$A_{ks}G_{ks}G_{ks}G_{ds}A_{ds}G_{ds}A_{ds}G_{ds}G_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}G_{ks}A_{ks}T_{k}$	96.9	6017	6032	663
570666	${}^{m}C_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}G_{ds}G_{ks}G_{ks}A_{k}$	74.7	6028	6043	664
570667	$G_{ks}T_{ks}G_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ks}A_{ks}G_{k}$	77.5	6031	6046	665
570668	$A_{ks}G_{ks}G_{ks}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}A_{ks}G_{k}$	76.7	6033	6048	666
570669	$A_{ks}G_{ks}A_{ks}G_{ds}G_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	43.3	6035	6050	667
570670	$A_{ks}G_{ks}A_{ks}G_{ds}A_{ds}G_{ds}G_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}G_{ks}{}^{m}C_{k}$	27.1	6037	6052	668
570671	$A_{ks}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}A_{k}$	42.6	6291	6306	669
570672	${}^{m}C_{ks}T_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ks}{}^{m}C_{ks}T_{k}$	44.9	6293	6308	670
570673	$A_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}G_{k}$	36.6	6295	6310	671
570674	$G_{ks}T_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	52	6297	6312	672
570675	$A_{ks}G_{ks}G_{ks}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	56.4	6299	6314	673
570676	$G_{ks}G_{ks}G_{ks}A_{ds}G_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	51.4	6329	6344	674
570677	$G_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}T_{ds}T_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}{}^{m}C_{ks}T_{ks}T_{k}$	28	6360	6375	675
570678	${}^{m}C_{ks}T_{ks}G_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}A_{ks}{}^{m}C_{k}$	33.6	6362	6377	676
570679	${}^{m}C_{ks}A_{ks}{}^{m}C_{ks}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	7.9	6364	6379	677
570680	$G_{ks}G_{ks}{}^{m}C_{ks}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}A_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	20.2	6366	6381	678
570681	$T_{ks}A_{ks}G_{ks}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ks}A_{ks}{}^{m}C_{k}$	38.3	6368	6383	679
570682	$G_{ks}G_{ks}T_{ks}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}T_{k}$	13.9	6370	6385	680
570683	$G_{ks}T_{ks}{}^{m}C_{ks}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}T_{k}$	29	6445	6460	681
570684	$G_{ks}G_{ks}T_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}G_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	21.3	6446	6461	43
570685	$A_{ks}G_{ks}G_{ks}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}G_{ks}T_{ks}{}^{m}C_{k}$	16.9	6447	6462	682
570686	${}^{m}C_{ks}T_{ks}A_{ks}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ks}G_{ks}G_{k}$	19.6	6449	6464	683
570687	$G_{ks}T_{ks}{}^{m}C_{ks}T_{ds}A_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ks}T_{ks}G_{k}$	15.7	6451	6466	684
570688	$A_{ks}A_{ks}G_{ks}T_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ks}G_{ks}{}^{m}C_{k}$	16.6	6453	6468	685
570689	$G_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}A_{k}$	13.2	6530	6545	686
570690	${}^{m}C_{ks}T_{ks}G_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}G_{ds}T_{ks}{}^{m}C_{ks}T_{k}$	50.1	6532	6547	687
570691	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ks}G_{ks}T_{k}$	48.4	6534	6549	688
570692	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}T_{ks}T_{k}$	74	6536	6551	689
570693	${}^{m}C_{ks}T_{ks}T_{ks}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ks}A_{ks}G_{k}$	25.3	6559	6574	690
570694	$T_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ks}G_{ks}G_{k}$	39.5	6561	6576	691

570695	${}^{m}C_{ks}T_{ks}T_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ks}{}^{m}C_{ks}A_{k}$	22.9	6563	6578	692
570696	$A_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ks}G_{ks}T_{k}$	52.5	6565	6580	693
570697	$G_{ks}G_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ks}G_{ks}A_{k}$	37.6	6567	6582	694
570698	${}^{m}C_{ks}A_{ks}G_{ks}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ks}{}^{m}C_{ks}T_{k}$	44.2	6569	6584	695
570699	$A_{ks}G_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}T_{k}$	26.6	6576	6591	696
570700	$T_{ks}A_{ks}G_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}G_{k}$	33.6	6594	6609	697
570701	$G_{ks}A_{ks}T_{ks}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	20.4	6596	6611	698
570702	${}^{m}C_{ks}A_{ks}G_{ks}A_{ds}T_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}{}^{m}C_{ks}T_{k}$	33.8	6598	6613	699
570703	${}^{m}C_{ks}T_{ks}{}^{m}C_{ks}A_{ds}G_{ds}A_{ds}T_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	25.8	6600	6615	700
570704	$A_{ks}G_{ks}{}^{m}C_{ks}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}T_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	29.1	6602	6617	701
570705	$T_{ks}{}^{m}C_{ks}A_{ks}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}T_{ds}A_{ds}G_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	47.4	6604	6619	702
570706	$T_{ks}{}^{m}C_{ks}T_{ks}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}T_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	33.4	6606	6621	703
570707	$G_{ks}A_{ks}G_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ks}T_{ks}T_{k}$	49	6636	6651	704
570708	$G_{ks}G_{ks}A_{ks}G_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}T_{k}$	79.2	6640	6655	705
570709	$G_{ks}A_{ks}G_{ks}G_{ds}A_{ds}G_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	63.3	6642	6657	706
570710	${}^{m}C_{ks}A_{ks}A_{ks}A_{ds}A_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}G_{ks}A_{k}$	38.8	6713	6728	707
570711	$A_{ks}G_{ks}{}^{m}C_{ks}A_{ds}A_{ds}A_{ds}A_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	13.7	6715	6730	708
570712	$G_{ks}G_{ks}A_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}A_{ds}T_{ds}T_{ks}G_{ks}T_{k}$	45.8	6733	6748	709
570713	${}^{m}C_{ks}T_{ks}G_{ks}G_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}A_{ks}T_{ks}T_{k}$	45.6	6735	6750	710
570714	$T_{ks}G_{ks}{}^{m}C_{ks}T_{ds}G_{ds}G_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ks}T_{ks}A_{k}$	43.6	6737	6752	711
570715	$A_{ks}T_{ks}T_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ks}A_{ks}A_{k}$	18.3	6789	6804	712
570716	$T_{ks}A_{ks}A_{ks}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}T_{ks}G_{ks}{}^{m}C_{k}$	15.1	6791	6806	713
570717	$T_{ks}{}^{m}C_{ks}T_{ks}A_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}A_{ks}{}^{m}C_{ks}T_{k}$	49.9	6793	6808	714
570718	$T_{ks}{}^{m}C_{ks}T_{ks}{}^{m}C_{ds}T_{ds}A_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}A_{ks}G_{ks}A_{k}$	77.6	6795	6810	715
570719	${}^{m}C_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}T_{ds}A_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ks}A_{ks}A_{k}$	42	6804	6819	716
570720	$A_{ks}{}^{m}C_{ks}T_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}A_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	28.5	6807	6822	717
570721	$A_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}A_{ds}A_{ds}T_{ks}T_{ks}{}^{m}C_{k}$	27.4	6809	6824	718
570722	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}A_{ks}A_{ks}T_{k}$	35.4	6811	6826	719
570723	$T_{ks}G_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}T_{ks}A_{k}$	45	6813	6828	720

Table 16

Inhibition of human DMPK RNA transcript in HepG2 cells targeting SEQ ID NO: 2

ISIS No.	Sequence	% Target Expression	Start Site on Seq ID: 2	Stop Site on Seq ID: 2	Seq ID No.
UTC	N/A	100	N/A	N/A	
445569	${}^{m}C_{es}G_{es}G_{es}A_{es}G_{es}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{es}T_{es}G_{es}G_{es}{}^{m}C_{e}$	33.9	13226	13245	24
486178	$A_{ks}{}^{m}C_{ks}A_{ks}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ks}G_{ks}G_{k}$	21.5	13836	13851	23
570339	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}A_{ds}T_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}G_{ks}{}^{m}C_{k}$	56.2	1534	1549	721
570340	$G_{ks}G_{ks}A_{ks}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}G_{ds}A_{ds}A_{ds}A_{ds}T_{ds}G_{ds}T_{ks}T_{ks}G_{k}$	46.7	1597	1612	722
570341	$G_{ks}G_{ks}{}^{m}C_{ks}A_{ds}T_{ds}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}G_{ks}A_{ks}A_{k}$	35.6	1603	1618	723
570342	$G_{ks}T_{ks}G_{ks}G_{ds}{}^{m}C_{ds}A_{ds}T_{ds}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}G_{ks}A_{ks}G_{k}$	34.8	1605	1620	724
570343	$T_{ks}G_{ks}G_{ks}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}T_{ds}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ks}A_{ks}G_{k}$	60.3	1607	1622	725
570344	${}^{m}C_{ks}T_{ks}T_{ks}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	49.6	1627	1642	726
570345	$A_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}T_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}T_{k}$	48.6	1629	1644	727
570346	$T_{ks}G_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	36.8	1631	1646	728
570347	$G_{ks}{}^{m}C_{ks}T_{ks}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ks}G_{ks}{}^{m}C_{k}$	53.5	1633	1648	729
570348	${}^{m}C_{ks}T_{ks}G_{ks}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}A_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}T_{k}$	59	1635	1650	730
570349	${}^{m}C_{ks}T_{ks}{}^{m}C_{ks}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}A_{ks}{}^{m}C_{ks}T_{k}$	70.8	1637	1652	731
570350	$G_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}T_{ks}A_{k}$	54	1639	1654	732
570351	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ks}{}^{m}C_{ks}A_{k}$	52.6	1666	1681	733
570352	$A_{ks}G_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ks}G_{ks}T_{k}$	60.7	1668	1683	734
570353	$T_{ks}A_{ks}A_{ks}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ks}G_{ks}A_{k}$	82.3	1670	1685	735
570354	$T_{ks}A_{ks}G_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	40.8	1687	1702	736
570355	$A_{ks}T_{ks}G_{ks}G_{ds}G_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}T_{ds}G_{ks}G_{ks}{}^{m}C_{k}$	90.7	1707	1722	737
570356	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}T_{ds}G_{ds}G_{ds}G_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ks}T_{ks}G_{k}$	73.9	1709	1724	738
570357	$G_{ks}G_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}T_{ds}G_{ds}G_{ds}G_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ks}G_{ks}T_{k}$	94.9	1711	1726	739
570358	$G_{ks}T_{ks}G_{ks}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}G_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}T_{ks}G_{k}$	73.5	1720	1735	740
570359	$G_{ks}A_{ks}G_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}T_{ds}G_{ks}A_{ks}{}^{m}C_{k}$	70.2	1759	1774	741
570360	$A_{ks}G_{ks}G_{ks}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ks}A_{ks}T_{k}$	56.1	1762	1777	742
570361	$G_{ks}{}^{m}C_{ks}{}^{m}C_{ks}A_{ds}T_{ds}A_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ks}T_{ks}T_{k}$	54.9	1799	1814	743
570362	$G_{ks}G_{ks}G_{ks}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}A_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}{}^{m}C_{k}$	78.1	1801	1816	744
570363	$A_{ks}T_{ks}G_{ks}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}G_{ks}G_{k}$	76.2	1848	1863	745
570364	$A_{ks}G_{ks}{}^{m}C_{ks}T_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ks}G_{ks}G_{k}$	92.6	1857	1872	746
570365	${}^{m}C_{ks}G_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ks}G_{ks}{}^{m}C_{k}$	73.6	1867	1882	747
570366	$T_{ks}G_{ks}{}^{m}C_{ks}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ks}{}^{m}C_{ks}T_{k}$	76.6	1869	1884	748
570367	$G_{ks}{}^{m}C_{ks}T_{ks}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ks}A_{ks}G_{k}$	79.1	1871	1886	749

570368	${}^{m}C_{ks}G_{ks}G_{ks}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ks}G_{ks}{}^{m}C_{k}$	82.9	1873	1888	750
570369	$G_{ks}T_{ks}{}^{m}C_{ks}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}G_{k}$	47.5	1875	1890	751
570370	${}^{m}C_{ks}T_{ks}G_{ks}T_{ds}{}^{m}C_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	79.6	1877	1892	752
570371	$G_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}G_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	58.4	1879	1894	753
570372	${}^{m}C_{ks}T_{ks}G_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ks}{}^{m}C_{ks}G_{k}$	49.9	1881	1896	754
570373	$A_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ds}G_{ds}{}^{m}C_{ks}T_{ks}G_{k}$	27.4	1883	1898	755
570374	$A_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}G_{ks}G_{ks}{}^{m}C_{k}$	54.3	1885	1900	756
570375	$G_{ks}A_{ks}A_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ks}{}^{m}C_{ks}G_{k}$	50.5	1887	1902	757
570376	${}^{m}C_{ks}{}^{m}C_{ks}G_{ks}A_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}G_{ks}T_{k}$	57.7	1889	1904	758
570377	${}^{m}C_{ks}G_{ks}{}^{m}C_{ks}{}^{m}C_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ks}{}^{m}C_{ks}T_{k}$	69.3	1891	1906	759
570378	${}^{m}C_{ks}{}^{m}C_{ks}T_{ks}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}T_{ks}G_{ks}G_{k}$	188.2	1925	1940	760
570379	$G_{ks}T_{ks}G_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}G_{ks}T_{k}$	111.5	1928	1943	761
570380	${}^{m}C_{ks}G_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}G_{ds}{}^{m}C_{ks}{}^{m}C_{ks}T_{k}$	78	1938	1953	762
570381	$A_{ks}{}^{m}C_{ks}{}^{m}C_{ks}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ks}G_{ks}{}^{m}C_{k}$	74.9	1940	1955	763
570382	$T_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}G_{ks}T_{k}$	71.6	1942	1957	764
570383	$A_{ks}G_{ks}T_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	62.1	1944	1959	765
570384	$T_{ks}G_{ks}A_{ks}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	65.6	1946	1961	766
570385	${}^{m}C_{ks}G_{ks}T_{ks}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}T_{k}$	37.3	1948	1963	767
570386	${}^{m}C_{ks}A_{ks}A_{ks}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	30.5	1974	1989	768
570387	$T_{ks}G_{ks}{}^{m}C_{ks}A_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	35.8	1976	1991	769
570388	$T_{ks}{}^{m}C_{ks}T_{ks}G_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}T_{ks}T_{ks}{}^{m}C_{k}$	30.1	1978	1993	770
570389	$T_{ks}G_{ks}T_{ks}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ks}G_{ks}T_{k}$	50.1	1980	1995	771
570390	${}^{m}C_{ks}{}^{m}C_{ks}T_{ks}G_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ks}T_{ks}G_{k}$	36	1982	1997	772
570391	${}^{m}C_{ks}G_{ks}{}^{m}C_{ks}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	31.1	1984	1999	773
570392	$T_{ks}T_{ks}G_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}A_{ks}T_{ks}{}^{m}C_{k}$	62.9	2022	2037	774
570393	$A_{ks}G_{ks}T_{ks}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ks}G_{ks}A_{k}$	57.1	2024	2039	775
570394	$A_{ks}A_{ks}A_{ks}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}G_{k}$	56.2	2026	2041	776
570395	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}A_{ds}A_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	48.9	2028	2043	777
570396	$A_{ks}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}T_{k}$	59.9	2030	2045	778
570397	$G_{ks}A_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	47.9	2032	2047	779
570398	$G_{ks}A_{ks}A_{ks}G_{ds}A_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}G_{ds}T_{ks}T_{ks}G_{k}$	60	2035	2050	780
570399	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}G_{ds}A_{ds}A_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ks}A_{ks}G_{k}$	51.2	2038	2053	781
570400	${}^{m}C_{ks}A_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}A_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	51.1	2041	2056	782
570401	$G_{ks}{}^{m}C_{ks}A_{ks}G_{ds}A_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}A_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ks}A_{ks}G_{k}$	44.9	2066	2081	783

570402	$G_{ks}T_{ks}G_{ks}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}A_{ds}{}^{m}C_{ds}A_{ks}A_{ks}A_{k}$	53	2068	2083	784
570403	$G_{ks}G_{ks}G_{ks}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}A_{ks}{}^{m}C_{ks}A_{k}$	51.5	2070	2085	785
570404	$G_{ks}T_{ks}G_{ks}G_{ds}G_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}A_{k}$	57.4	2072	2087	786
570405	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}T_{ds}A_{ks}G_{ks}G_{k}$	54.3	2116	2131	787
570406	$A_{ks}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ks}T_{ks}A_{k}$	43.6	2118	2133	788
570407	$T_{ks}G_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}A_{k}$	44	2120	2135	789
570408	$G_{ks}{}^{m}C_{ks}T_{ks}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}G_{ds}G_{ks}{}^{m}C_{ks}T_{k}$	56.5	2122	2137	790
570409	$T_{ks}G_{ks}G_{ks}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ks}G_{ks}G_{k}$	54.8	2124	2139	791
570410	$G_{ks}G_{ks}T_{ks}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ks}A_{ks}{}^{m}C_{k}$	46.8	2126	2141	792
570411	$A_{ks}T_{ks}G_{ks}G_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}{}^{m}C_{k}$	73.8	2128	2143	793
570412	$G_{ks}A_{ks}A_{ks}T_{ds}G_{ds}G_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	43.5	2130	2145	794
570413	${}^{m}C_{ks}T_{ks}A_{ks}A_{ds}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ks}G_{ks}A_{k}$	54.4	2159	2174	795
570414	$A_{ks}A_{ks}{}^{m}C_{ks}T_{ds}A_{ds}A_{ds}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}A_{ks}G_{ks}G_{k}$	49.1	2161	2176	796
570415	$G_{ks}A_{ks}G_{ks}A_{ds}A_{ds}{}^{m}C_{ds}T_{ds}A_{ds}A_{ds}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ks}G_{ks}{}^{m}C_{k}$	35.4	2164	2179	797

Table 17

Inhibition of human DMPK RNA transcript in HepG2 cells targeting SEQ ID NO: 2

ISIS No.	Sequence	% Target Expression	Start Site on Seq ID: 2	Stop Site on Seq ID: 2	Seq ID No.
UTC	N/A	100	N/A	N/A	
445569	${}^{m}C_{es}G_{es}G_{es}A_{es}G_{es}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{es}T_{es}G_{es}G_{es}{}^{m}C_{e}$	41.4	13226	13245	24
486178	$A_{ks}{}^{m}C_{ks}A_{ks}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ks}G_{ks}G_{k}$	24	13836	13851	23
570493	$A_{ks}T_{ks}T_{ks}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	112.1	3973	3988	798
570494	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}T_{ds}T_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}G_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	91.3	3975	3990	799
570495	$G_{ks}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}A_{ks}G_{k}$	103.4	3977	3992	800
570496	$A_{ks}{}^{m}C_{ks}G_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	67.8	3979	3994	801
570497	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}G_{ds}G_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	77.3	3981	3996	802
570498	${}^{m}C_{ks}A_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}G_{ks}G_{ks}T_{k}$	98.3	3983	3998	803
570499	$A_{ks}G_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	63.7	4036	4051	804
570500	$T_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}T_{ks}T_{k}$	43	4181	4196	805
570501	${}^{m}C_{ks}{}^{m}C_{ks}T_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	38.1	4183	4198	806
570502	$A_{ks}G_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}G_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	85.4	4187	4202	807

570503	${}^{m}C_{ks}T_{ks}{}^{m}C_{ks}A_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}{}^{m}C_{ks}G_{k}$	115.8	4210	4225	808
570504	$A_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	114.5	4213	4228	809
570505	$G_{ks}G_{ks}A_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	88.1	4215	4230	810
570506	$G_{ks}{}^{m}C_{ks}G_{ks}G_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}G_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	93.1	4217	4232	811
570507	$G_{ks}{}^{m}C_{ks}G_{ks}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}A_{ks}A_{ks}G_{k}$	102.9	4219	4234	812
570508	$G_{ks}G_{ks}G_{ks}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}A_{ks}A_{k}$	78.5	4221	4236	813
570509	$G_{ks}A_{ks}G_{ks}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ks}G_{ks}A_{k}$	192.2	4239	4254	814
570510	$A_{ks}G_{ks}G_{ks}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ks}G_{ks}A_{k}$	219.8	4241	4256	815
570511	${}^{m}C_{ks}G_{ks}G_{ks}A_{ds}G_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	128.6	4244	4259	816
570512	$A_{ks}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}G_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ks}{}^{m}C_{ks}A_{k}$	89.9	4247	4262	817
570513	$G_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}G_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ks}T_{ks}G_{k}$	96.1	4249	4264	818
570514	$G_{ks}G_{ks}G_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}G_{ds}G_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	67.8	4251	4266	819
570515	${}^{m}C_{ks}A_{ks}G_{ks}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}G_{ks}G_{ks}A_{k}$	64.2	4253	4268	820
570516	$T_{ks}G_{ks}{}^{m}C_{ks}A_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}G_{ks}A_{ks}G_{k}$	62.2	4255	4270	821
570517	${}^{m}C_{ks}{}^{m}C_{ks}T_{ks}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}G_{ks}G_{k}$	77.7	4257	4272	822
570518	${}^{m}C_{ks}G_{ks}A_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}G_{ks}{}^{m}C_{ks}A_{k}$	79	4262	4277	823
570519	${}^{m}C_{ks}A_{ks}{}^{m}C_{ks}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ks}G_{ks}G_{k}$	68.5	4264	4279	824
570520	$A_{ks}G_{ks}{}^{m}C_{ks}A_{ds}{}^{m}C_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ks}A_{ks}G_{k}$	39.8	4266	4281	825
570521	$G_{ks}A_{ks}A_{ks}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}G_{ks}{}^{m}C_{k}$	32.4	4268	4283	826
570522	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}G_{ds}G_{ds}T_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ks}T_{ks}{}^{m}C_{k}$	41	4353	4368	827
570523	${}^{m}C_{ks}A_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}T_{ds}A_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}A_{k}$	71.9	4355	4370	828
570524	${}^{m}C_{ks}T_{ks}{}^{m}C_{ks}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}T_{ds}A_{ds}G_{ds}T_{ds}T_{ks}{}^{m}C_{ks}T_{k}$	105.9	4357	4372	829
570525	$A_{ks}G_{ks}{}^{m}C_{ks}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}T_{ds}A_{ds}G_{ks}T_{ks}T_{k}$	99.3	4359	4374	830
570526	$G_{ks}G_{ks}A_{ks}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}T_{ks}A_{ks}G_{k}$	85.2	4361	4376	831
570527	${}^{m}C_{ks}{}^{m}C_{ks}G_{ks}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ks}G_{ks}T_{k}$	82.5	4363	4378	832
570528	$G_{ks}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ds}G_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}G_{k}$	60.5	4365	4380	833
570529	$T_{ks}A_{ks}G_{ks}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	35.4	4435	4450	834
570530	${}^{m}C_{ks}{}^{m}C_{ks}T_{ks}A_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	29.4	4437	4452	835
570531	$A_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	30.4	4439	4454	836
570532	${}^{m}C_{ks}A_{ks}A_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	30.3	4441	4456	837
570533	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ks}T_{ks}T_{k}$	54.1	4443	4458	838
570534	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	60.1	4445	4460	839
570535	${}^{m}C_{ks}A_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}A_{ks}G_{ks}A_{k}$	68.5	4447	4462	840
570536	$A_{ks}G_{ks}{}^{m}C_{ks}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}A_{k}$	37.5	4449	4464	841

570537	$G_{ks}{}^{m}C_{ks}A_{ks}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	50.9	4451	4466	842
570538	$G_{ks}G_{ks}G_{ks}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}A_{ks}T_{k}$	67.7	4453	4468	843
570539	$T_{ks}G_{ks}A_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}T_{ks}A_{ks}{}^{m}C_{k}$	55.9	4498	4513	844
570540	${}^{m}C_{ks}{}^{m}C_{ks}T_{ks}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}T_{ks}T_{k}$	45.1	4500	4515	845
570541	${}^{m}C_{ks}A_{ks}{}^{m}C_{ks}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	30.9	4502	4517	846
570542	$T_{ks}{}^{m}C_{ks}{}^{m}C_{ks}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	35	4504	4519	847
570543	${}^{m}C_{ks}A_{ks}T_{ks}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ks}A_{ks}{}^{m}C_{k}$	48	4506	4521	848
570544	${}^{m}C_{ks}T_{ks}{}^{m}C_{ks}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}{}^{m}C_{ks}A_{ks}{}^{m}C_{k}$	37.1	4508	4523	849
570545	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}{}^{m}C_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ks}A_{ks}{}^{m}C_{k}$	46	4510	4525	850
570546	$G_{ks}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}G_{k}$	79.2	4512	4527	851
570547	$A_{ks}G_{ks}G_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	40.7	4514	4529	852
570548	$G_{ks}A_{ks}A_{ks}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	35.9	4516	4531	853
570549	$A_{ks}G_{ks}G_{ks}T_{ds}A_{ds}A_{ds}G_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	18.8	4613	4628	854
570550	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}G_{ds}G_{ds}T_{ds}A_{ds}A_{ds}G_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	16.2	4615	4630	855
570551	$T_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}T_{ds}A_{ds}A_{ds}G_{ds}A_{ds}G_{ds}A_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	38.9	4617	4632	856
570552	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}T_{ds}A_{ds}A_{ds}G_{ks}A_{ks}G_{k}$	28.6	4620	4635	857
570553	$T_{ks}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}T_{ds}A_{ks}A_{ks}G_{k}$	42.6	4622	4637	858
570554	$T_{ks}A_{ks}T_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ks}T_{ks}A_{k}$	31.8	4624	4639	859
570555	${}^{m}C_{ks}{}^{m}C_{ks}T_{ks}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}G_{ks}G_{k}$	62	4626	4641	860
570556	$G_{ks}A_{ks}{}^{m}C_{ks}{}^{m}C_{ds}T_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	20	4628	4643	861
570557	$A_{ks}A_{ks}G_{ks}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ks}T_{ks}{}^{m}C_{k}$	29.8	4630	4645	862
570558	$T_{ks}G_{ks}A_{ks}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}T_{k}$	45.5	4632	4647	863
570559	$T_{ks}G_{ks}G_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}T_{ds}T_{ds}A_{ds}G_{ds}A_{ds}A_{ks}T_{ks}T_{k}$	72.7	4650	4665	864
570560	$A_{ks}G_{ks}T_{ks}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}T_{ds}T_{ds}A_{ds}G_{ks}A_{ks}A_{k}$	33.7	4652	4667	865
570561	$G_{ks}{}^{m}C_{ks}A_{ks}G_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}T_{ds}T_{ks}A_{ks}G_{k}$	17.5	4654	4669	866
570562	$A_{ks}G_{ks}G_{ks}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ks}T_{ks}T_{k}$	27.9	4656	4671	867
570563	${}^{m}C_{ks}T_{ks}A_{ks}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}G_{k}$	31.3	4658	4673	868
570564	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}G_{ds}G_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	23.8	4660	4675	869
570565	$A_{ks}G_{ks}G_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	17.2	4678	4693	870
570566	$A_{ks}T_{ks}A_{ks}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}A_{ks}{}^{m}C_{ks}T_{k}$	33.1	4680	4695	871
570567	$G_{ks}A_{ks}A_{ks}T_{ds}A_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ks}{}^{m}C_{ks}A_{k}$	51.8	4682	4697	872
570568	$G_{ks}A_{ks}G_{ks}A_{ds}A_{ds}T_{ds}A_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}G_{ks}A_{k}$	20.3	4684	4699	873
570569	${}^{m}C_{ks}A_{ks}G_{ks}A_{ds}G_{ds}A_{ds}A_{ds}T_{ds}A_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	19	4686	4701	874

Table 18

Inhibition of human DMPK RNA transcript in HepG2 cells targeting SEQ ID NO: 2

ISIS No.	Sequence	% Target Expression	Start Site on Seq ID: 2	Stop Site on Seq ID: 2	Seq ID No.
UTC	N/A	100	N/A	N/A	
445569	${}^{m}C_{es}G_{es}G_{es}A_{es}G_{es}{}^{m}C_{ds}G_{ds}G_{ds}T_{ds}T_{ds}G_{ds}T_{ds}G_{ds}A_{ds}A_{ds}{}^{m}C_{es}T_{es}G_{es}G_{es}{}^{m}C_{e}$	33.8	13226	13245	24
486178	$A_{ks}{}^{m}C_{ks}A_{ks}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}A_{ks}G_{ks}G_{k}$	24.4	13836	13851	23
570647	$G_{ks}{}^{m}C_{ks}T_{ks}T_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}T_{k}$	60.6	5718	5733	645
570648	$A_{ks}G_{ks}G_{ks}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	82	5720	5735	646
570649	${}^{m}C_{ks}G_{ks}A_{ks}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}{}^{m}C_{k}$	133.4	5722	5737	647
570650	$A_{ks}G_{ks}{}^{m}C_{ks}G_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	54.1	5724	5739	648
570651	$A_{ks}G_{ks}A_{ks}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}G_{ks}G_{ks}{}^{m}C_{k}$	88.5	5726	5741	649
570652	$G_{ks}{}^{m}C_{ks}A_{ks}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}T_{ds}T_{ks}G_{ks}G_{k}$	162.9	5728	5743	650
570653	$G_{ks}A_{ks}G_{ks}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ks}T_{ks}T_{k}$	130	5730	5745	651
570654	$A_{ks}A_{ks}A_{ks}G_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}G_{ks}A_{ks}G_{k}$	66.5	5734	5749	652
570655	${}^{m}C_{ks}A_{ks}A_{ks}A_{ds}A_{ds}G_{ds}G_{ds}A_{ds}G_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}G_{ks}{}^{m}C_{ks}G_{k}$	79	5736	5751	653
570656	$T_{ks}G_{ks}G_{ks}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}A_{ds}G_{ds}G_{ds}A_{ds}G_{ks}{}^{m}C_{ks}A_{k}$	57.4	5741	5756	654
570657	${}^{m}C_{ks}{}^{m}C_{ks}T_{ks}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}A_{ds}G_{ds}G_{ks}A_{ks}G_{k}$	129.2	5743	5758	655
570658	${}^{m}C_{ks}A_{ks}{}^{m}C_{ks}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}A_{ds}A_{ks}G_{ks}G_{k}$	66.3	5745	5760	656
570659	${}^{m}C_{ks}G_{ks}{}^{m}C_{ks}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ks}A_{ks}A_{k}$	58.7	5747	5762	657
570660	$G_{ks}A_{ks}{}^{m}C_{ks}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	55.4	5750	5765	658
570661	$A_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}T_{ds}G_{ds}T_{ds}A_{ds}G_{ds}T_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ks}G_{ks}A_{k}$	45.4	5951	5966	659
570662	$T_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}T_{ds}A_{ds}G_{ds}T_{ds}G_{ds}G_{ks}A_{ks}{}^{m}C_{k}$	63.5	5953	5968	660
570663	$G_{ks}{}^{m}C_{ks}T_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}T_{ds}A_{ds}G_{ds}T_{ks}G_{ks}G_{k}$	56.6	5955	5970	661
570664	$G_{ks}G_{ks}A_{ks}G_{ds}A_{ds}G_{ds}G_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}G_{ds}A_{ds}T_{ks}A_{ks}G_{k}$	125.6	6015	6030	662
570665	$A_{ks}G_{ks}G_{ks}G_{ds}A_{ds}G_{ds}A_{ds}G_{ds}G_{ds}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}G_{ks}A_{ks}T_{k}$	64.2	6017	6032	663
570666	${}^{m}C_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}G_{ds}G_{ks}G_{ks}A_{k}$	59	6028	6043	664
570667	$G_{ks}T_{ks}G_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ks}A_{ks}G_{k}$	82.3	6031	6046	665
570668	$A_{ks}G_{ks}G_{ks}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}A_{ks}G_{k}$	96.2	6033	6048	666
570669	$A_{ks}G_{ks}A_{ks}G_{ds}G_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	26.2	6035	6050	667
570670	$A_{ks}G_{ks}A_{ks}G_{ds}A_{ds}G_{ds}G_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ks}G_{ks}{}^{m}C_{k}$	18.2	6037	6052	668
570671	$A_{ks}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}A_{k}$	29.2	6291	6306	669

570672	${}^{m}C_{ks}T_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ks}{}^{m}C_{ks}T_{k}$	50.3	6293	6308	670
570673	$A_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}G_{k}$	26.8	6295	6310	671
570674	$G_{ks}T_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	40.8	6297	6312	672
570675	$A_{ks}G_{ks}G_{ks}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	56.1	6299	6314	673
570676	$G_{ks}G_{ks}G_{ks}A_{ds}G_{ds}G_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}G_{ds}{}^{m}C_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	95	6329	6344	674
570677	$G_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}T_{ds}T_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}A_{ds}{}^{m}C_{ks}T_{ks}T_{k}$	23	6360	6375	675
570678	${}^{m}C_{ks}T_{ks}G_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}A_{ks}{}^{m}C_{k}$	23.4	6362	6377	676
570679	${}^{m}C_{ks}A_{ks}{}^{m}C_{ks}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	7.4	6364	6379	677
570680	$G_{ks}G_{ks}{}^{m}C_{ks}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}A_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	20.6	6366	6381	678
570681	$T_{ks}A_{ks}G_{ks}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ks}A_{ks}{}^{m}C_{k}$	29	6368	6383	679
570682	$G_{ks}G_{ks}T_{ks}A_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}T_{k}$	10.5	6370	6385	680
570683	$G_{ks}T_{ks}{}^{m}C_{ks}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}T_{k}$	23	6445	6460	681
570684	$G_{ks}G_{ks}T_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}G_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	22.5	6446	6461	433
570685	$A_{ks}G_{ks}G_{ks}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}G_{ds}G_{ks}T_{ks}{}^{m}C_{k}$	10.2	6447	6462	682
570686	${}^{m}C_{ks}T_{ks}A_{ks}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ks}G_{ks}G_{k}$	11.1	6449	6464	683
570687	$G_{ks}T_{ks}{}^{m}C_{ks}T_{ds}A_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ks}T_{ks}G_{k}$	11.7	6451	6466	684
570688	$A_{ks}A_{ks}G_{ks}T_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ks}G_{ks}{}^{m}C_{k}$	14.6	6453	6468	685
570689	$G_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}G_{ds}T_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}A_{k}$	10.1	6530	6545	686
570690	${}^{m}C_{ks}T_{ks}G_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ds}G_{ds}T_{ks}{}^{m}C_{ks}T_{k}$	35.4	6532	6547	687
570691	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}T_{ks}G_{ks}T_{k}$	33.6	6534	6549	688
570692	${}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}T_{ks}T_{k}$	77.3	6536	6551	689
570693	${}^{m}C_{ks}T_{ks}T_{ks}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ks}A_{ks}G_{k}$	18.9	6559	6574	690
570694	$T_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}A_{ks}G_{ks}G_{k}$	30.9	6561	6576	691
570695	${}^{m}C_{ks}T_{ks}T_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ds}G_{ds}T_{ks}{}^{m}C_{ks}A_{k}$	21	6563	6578	692
570696	$A_{ks}{}^{m}C_{ks}{}^{m}C_{ks}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ds}G_{ds}A_{ks}G_{ks}T_{k}$	50.3	6565	6580	693
570697	$G_{ks}G_{ks}A_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ds}{}^{m}C_{ds}T_{ks}G_{ks}A_{k}$	28.3	6567	6582	694
570698	${}^{m}C_{ks}A_{ks}G_{ks}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}T_{ds}G_{ks}{}^{m}C_{ks}T_{k}$	47.6	6569	6584	695
570699	$A_{ks}G_{ks}{}^{m}C_{ks}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}G_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ks}T_{ks}T_{k}$	17.9	6576	6591	696
570700	$T_{ks}A_{ks}G_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ks}A_{ks}G_{k}$	24.1	6594	6609	697
570701	$G_{ks}A_{ks}T_{ks}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	12.9	6596	6611	698
570702	${}^{m}C_{ks}A_{ks}G_{ks}A_{ds}T_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}{}^{m}C_{ks}T_{k}$	24	6598	6613	699
570703	${}^{m}C_{ks}T_{ks}{}^{m}C_{ks}A_{ds}G_{ds}A_{ds}T_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	22.3	6600	6615	700
570704	$A_{ks}G_{ks}{}^{m}C_{ks}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}T_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}{}^{m}C_{k}$	31.8	6602	6617	701
570705	$T_{ks}{}^{m}C_{ks}A_{ks}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}T_{ds}A_{ds}G_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	33.9	6604	6619	702

570706	$T_{ks}{}^{m}C_{ks}T_{ks}{}^{m}C_{ds}A_{ds}G_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}A_{ds}G_{ds}A_{ds}T_{ds}A_{ks}G_{ks}{}^{m}C_{k}$	28.1	6606	6621	703
570707	$G_{ks}A_{ks}G_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ks}T_{ks}T_{k}$	37.2	6636	6651	704
570708	$G_{ks}G_{ks}A_{ks}G_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}{}^{m}C_{ks}T_{k}$	66.3	6640	6655	705
570709	$G_{ks}A_{ks}G_{ks}G_{ds}A_{ds}G_{ds}G_{ds}A_{ds}G_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	52.7	6642	6657	706
570710	${}^{m}C_{ks}A_{ks}A_{ks}A_{ds}A_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}G_{ks}A_{k}$	31.8	6713	6728	707
570711	$A_{ks}G_{ks}{}^{m}C_{ks}A_{ds}A_{ds}A_{ds}A_{ds}G_{ds}G_{ds}G_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}{}^{m}C_{ks}{}^{m}C_{ks}A_{k}$	12.3	6715	6730	708
570712	$G_{ks}G_{ks}A_{ks}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}A_{ds}T_{ds}T_{ks}G_{ks}T_{k}$	37.1	6733	6748	709
570713	${}^{m}C_{ks}T_{ks}G_{ks}G_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ds}T_{ds}A_{ks}T_{ks}T_{k}$	42.4	6735	6750	710
570714	$T_{ks}G_{ks}{}^{m}C_{ks}T_{ds}G_{ds}G_{ds}A_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}G_{ks}T_{ks}A_{k}$	31.4	6737	6752	711
570715	$A_{ks}T_{ks}T_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}T_{ds}G_{ds}{}^{m}C_{ks}A_{ks}A_{k}$	12.1	6789	6804	712
570716	$T_{ks}A_{ks}A_{ks}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}A_{ds}{}^{m}C_{ds}T_{ks}G_{ks}{}^{m}C_{k}$	9	6791	6806	713
570717	$T_{ks}{}^{m}C_{ks}T_{ks}A_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}A_{ds}G_{ds}A_{ks}{}^{m}C_{ks}T_{k}$	32.1	6793	6808	714
570718	$T_{ks}{}^{m}C_{ks}T_{ks}{}^{m}C_{ds}T_{ds}A_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}A_{ks}G_{ks}A_{k}$	71.4	6795	6810	715
570719	${}^{m}C_{ks}T_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}T_{ds}A_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ks}A_{ks}A_{k}$	36.9	6804	6819	716
570720	$A_{ks}{}^{m}C_{ks}T_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}A_{ds}A_{ds}T_{ds}T_{ds}{}^{m}C_{ks}T_{ks}{}^{m}C_{k}$	17.1	6807	6822	717
570721	$A_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}A_{ds}A_{ds}T_{ks}T_{ks}{}^{m}C_{k}$	23.7	6809	6824	718
570722	${}^{m}C_{ks}{}^{m}C_{ks}A_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ds}T_{ds}A_{ks}A_{ks}T_{k}$	34.4	6811	6826	719
570723	$T_{ks}G_{ks}{}^{m}C_{ks}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}A_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}T_{ds}{}^{m}C_{ds}{}^{m}C_{ds}A_{ks}T_{ks}A_{k}$	38.7	6813	6828	720

Example 10: Dose response studies with antisense oligonucleotides targeting human dystrophia myotonica-protein kinase (DMPK) in HepG2 Cells

Antisense oligonucleotides targeted to a human DMPK nucleic acid were tested for their effect on human DMPK RNA transcript *in vitro*. Cultured HepG2 cells at a density of 20,000 cells per well were transfected using electroporation with 61.7 nM, 185.2 nM, 555.6 nM, 1666.7 nM, 5000.0 nM, and 15000.0 nM concentrations of each antisense oligonucleotide. After approximately 24 hours, RNA was isolated from the cells and DMPK RNA transcript levels were measured by quantitative real-time PCR using primer probe set RTS3164 (forward sequence AGCCTGAGCCGGGAGATG, designated herein as SEQ ID NO: 20; reverse sequence GCGTAGTTGACTGGCGAAGTT, designated herein as SEQ ID NO: 21; probe sequence AGGCCATCCGCACGGACAACCX, designated herein as SEQ ID NO: 22). Human DMPK RNA transcript levels were adjusted according to total RNA content, as measured by RIBOGREEN®.

Results are presented as percent expression of human DMPK, relative to untreated control (UTC) cells. For example, if the UTC is 100 and a dose of 5000 nM of ISIS No. 445569 yields a % Expression of human DMPK of 35 then the 5000 nM dose of ISIS reduced expression of human DMPK by 65% relative to the UTC. The half maximal inhibitory concentration (IC_{50}) of each oligonucleotide is presented in the table below and was calculated by plotting the concentrations of oligonucleotides used versus the percent inhibition of human DMPK mRNA expression achieved at each concentration, and noting the concentration of oligonucleotide at which 50% inhibition of human DMPK mRNA expression was achieved compared to the control. The results are presented in Table 19.

The tested antisense oligonucleotide sequences demonstrated dose-dependent inhibition of human DMPK mRNA levels under the conditions specified above.

Table 19

Dose response studies for with antisense oligonucleotides targeting hDMPK in HepG2 Cells

ISIS No.	Dose (nM)	% Expression of human DMPK	IC_{50}
UTC	ND	100	ND
445569	61.7	115.3	2.3
	185.2	87.9	
	555.6	69.0	
	1666.7	57.2	
	5000.0	35.0	
	15000.0	22.6	
512497	61.7	108.6	2
	185.2	98.4	
	555.6	77.9	
	1666.7	57.2	
	5000.0	28.0	
	15000.0	12.8	
486178	61.7	88.2	0.7
	185.2	67.1	
	555.6	49.4	
	1666.7	32.8	
	5000.0	26.7	
	15000.0	11.8	

569473	61.7	107.9	0.6
	185.2	66.5	
	555.6	33.6	
	1666.7	23.5	
	5000.0	12.8	
	15000.0	9.2	
570808	61.7	77.2	0.2
	185.2	52.7	
	555.6	20.6	
	1666.7	8.1	
	5000.0	7.2	
	15000.0	5.4	
594292	61.7	96.2	5.5
	185.2	99.6	
	555.6	80.0	
	1666.7	59.0	
	5000.0	45.5	
	15000.0	42.8	
594300	61.7	101.7	>15
	185.2	104.3	
	555.6	101.6	
	1666.7	93.6	
	5000.0	74.9	
	15000.0	66.8	
598768	61.7	95.5	1.2
	185.2	83.6	
	555.6	70.6	
	1666.7	40.7	
	5000.0	22.2	
	15000.0	7.3	
598769	61.7	103.9	1.9
	185.2	105.3	
	555.6	76.1	
	1666.7	50.4	
	5000.0	29.8	
	15000.0	12.1	
598777	61.7	96.4	0.9
	185.2	69.4	
	555.6	41.8	
	1666.7	42.8	

	5000.0	16.4	
	15000.0	27.1	

Example 11: Dose response studies with antisense oligonucleotides targeting human dystrophia myotonica-protein kinase (hDMPK) in Steinert DM1 Myoblast Cells

Antisense oligonucleotides targeted to a human DMPK nucleic acid were tested for their effect on human DMPK RNA transcript *in vitro*. Cultured Steinert DM1 myoblast cells at a density of 20,000 cells per well were transfected using electroporation with 61.7 nM, 185.2 nM, 555.6 nM, 1666.7 nM, 5000.0 nM, and 15000.0 nM concentrations of each antisense oligonucleotide. After approximately 24 hours, RNA was isolated from the cells and DMPK RNA transcript levels were measured by quantitative real-time PCR using primer probe set RTS3164 described above. Human DMPK RNA transcript levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent (%) expression of human DMPK, relative to untreated control (UTC) cells. The half maximal inhibitory concentration (IC_{50}) of each oligonucleotide is presented in the table below and was calculated by plotting the concentrations of oligonucleotides used versus the percent inhibition of human DMPK mRNA expression achieved at each concentration, and noting the concentration of oligonucleotide at which 50% inhibition of human DMPK mRNA expression was achieved compared to the control. The results are presented in Table 20.

The tested antisense oligonucleotide sequences demonstrated dose-dependent inhibition of human DMPK mRNA levels under the conditions specified above.

Table 20

Dose response studies for with antisense oligonucleotides targeting hDMPK in Steinert DM1 Cells

ISIS No.	Dose (nM)	% Expression of human DMPK	IC_{50}
UTC	ND	100	ND
445569	61.7	58.3	0.4
	185.2	56.7	
	555.6	58.5	
	1666.7	40.9	
	5000.0	26.0	

	15000.0	23.5	
512497	61.7	78.1	5.1
	185.2	77.5	
	555.6	98.8	
	1666.7	71.2	
	5000.0	51.3	
	15000.0	22.8	
486178	61.7	78.0	0.5
	185.2	61.3	
	555.6	43.3	
	1666.7	27.4	
	5000.0	24.6	
	15000.0	16.9	
569473	61.7	83.3	0.6
	185.2	54.8	
	555.6	64.5	
	1666.7	26.1	
	5000.0	19.4	
	15000.0	15.4	
570808	61.7	103.6	0.9
	185.2	77.8	
	555.6	46.7	
	1666.7	25.2	
	5000.0	20.8	
	15000.0	19.3	
594292	61.7	100.1	5.6
	185.2	109.7	
	555.6	72.6	
	1666.7	66.2	
	5000.0	39.5	
	15000.0	45.7	
594300	61.7	96.2	5.6
	185.2	87.1	
	555.6	70.3	
	1666.7	66.4	
	5000.0	58.1	
	15000.0	33.2	
598768	61.7	77.0	0.7
	185.2	62.9	
	555.6	62.0	

	1666.7	35.6	
	5000.0	24.5	
	15000.0	21.0	
598769	61.7	70.3	0.4
	185.2	49.2	
	555.6	55.3	
	1666.7	33.2	
	5000.0	27.1	
	15000.0	13.4	
598777	61.7	87.7	1
	185.2	61.7	
	555.6	57.3	
	1666.7	37.9	
	5000.0	30.0	
	15000.0	29.7	

Example 12: Dose response studies with antisense oligonucleotides targeting rhesus monkey dystrophia myotonica-protein kinase (DMPK) in cynomolgus monkey primary hepatocytes

Antisense oligonucleotides targeted to a rhesus monkey DMPK nucleic acid were tested for their effect on rhesus monkey DMPK RNA transcript *in vitro*. Cultured cynomolgus monkey primary hepatocytes cells at a density of 20,000 cells per well were transfected using electroporation with 61.7 nM, 185.2 nM, 555.6 nM, 1666.7 nM, 5000.0 nM, and 15000.0 nM concentrations of each antisense oligonucleotide. After approximately 24 hours, RNA was isolated from the cells and DMPK RNA transcript levels were measured by quantitative real-time PCR using primer probe set RTS3164 described above. Rhesus monkey DMPK RNA transcript levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent (%) expression of rhesus monkey DMPK, relative to untreated control (UTC) cells. The half maximal inhibitory concentration (IC_{50}) of each oligonucleotide is presented in the table below and was calculated by plotting the concentrations of oligonucleotides used versus the percent inhibition of rhesus monkey DMPK mRNA expression achieved at each concentration, and noting the concentration of oligonucleotide at which 50% inhibition of rhesus monkey DMPK mRNA expression was achieved compared to the control.

The tested antisense oligonucleotide sequences demonstrated dose-dependent inhibition of rhesus monkey DMPK mRNA levels under the conditions specified above.

Table 21

Dose response studies for with antisense oligonucleotides targeting rhesus monkey DMPK in cynomolgus monkey primary hepatocytes

ISIS No.	Dose (nM)	% Expression of human DMPK	IC_{50}
UTC	ND	100	ND
445569	61.7	79.7	1.4
	185.2	41.1	
	555.6	58.1	
	1666.7	33.5	
	5000.0	46.9	
	15000.0	50.0	
512497	61.7	123.4	1.5
	185.2	63.7	
	555.6	44.8	
	1666.7	34.1	
	5000.0	51.2	
	15000.0	23.5	
486178	61.7	51.1	<.06
	185.2	30.6	
	555.6	22.0	
	1666.7	23.5	
	5000.0	9.8	
	15000.0	19.2	
569473	61.7	82.1	.2
	185.2	39.4	
	555.6	17.7	
	1666.7	28.5	
	5000.0	20.0	
	15000.0	15.6	
570808	61.7	74.6	0.1
	185.2	27.6	
	555.6	16.4	
	1666.7	25.6	
	5000.0	8.8	
	15000.0	21.9	
594292	61.7	93.0	>15

	185.2	82.1	
	555.6	106.0	
	1666.7	91.1	
	5000.0	62.2	
	15000.0	70.4	
594300	61.7	105.5	>15
	185.2	91.8	
	555.6	114.9	
	1666.7	65.7	
	5000.0	110.2	
	15000.0	118.8	
598768	61.7	70.3	0.4
	185.2	57.8	
	555.6	58.5	
	1666.7	16.5	
	5000.0	24.0	
	15000.0	13.4	
598769	61.7	76.5	1.1
	185.2	65.1	
	555.6	64.0	
	1666.7	34.4	
	5000.0	60.9	
	15000.0	8.6	
598777	61.7	161.4	2.1
	185.2	51.7	
	555.6	47.5	
	1666.7	34.6	
	5000.0	27.8	
	15000.0	52.9	

Example 13: *In vivo* antisense inhibition of hDMPK in DMSXL transgenic mice

To test the effect of antisense inhibition for the treatment of myotonic dystrophy type 1 (DM1), an appropriate mouse model was required. The transgenic mouse model, DMSXL carrying the hDMPK gene with large expansions of over 1000 CTG repeats was generated (Huguet *et al., PLOS Genetics*, 2012, *8(11),* e1003034- e1003043). These DMSXL mice express the mutant hDMPK allele and display muscle weakness phenotype similar to that seen in DM1 patients.

ISIS 486178 from Table 1 was selected and tested for antisense inhibition of hDMPK transcript *in vivo.* ISIS 445569 was included in the study for comparison.

Treatment

DMSXL mice were maintained on a 12-hour light/dark cycle and fed *ad libitum* normal Purina mouse chow. Animals were acclimated for at least 7 days in the research facility before initiation of the experiment. Antisense oligonucleotides (ASOs) were prepared in PBS and sterilized by filtering through a 0.2 micron filter. ASOs were dissolved in 0.9% PBS for injection.

DMSXL mice received subcutaneous injections of ISIS 445569 at 50 mg/kg or ISIS 486178 at 25 mg/kg twice per week for 4 weeks. The control group received subcutaneous injections of PBS twice weekly for 4 weeks. Each treatment group consisted of 4 animals.

Inhibition of hDMPK mRNA levels

Twenty four hours after the final dose, the mice were sacrificed and tissues were collected. mRNA was isolated for real-time PCR analysis of hDMPK and normalized to 18s RNA. Human primer probe set RTS3164 was used to measure mRNA levels. The results are expressed as the average percent of hDMPK mRNA levels for each treatment group, relative to PBS control.

Human primer probe set RTS3164 (forward sequence AGCCTGAGCCGGGAGATG, designated herein as SEQ ID NO: 20; reverse sequence GCGTAGTTGACTGGCGAAGTT, designated herein as SEQ ID NO: 21; probe sequence AGGCCATCCGCACGGACAACCX, designated herein as SEQ ID NO: 22).

As presented in Table 22 below, treatment with antisense oligonucleotides reduced hDMPK transcript expression. The results indicate that treatment with ISIS 445569 and 486178 resulted in reduction of hDMPK mRNA levels in DMSXL mice.

Table 22

Effect of antisense oligonucleotides on hDMPK inhibition in DMSXL mice

ISIS No.	Dosage (mg/kg)	Tissue Type	hDMPK mRNA levels (% PBS)	Motif/Length
PBS	0			
486178	25	Tibialis Anterior	70.7	kkk-d10-kkk (16 mer)
		Soleus	67.3	
		Quadriceps	73.9	

		Latissiumus grand dorsi	71.0	
		Triceps	67.1	
		Diaphragm	68.9	
		Heart	30.8	
		Brain	11.8	
445569	50	Tibialis Anterior	38.4	e5-d10-e5 (20 mer)
		Soleus	47.5	
		Quadriceps	41.3	
		Latissiumus grand dorsi	35.7	
		Triceps	30.5	
		Diaphragm	44.7	
		Heart	7.6	
		Brain	13.1	

Example 14: Effect of ASO treatment on muscle strength in DMSXL mice targeting hDMPK

Griptest

Mice were assessed for grip strength performance in wild-type (WT) and DMSXL forelimb using a commercial grip strength dynamometer as described in the literature ((Huguet *et al., PLOS Genetics,* 2012, *8(11),* e1003034- e1003043).

DMSXL mice received subcutaneous injections of ISIS 486178 at 25 mg/kg or ISIS 445569 at 50 mg/kg twice per week for 4 weeks. The control DMSXL group received subcutaneous injections of PBS twice weekly for 4 weeks. Each treatment group consisted of 4 animals. The forelimb force for each treatment group and WT was measured at day 0, 30, and 60 using the griptest. The grip strength performance was determined by measuring the force difference between day 60 and day 0. Results are presented as the average forelimb force from each group.

As illustrated in Table 23, below, treatment with ASOs targeting hDMPK improved muscle strength in DMSXL mice compared to untreated control. ISIS 486178, an ASO with cEt modifications, demonstrated substantial improvement in the forelimb strength (+3.4) compared to ISIS 445569 with MOE modifications (+0.38).

Table 23

Effect of ASO treatment on muscle strength in DMSXL mice targeting hDMPK

Treatment group	Forelimb force (g)			
	Day 0	Day 30	Day 60	Δ = Day 60 - Day 0
Untreated control	72.2	70.2	67.5	-4.6
ASO 486178	62.3	65.7	65.6	+3.4
ASO 445569	64.3	68	64.7	+0.38
Wild type (WT)	75.2	76.5	78.4	+3.2

Example 15: Effect of ASO treatment on muscle fiber distribution in DMSXL mice targeting hDMPK

The muscle fiber distribution in DMSXL mice targeting hDMPK in the presence and absence of ISIS 445569 and 486178 was also assessed. Both ASOs were previously described in Table 1, above.

DMSXL mice received subcutaneous injections of ISIS 486178 at 25 mg/kg or ISIS 445569 at 50 mg/kg twice per week for 4 weeks. The control DMSXL group received subcutaneous injections of PBS twice weekly for 4 weeks. Each treatment group consisted of 4 animals. The muscle fiber distribution was assessed and the results are presented Table 44, below.

As illustrated, treatment with ASOs targeting hDMPK decreased the distribution of DM1 Associated Type 2c muscle fiber in the tibialis anterior (TA) of DMSXL mice compared to untreated control. The results demonstrated that normal pattern of fiber distribution in the skeletal muscles can be restored with ASO treatment. ISIS 445569 demonstrated an improvement in the muscle fiber distribution as compared to the untreated control; however ISIS 486178, an ASO with cEt modifications, demonstrated muscle fiber distribution that was more consistent with the muscle fiber distribution found in the wild-type mice.

Table 24

Effect of ASO treatment on muscle fiber distribution in DMSXL mice targeting hDMPK

Treatment group	Fiber Type Distribution in TA muscle		
	Fiber 1	Fiber 2a	Fiber 2c
Untreated control	4%	25%	5.90%
ASO 486178	3.10%	15%	0.70%
ASO 445569	4%	21%	2%
Wild type (WT)	3.30%	15%	0.00%

Example 16: Dose-dependent antisense inhibition of hDMPK in DMSXL transgenic mice

The newly designed ASOs from Table 1, above, were further evaluated in a dose-response study for antisense inhibition of hDMPK transcript *in vivo*. ISIS 445569 was included in the study for comparison.

Treatment

DMSXL mice were maintained on a 12-hour light/dark cycle and fed *ad libitum* normal Purina mouse chow. Animals were acclimated for at least 7 days in the research facility before initiation of the experiment. Antisense oligonucleotides (ASOs) were prepared in PBS and sterilized by filtering through a 0.2 micron filter. ASOs were dissolved in 0.9% PBS for injection.

DMSXL mice received subcutaneous injections of PBS or ASOs from Table 1, above, targeting hDMPK. The ASO was dosed twice per week for 4 weeks at the indicated doses in Table 25, below. The control group received subcutaneous injections of PBS twice weekly for 4 weeks. Each treatment group consisted of 4 animals.

Inhibition of hDMPK mRNA levels

Forty eight hours after the final dose, the mice were sacrificed and tissue from the tibialis anterior muscles, quadriceps muscles (left), gastrocnemius muscles, heart and diaphragm was isolated. mRNA was isolated for real-time PCR analysis of hDMPK and normalized to RIBOGREEN®. Human primer probe set RTS3164 was used to measure mRNA levels. The results summarized in Table 25, below, were independently generated from various dose-response studies. The results are presented as the average percent of hDMPK mRNA expression levels for each treatment group, relative to PBS control.

As presented, treatment with antisense oligonucleotides reduced hDMPK transcript expression in a dose-dependent manner.

Table 25

Dose-dependent inhibition of hDMPK mRNA levels in DMSXL mice

ISIS No.	mg/kg/wk	hDMPK mRNA levels (% PBS)				
		TA	Quad (Left)	Gastroc	Heart	Diaphragm
PBS	0	100	100	100	100	100
445569	50	54.7	80.3	97.1	55.4	21.7
	100	28.3	42.1	71.3	48.9	19.7
	200	22.2	33.9	45.2	34.2	10.0
512497	50	23.8	48.9	52.9	44.4	35.0

	100	9.7	28.7	24.8	43.8	24.2
	200	11.4	22.4	16.4	42.0	15.2
486178	25	59.1	56.1	63.1	75.3	39.1
	50	33.8	61.9	58.7	59.2	32.5
	100	36.6	65.8	51.6	47.3	26.2
570808	25	26.3	41.1	39.8	44.9	17.3
	50	12.2	13.0	36.3	18.4	8.1
	100	6.1	5.4	7.9	10.2	3.0
594292	25	48.8	32.2	68.8	70.6	72.7
	50	32.0	30.4	41.1	85.1	48.3
	100	31.6	39.6	53.3	63.9	40.2
598768	25	16.9	27.1	27.5	56.3	26.9
	50	10.2	33.6	24.1	30.8	20.2
	100	6.8	22.0	25.5	22.6	13.1
598769	25	21.6	50.8	48.1	61.0	30.3
	50	12.7	25.1	42.3	36.4	16.7
	100	12.8	18.4	33.2	32.0	20.2
569473	25	42.0	21.8	48.9	51.8	34.8
	50	41.6	16.2	47.6	55.6	23.6
	100	31.9	19.2	31.9	35.6	20.5
594300	25	114.5	56.7	96.2	91.0	62.6
	50	44.3	22.3	52.8	69.3	54.7
	100	73.0	22.6	56.6	78.3	44.5
598777	25	49.4	28.8	76.1	97.1	58.7
	50	44.8	13.6	36.5	87.4	40.8
	100	31.8	10.1	22.5	86.8	33.6

TA = Tibialis Anterior; Quad = Quadriceps; Gastroc = Gastrocnemius

Example 17: Six Week *in vivo* Tolerability Study in CD-1 Mice

The newly designed ASOs from Table 1, above, were further evaluated in a 6 week study to assess plasma chemistry, body/organ weights and histology. Groups of CD-1 mice were administered 100 mg/kg/wk of ISIS 445569 or ISIS 512497. Further groups of CD-1 mice were administered 50 mg/kg/wk of ISIS 486178, ISIS 570808, ISIS 594292, ISIS 598768, ISIS 598769, ISIS 569473, ISIS 594300, and ISIS

598777. After six weeks and two days after each group of mice received the last dose, the mice were sacrificed and tissues were collected for analysis. For each group of mice, analysis to measure alanine transaminase levels, aspartate aminotransferase levels, blood urea nitrogen (BUN) levels, albumin levels, total bilirubin, and creatine levels was measured. Additionally, organ weights were also measured, the results of which are presented in the tables below.

Table 26

Plasma Chemistry in CD-1 mice

ISIS No.	ALT (U/L)	AST (U/L)	BUN (mg/dL)	Albumin (g/dL)	T. Bil (mg/dL)	Creatinine (mg/dL)
PBS	31.75	60.75	32.73	2.99	0.23	0.16
486178	65.00	103.00	27.18	2.90	0.19	0.13
445569	162.75	195.25	29.70	3.38	0.26	0.14
570808	313.50	332.50	32.40	2.81	0.28	0.15
594292	58.75	133.00	28.15	2.94	0.21	0.13
598768	45.50	92.00	26.85	2.90	0.21	0.11
598769	69.25	94.25	32.73	2.89	0.18	0.13
512497	101.25	144.50	26.90	2.90	0.19	0.12
569473	75.75	137.00	28.98	3.05	0.26	0.13
594300	46.00	76.75	24.70	2.94	0.18	0.11
598777	186.50	224.25	24.68	2.97	0.30	0.11

Table 27

Body & Organ Weights in CD-1 mice

ISIS No.	*Kidney % BW	*Liver % BW	*Spleen % BW
PBS	1.00	1.00	1.00
486178	1.05	1.05	1.03
445569	1.07	1.09	1.23
570808	0.94	1.27	1.43
594292	1.03	1.03	1.16
598768	1.14	1.08	0.97
598769	0.97	1.05	1.04
512497	0.99	1.17	1.38
569473	1.02	1.01	1.09
594300	1.14	1.07	1.02
598777	1.05	1.20	1.01

* Fold change over Saline control group

Example 18: Six Week *in vivo* Tolerability Study in Sprague-Dawley Rats

The newly designed ASOs from Table 1, above, were further evaluated in a 6 week study to assess plasma chemistry, body/organ weights and histology. Groups of Sprague-Dawley rats were administered 100 mpk/wk of ISIS 445569 or ISIS 512497. Further groups of Groups of Sprague-Dawley rats were administered 50 mpk/wk of ISIS 486178, ISIS 570808, ISIS 594292, ISIS 598768, ISIS 598769, ISIS

569473, ISIS 594300, and ISIS 598777. After six weeks and two days after each group of mice received the last dose, the mice were sacrificed and tissues were collected for analysis. For each group of mice, analysis to measure alanine transaminase levels, aspartate aminotransferase levels, blood urea nitrogen (BUN) levels, albumin levels, total bilirubin, creatine levels, and urinary creatine levels was measured. Additionally, organ weights were also measured, the results of which are presented in the tables below.

Table 28

Plasma Chemistry & Urine Analysis in Sprague-Dawley Rats

ISIS No.	ALT (U/L)	AST (U/L)	BUN (mg/dl)	Total protein (mg/dl)	T.Bil (mg/dl)	Creatinine (mg/dl)	Urine MTP/Creatine
Saline	59.25	100.35	18.05	3.47	0.158	0.30	1.09
569473	101	198.25	25.9	2.74	0.195	0.4025	4.59
512497	211	240.25	19.32	3.58	0.17	0.39	6.18
598768	78.2	103.5	20.6	3.36	0.14	0.38	3.85
598769	84.5	104.5	18.6	3.52	0.15	0.34	3.02
570808	82	141	23.8	3.08	0.21	0.4	2.71
598777	109	119.5	21.65	3.79	0.22	0.37	2.56
445569	117.5	163.2	22.45	3.86	0.18	0.47	6.4
594300	66	80.75	17.53	3.59	0.12	0.29	4.72
486178	56.8	80.75	23.3	5.28	0.08	3.0	4.5
594292	64.5	80.5	19.62	3.38	0.098	0.29	5.17

Table 29

Plasma Chemistry & Urine Analysis in Sprague-Dawley Rats

ISIS No.	Kidney (fold)*	Liver (fold)*	Spleen (fold)*
Saline	1	1	1
569473	1.46	1.20	0.82
512497	1.03	1.22	1.94
598768	0.92	0.92	1.49
598769	0.93	1.04	0.98
570808	1.18	0.98	2.43
598777	1.07	0.93	2.31
445569	1	1.13	3.25
594300	1.03	1.04	1.94
486178	0.87	0.89	1.45
594292	1.08	1.01	2.04

* Fold change over Saline control group

Example 19: Thirteen (13) Week *in vivo* Study in Cynomolgus Monkeys

Groups of 4 cynomolgus male monkeys were administered 40 mg/kg/wk of ISIS 445569, ISIS 512497, ISIS 486178, ISIS 570808, ISIS 594292, ISIS 598768, ISIS 598769, ISIS 569473, ISIS 594300, and

ISIS 598777 via subcutaneous injection. Thirteen weeks after the first dose, the animals were sacrificed and tissue analysis was performed. mRNA was isolated for real-time PCR analysis of rhesus monkey DMPK and normalized to RIBOGREEN®. Primer probe set RTS3164 (described above) was used to measure mRNA levels and the results are shown in Table 30 below. Additionally, further mRNA was isolated for real-time PCR analysis of rhesus monkey DMPK and normalized to RIBOGREEN® using primer probe set RTS4447 and the results are shown in Table 31 below. RTS4447 (forward sequence AGCCTGAGCCGGGAGATG, designated herein as SEQ ID NO: 20; reverse sequence GCGTAGTTGACTGGCAAAGTT, designated herein as SEQ ID NO: 21; probe sequence AGGCCATCCGCATGGCCAACC, designated herein as SEQ ID NO: 22).

Table 30

Dose-dependent inhibition of DMPK mRNA levels in Cynomolgus Monkeys using Primer Probe Set RTS3164

ISIS No.	mg/kg/wk	hDMPK mRNA levels (% PBS)					
		TA	Quad (Left)	Gastroc	Kidney	Heart	Liver
PBS	0	100	100	100	100	100	100
486178	40	26.1	30.8	49.3	55.3	45.8	44.9
445569	40	68.5	82.2	128.9	65.6	91.2	113.5
512497	40	60.3	58.7	66.7	61.9	74.2	68.1
598768	40	69.1	64.9	80.7	58.1	70.6	100.8
594300	40	73.6	80.2	106.0	57.9	97.5	91.6
594292	40	55.6	52.0	71.9	46.2	72.1	81.6
569473	40	44.8	31.7	61.6	44.0	58.7	28.0
598769	40	31.7	28.9	49.7	26.8	45.0	38.6
570808	40	2.5	4.4	6.4	29.7	17.5	7.2
598777	40	53.3	31.8	76.4	42.7	44.6	111.6

Table 31

Dose-dependent inhibition of DMPK mRNA levels in Cynomolgus Monkeys using Primer Probe Set RTS4447

ISIS No.	mg/kg/wk	hDMPK mRNA levels (% PBS)					
		TA	Quad (Left)	Gastroc	Kidney	Heart	Liver
PBS	0	100.0	100.0	100.0	100.0	100.0	100.0
486178	40	26.7	29.0	32.9	57.0	49.4	58.1

445569	40	85.4	87.4	147.1	77.1	97.2	93.6
512497	40	66.4	70.4	94.2	81.9	87.6	79.5
598768	40	48.3	76.4	106.7	73.7	81.0	85.1
594300	40	100.9	113.5	219.6	96.9	131.0	118.9
594292	40	76.5	75.7	151.7	86.6	107.1	108.6
569473	40	52.6	51.7	114.2	72.9	87.2	53.7
598769	40	45.2	57.6	86.3	56.6	65.4	72.5
570808	40	6.6	8.3	14.8	60.7	27.9	35.0
598777	40	55.1	56.8	124.1	78.6	88.9	131.2

Example 20: Thirteen (13) Week *in vivo* Tolerability Study in Cynomolgus Monkeys

Groups of cynomolgus male monkeys were administered 40 mg/kg of ISIS 445569, ISIS 512497, ISIS 486178, ISIS 570808, ISIS 594292, ISIS 598768, ISIS 598769, ISIS 569473, ISIS 594300, and ISIS 598777 via subcutaneous injection on days 1, 3, 5, and 7. Following administration on day 7, each monkey was administered 40 mg/kg/wk of ISIS 445569, ISIS 512497, ISIS 486178, ISIS 570808, ISIS 594292, ISIS 598768, ISIS 598769, ISIS 569473, ISIS 594300, and ISIS 598777 via subcutaneous injection.

48 hours after each monkey received a subcutaneous dose on days 28 and 91, blood and urine samples were taken for analysis. Some of the monkeys had blood and urine taken 48 hours after the dose given on day 56. Alanine aminotransferase (ALT), aspartate aminotransferase (AST), lactate dehydrogenase (LDH), and creatine kinase (CK) were measured for each animal in a treatment group and the average values are presented in the table below. Day of Sample values with a negative represent time point before treatment began. For example, a Day of Treatment value of -7 represents a sample taken 7 days before the first dose. Thirteen weeks after the first dose, the animals were sacrificed and tissue analysis was performed.

Table 32

Plasma Chemistry & Urine Analysis in Cynomolgus Monkeys

ISIS No.	Day of Sample	ALT (U/L)	AST (U/L)	LDH (mg/dl)	CK (mg/dl)
Saline	-14	34.2	25.9	604.0	160.8
	-7	38.8	27.8	861.3	249.0
	30	43.0	34.4	1029.0	300.0

	93	66.1	43.0	1257.3	898.8
486178	-14	37.6	40.5	670.0	236.8
	-7	49.8	55.0	1039.8	380.8
	30	47.0	41.2	875.4	415.0
	93	59.7	43.6	960.6	809.6
594292	-14	38.9	32.0	776.3	375.8
	-7	37.8	38.4	877.3	210.0
	30	35.4	39.6	666.0	93.8
	93	49.8	46.3	958.5	339.0
569473	-14	49.4	49.8	1185.3	365.3
	-7	50.4	59.7	1609.5	261.0
	30	46.7	52.5	1390.8	107.8
	93	56.3	49.8	1483.3	524.5
570808	-14	47.1	46.8	896.0	448.3
	-7	44.4	63.6	913.3	257.3
	30	47.1	57.7	660.5	125.0
	93	79.8	92.2	813.5	294.0
598768	-14	37.9	41.6	666.3	253.8
	-7	41.4	53.5	754.0	231.5
	30	37.2	38.9	652.3	106.3
	93	45.8	41.5	721.3	238.3
598769	-14	44.2	36.1	1106.8	456.8
	-7	45.7	41.5	1323.3	214.0

	30	40.3	42.0	981.0	147.8
	58	56.7	49.9	1101.5	552.3
	93	69.0	50.3	1167.3	749.5
512497	-14	31.5	34.3	689.3	293.8
	-7	39.0	45.4	1110.3	286.0
	30	47.2	60.2	960.5	202.5
	93	69.6	87.1	997.0	1118.5
594300	-14	42.0	34.0	935.5	459.5
	-7	42.1	53.6	1020.5	272.0
	30	28.0	34.6	620.8	124.5
	58	42.9	48.5	883.5	169.8
	93	45.7	45.7	835.5	252.3
598777	-14	45.6	37.7	707.0	558.5
	-7	43.3	50.0	705.8	200.3
	30	50.2	47.3	585.3	159.3
	93	79.2	56.1	1029.0	785.0
445569	-14	40.2	44.2	835.8	404.0
	-7	41.0	46.1	1074.3	305.5
	30	45.9	61.7	994.8	283.0
	58	51.6	85.1	739.0	117.8
	93	99.3	97.5	1583.5	2114.0

What is claimed is:

1. A compound comprising a modified oligonucleotide consisting of 10-30 linked nucleosides and having a nucleobase sequence comprising a complementary region comprising at least 8 contiguous nucleobases complementary to a target region of equal length of a DMPK nucleic acid.

2. The compound of claim 1, wherein at least one nucleoside of the modified oligonucleotide comprises a bicyclic sugar selected from among cEt, LNA, α-L-LNA, ENA and 2'-thio LNA.

3. The compound of any of claims 1 to 2, wherein the target region is exon 9 of a DMPK nucleic acid.

4. The compound of any of claims 1 to 3, wherein the complementary region comprises at least 10 contiguous nucleobases complementary to a target region of equal length of a DMPK transcript.

5. The compound of any of claims 1 to 3, wherein the complementary region comprises at least 12 contiguous nucleobases complementary to a target region of equal length of a DMPK nucleic acid.

6. The compound of any of claims 1 to 3, wherein the complementary region comprises at least 14 contiguous nucleobases complementary to a target region of equal length of a DMPK nucleic acid.

7. The compound of any of claims 1 to 3, wherein the complementary region comprises at least 16 contiguous nucleobases complementary to a target region of equal length of a DMPK nucleic acid.

8. The compound of any of claims 1 to 7, wherein the DMPK nucleic acid is a DMPK pre-mRNA

9. The compound of any of claims 1 to 7, wherein the DMPK nucleic acid is a DMPK mRNA.

10. The compound of any of claims 1 to 9, wherein the DMPK nucleic acid has a nucleobase sequence selected from among SEQ ID NO: 1 and SEQ ID NO: 2.

11. The compound of any of claims 1 to 10, wherein the modified oligonucleotide has a nucleobase sequence comprising a complementary region comprising at least 10 contiguous nucleobases complementary to a target region of equal length of SEQ ID NO: 1 or SEQ ID NO: 2.

12. The compound of claims 1 to 10, wherein the modified oligonucleotide has a nucleobase sequence comprising a complementary region comprising at least 12 contiguous nucleobases complementary to a target region of equal length of SEQ ID NO: 1 or SEQ ID NO: 2.

13. The compound of claims 1 to 10, wherein the modified oligonucleotide has a nucleobase sequence comprising a complementary region comprising at least 14 contiguous nucleobases complementary to a target region of equal length of SEQ ID NO: 1 or SEQ ID NO: 2.

14. The compound of claims 1 to 10, wherein the modified oligonucleotide has a nucleobase sequence comprising a complementary region comprising at least 16 contiguous nucleobases complementary to a target region of equal length of SEQ ID NO: 1 or SEQ ID NO: 2.

15. The compound of any of claims 1 to 14, wherein the target region is from nucleobase 1343 to nucleobase 1368 of SEQ ID NO.: 1.

16. The compound of any of claims 1 to 14, wherein the target region is from nucleobase 1317 to nucleobase 1366 of SEQ ID NO.: 1.

17. The compound of any of claims 1 to 14, wherein the target region is from nucleobase 2748 to nucleobase 2791 of SEQ ID NO.: 1.

18. The compound of any of claims 1 to 14, wherein the target region is from nucleobase 730 to nucleobase 748 of SEQ ID NO.: 1.

19. The compound of any of claims 1 to 14, wherein the target region is from nucleobase 8603 to nucleobase 8619 of SEQ ID NO.: 2.

20. The compound of any of claims 1 to 14, wherein the target region is from nucleobase 13836 to nucleobase 13851 of SEQ ID NO.: 2.

21. The compound of any of claims 1 to 14, wherein the target region is from nucleobase 10201 to nucleobase 10216 of SEQ ID NO.: 2.

22. The compound of any of claims 1 to 14, wherein the target region is from nucleobase 10202 to nucleobase 10218 of SEQ ID NO.: 2.

23. The compound of any of claims 1 to 22, wherein the modified oligonucleotide has a nucleobase sequence that is at least 80% complementary to the target region over the entire length of the oligonucleotide.

24. The compound of any of claims 1 to 22, wherein the modified oligonucleotide has a nucleobase sequence that is at least 90% complementary to the target region over the entire length of the oligonucleotide.

25. The compound of any of claims 1 to 22, wherein the modified oligonucleotide has a nucleobase sequence that is at least 100% complementary to the target region over the entire length of the oligonucleotide.

26. The compound of any of claims 1-25 having a nucleobase sequence comprising at least 8 contiguous nucleobases of a sequence recited in any of SEQ ID NOs: 23-874.

27. The compound of any of claims 1 to 25, wherein the modified oligonucleotide has a nucleobase sequence comprising at least 10 contiguous nucleobases of a sequence recited in SEQ ID NOs: 23-32.

28. The compound of any of claims 1 to 25, wherein the modified oligonucleotide has a nucleobase sequence comprising at least 12 contiguous nucleobases of a sequence recited in SEQ ID NOs: 23-32.

29. The compound of any of claims 1 to 25, wherein the modified oligonucleotide has a nucleobase sequence comprising at least 14 contiguous nucleobases of a sequence recited in SEQ ID NOs: 23-32.

30. The compound of any of claims 1 to 25, wherein the modified oligonucleotide has a nucleobase sequence comprising at least 16 contiguous nucleobases of a sequence recited in SEQ ID NOs: 23-32.

31. The compound of any of claims 1 to 30, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 23.

32. The compound of any of claims 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 25.

33. The compound of any of claims 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 26.

34. The compound of any of claims 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 27.

35. The compound of any of claims 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 28.

36. The compound of any of claims 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 29.

37. The compound of any of claims 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 30.

38. The compound of any of claims 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 31.

39. The compound of any of claims 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence that consists of the sequence recited in SEQ ID NO: 32.

40. The compound of any of claims 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence comprising the sequence recited in SEQ ID NO: 23, 24, 25, 26, 27, 28, 29, 30, 31, or 32.

41. The compound of any of claims 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence comprising the sequence recited in SEQ ID NO: 23, 25, 26, 27, 28, 29, 30, 31, or 32.

42. The compound of any of claims 1 to 14, wherein the modified oligonucleotide has a nucleobase sequence comprising the sequence recited in any of SEQ ID NOs: 33-874.

43. The compound of any of claims 1 to 42, wherein the nucleobase sequence of the modified oligonucleotide is at least 90% complementary to any of SEQ ID NOs: 1-19.

44. The compound of any of claims 1 to 34, wherein the nucleobase sequence of the modified oligonucleotide is 100% complementary to any of SEQ ID NOs: 1-19.

45. The compound of any of claims 1 to 30, wherein the modified oligonucleotide consists of 16 linked nucleosides.

46. The compound of any of claims 1 to 30, wherein the modified oligonucleotide consists of 17 linked nucleosides.

47. The compound of any of claims 1 to 30, wherein the modified oligonucleotide consists of 18 linked nucleosides.

48. The compound of any of claims 1 to 30, wherein the modified oligonucleotide consists of 19 linked nucleosides.

49. The compound of any of claims 1 to 30, wherein the modified oligonucleotide consists of 20 linked nucleosides.

50. The compound of any of claims 1 to 49, wherein the modified oligonucleotide is a single-stranded oligonucleotide.

51. The compound of any of claims 1 to 50 wherein at least one nucleoside comprises a modified sugar.

52. The compound of any of claims 1 to 51 wherein at least two nucleosides comprise a modified sugar.

53. The compound of claim 52, wherein each of the modified sugars have the same modification.

54. The compound of claim 52, wherein at least one the modified sugars has a different modification.

55. The compound of any of claims 51 to 54, wherein at least one modified sugar is a bicyclic sugar.

56. The compound of claim 55, wherein the bicyclic sugar is selected from among cEt, LNA, α-L-LNA, ENA and 2'-thio LNA.

57. The compound of claim 56, wherein the bicyclic sugar comprises cEt.

58. The compound of claim 56, wherein the bicyclic sugar comprises LNA.

59. The compound of claim 56, wherein the bicyclic sugar comprises α-L-LNA.

60. The compound of claim 56, wherein the bicyclic sugar comprises ENA.

61. The compound of claim 56, wherein the bicyclic sugar comprises 2'-thio LNA.

62. The compound of any of claims 1 to 61, wherein at least one modified sugar comprises a 2'-substituted nucleoside.

63. The compound of claim 62, wherein the 2'-substituted nucleoside is selected from among: 2'-OCH_3, 2'-F, and 2'-O-methoxyethyl.

64. The compound of any of claims 1 to 63, wherein at least one modified sugar comprises a 2'-O-methoxyethyl.

65. The compound of any of claims 1 to 64, wherein at least one nucleoside comprises a modified nucleobase.

66. The compound of claim 65, wherein the modified nucleobase is a 5-methylcytosine.

67. The compound of any of claims 1 to 67, wherein each cytosine is a 5-methylcytosine.

68. The compound of any of claims 1 to 67, wherein the modified oligonucleotide comprises:
   a. a gap segment consisting of linked deoxynucleosides;
   b. a 5' wing segment consisting of linked nucleosides;
   c. a 3' wing segment consisting of linked nucleosides;
   d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

69. The compound of claim 68, wherein the modified oligonucleotide consists of 16 linked nucleosides.

70. The compound of claim 68, wherein the modified oligonucleotide consists of 17 linked nucleosides.

71. The compound of claim 68, wherein the modified oligonucleotide consists of 18 linked nucleosides.

72. The compound of claim 68, wherein the modified oligonucleotide consists of 19 linked nucleosides.

73. The compound of claim 68, wherein the modified oligonucleotide consists of 20 linked nucleosides.

74. The compound of any of claims 68 to 73, wherein the 5'-wing segment consists of two linked nucleosides.

75. The compound of any of claims 68 to 73, wherein the 5'-wing segment consists of three linked nucleosides.

76. The compound of any of claims 68 to 73, wherein the 5'-wing segment consists of four linked nucleosides.

77. The compound of any of claims 68 to 73, wherein the 5'-wing segment consists of five linked nucleosides.

78. The compound of any of claims 68 to 73, wherein the 5'-wing segment consists of six linked nucleosides.

79. The compound of any of claims 68 to 78, wherein the 3'-wing segment consists of two linked nucleosides.

80. The compound of any of claims 68 to 78, wherein the 3'-wing segment consists of three linked nucleosides.

81. The compound of any of claims 68 to 78, wherein the 3'-wing segment consists of four linked nucleosides.

82. The compound of any of claims 68 to 78, wherein the 3'-wing segment consists of five linked nucleosides.

83. The compound of any of claims 68 to 78, wherein the 3'-wing segment consists of six linked nucleosides.

84. The compound of any of claims 68 to 83, wherein the gap segment consists of six linked deoxynucleosides.

85. The compound of any of claims 68 to 83, wherein the gap segment consists of seven linked deoxynucleosides.

86. The compound of any of claims 68 to 83, wherein the gap segment consists of eight linked deoxynucleosides.

87. The compound of any of claims 68 to 83, wherein the gap segment consists of nine linked deoxynucleosides.

88. The compound of any of claims 68 to 83, wherein the gap segment consists of ten linked deoxynucleosides.

89. The compound of any of claims 1 to 31, 33, 37 to 45, or 51 to 88, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:
    a. a gap segment consisting of ten linked deoxynucleosides;
    b. a 5' wing segment consisting of three linked nucleosides;
    c. a 3' wing segment consisting of three linked nucleosides;
    d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each nucleoside of each wing segment comprises a bicyclic sugar.

90. The compound of any of claims 1 to 31, 33, 37 to 45, or 51 to 88, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:
    a. a gap segment consisting of eight linked deoxynucleosides;
    b. a 5' wing segment consisting of four linked nucleosides and having an AABB 5'-wing motif;
    c. a 3' wing segment consisting of four linked nucleosides and having a BBAA 3'-wing motif;
    d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment.

91. The compound of any of claims 1 to 30, 34, 35, 46, or 50 to 88, wherein the modified oligonucleotide consists of 17 linked nucleosides and comprises:
    a. a gap segment consisting of seven linked deoxynucleosides;
    b. a 5' wing segment consisting of five linked nucleosides and having an AAABB 5'-wing motif;
    c. a 3' wing segment consisting of five linked nucleosides and having a BBAAA 3'-wing motif;
    d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment.

92. The compound of any of claims 1 to 31, 33, 37 to 45, or 51 to 88, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:
    a. a gap segment consisting of eight linked deoxynucleosides;
    b. a 5' wing segment consisting of four linked nucleosides and having a E-E-K-K 5'-wing motif;
    c. a 3' wing segment consisting of four linked nucleosides and having a K-K-E-E 3'-wing motif;
    d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each E represents 2'-O-methoxyethyl sugar and each K represents a cEt sugar.

93. The compound of any of claims 1 to 30, 34, 35, 46, or 50 to 88, wherein the modified oligonucleotide consists of 17 linked nucleosides and comprises:
    a. a gap segment consisting of seven linked deoxynucleosides;
    b. a 5' wing segment consisting of five linked nucleosides and having an E-E-E-K-K 5'-wing motif;
    c. a 3' wing segment consisting of five linked nucleosides and having a K-K-E-E-E 3'-wing motif;
    d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each E represents 2'-O-methoxyethyl sugar and each K represents a cEt sugar.

94. The compound of any of claims 1 to 30, 32, 33, or 49 to 88, wherein the modified oligonucleotide consists of 20 linked nucleosides and comprises:
    a. a gap segment consisting of ten linked deoxynucleosides;
    b. a 5' wing segment consisting of five linked nucleosides;
    c. a 3' wing segment consisting of five linked nucleosides;
    d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each nucleoside of each wing segment comprises a 2'-O-methoxyethyl sugar.

95. The compound of any of claims 1 to 31, 33, 34, 37 to 45, or 53 to 88, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:
    a. a gap segment consisting of ten linked deoxynucleosides;
    b. a 5' wing segment consisting of three linked nucleosides;

c. a 3' wing segment consisting of three linked nucleosides;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, and wherein each nucleoside of each wing segment comprises a cEt sugar.

96. The compound of any of claims 1 to 67, wherein the modified oligonucleotide comprises at least 8 contiguous nucleobases complementary to a target region within nucleobase 1343 and nucleobase 1368 of SEQ ID NO.: 1, and wherein the modified oligonucleotide comprises:
a. a gap segment consisting of linked deoxynucleosides;
b. a 5' wing segment consisting of linked nucleosides;
c. a 3' wing segment consisting of linked nucleosides;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

97. The compound of claim 96, wherein each modified sugar in the 5'-wing segment has the same modifications.

98. The compound of claim 96, wherein at least two modified sugars in the 5'-wing segment have different modifications.

99. The compound of any of claims 96 to 98 wherein each modified sugar in the 3'-wing segment has the same modifications.

100. The compound of any of claims 96 to 98, wherein at least two modified sugars in the 3'-wing segment have different modification.

101. The compound of claim 96, wherein at least one modified sugar is a bicyclic sugar selected from among cEt, LNA, α-L-LNA, ENA and 2'-thio LNAs.

102. The compound of claim 90 to 91, wherein each B represents a bicyclic sugar selected from among cEt, LNA, α-L-LNA, ENA and 2'-thio LNA.

103. The compound of claim 102, wherein the bicyclic sugar comprises BNA.

104. The compound of claim 102, wherein the bicyclic sugar comprises cEt.

105. The compound of claim 102, wherein the bicyclic sugar comprises LNA.

106. The compound of claim 102, wherein the bicyclic sugar comprises α-L-LNA.

107. The compound of claim 102, wherein the bicyclic sugar comprises ENA.

108. The compound of claim 102, wherein the bicyclic sugar comprises 2'-thio LNA.

109. The compound of claim 90 or 91, wherein each A represents a 2'-substituted nucleoside is selected from among: 2'-OCH_3, 2'-F, and 2'-O-methoxyethyl.

110. The compound of claim 109, wherein the 2'-substituted nucleoside comprises 2'-O-methoxyethyl.

111. The compound of any of claims 1 to 111, wherein at least one internucleoside linkage is a modified internucleoside linkage.

112. The compound of any of claims 1 to 111, wherein each internucleoside linkage is a phosphorothioate internucleoside linkage.

113. A compound consisting of ISIS 486178.

114. A compound consisting of ISIS 512497.

115. A compound consisting of ISIS 598768.

116. A compound consisting of ISIS 594300.

117. A compound consisting of ISIS 594292.

118. A compound consisting of ISIS 569473.

119. A compound consisting of ISIS 598769.

120. A compound consisting of ISIS 570808.

121. A compound consisting of ISIS 598777.

122. A compound having a nucleobase sequence as set forth in SEQ ID NO: 23, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:

a. a gap segment consisting of ten linked deoxynucleosides;
b. a 5' wing segment consisting of three linked nucleosides;
c. a 3' wing segment consisting of three linked nucleosides;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment;
e. wherein each nucleoside of each wing segment comprises a bicyclic sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

123. A compound having a nucleobase sequence as set forth in SEQ ID NO: 29, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:

a. a gap segment consisting of ten linked deoxynucleosides;
b. a 5' wing segment consisting of three linked nucleosides;
c. a 3' wing segment consisting of three linked nucleosides;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment;
e. wherein each nucleoside of each wing segment comprises a bicyclic sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

124. A compound having a nucleobase sequence as set forth in SEQ ID NO: 31, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:

a. a gap segment consisting of ten linked deoxynucleosides;
b. a 5' wing segment consisting of three linked nucleosides;
c. a 3' wing segment consisting of three linked nucleosides;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment;
e. wherein each nucleoside of each wing segment comprises a bicyclic sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

125. A compound having a nucleobase sequence as set forth in SEQ ID NO: 26, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:

a. a gap segment consisting of eight linked deoxynucleosides;

b. a 5' wing segment consisting of four linked nucleosides and having a E-E-K-K 5'-wing motif;
c. a 3' wing segment consisting of four linked nucleosides and having a K-K-E-E 3'-wing motif;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment;
e. wherein each E represents 2'-O-methoxyethyl sugar and each K represents a cEt sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

126. A compound having a nucleobase sequence as set forth in SEQ ID NO: 30, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:
a. a gap segment consisting of eight linked deoxynucleosides;
b. a 5' wing segment consisting of four linked nucleosides and having a E-E-K-K 5'-wing motif;
c. a 3' wing segment consisting of four linked nucleosides and having a K-K-E-E 3'-wing motif;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment;
e. wherein each E represents 2'-O-methoxyethyl sugar and each K represents a cEt sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

127. A compound having a nucleobase sequence as set forth in SEQ ID NO: 32, wherein the modified oligonucleotide consists of 16 linked nucleosides and comprises:
a. a gap segment consisting of eight linked deoxynucleosides;
b. a 5' wing segment consisting of four linked nucleosides and having a E-E-K-K 5'-wing motif;
c. a 3' wing segment consisting of four linked nucleosides and having a K-K-E-E 3'-wing motif;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment;
e. wherein each E represents 2'-O-methoxyethyl sugar and each K represents a cEt sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

128. A compound having a nucleobase sequence as set forth in SEQ ID NO: 27, wherein the modified oligonucleotide consists of 17 linked nucleosides and comprises:

a. a gap segment consisting of seven linked deoxynucleosides;
b. a 5' wing segment consisting of five linked nucleosides and having an E-E-E-K-K 5'-wing motif;
c. a 3' wing segment consisting of five linked nucleosides and having a K-K-E-E-E 3'-wing motif;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment;
e. wherein each E represents 2'-O-methoxyethyl sugar and each K represents a cEt sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

129. A compound having a nucleobase sequence as set forth in SEQ ID NO: 28, wherein the modified oligonucleotide consists of 17 linked nucleosides and comprises:

a. a gap segment consisting of seven linked deoxynucleosides;
b. a 5' wing segment consisting of five linked nucleosides and having an E-E-E-K-K 5'-wing motif;
c. a 3' wing segment consisting of five linked nucleosides and having a K-K-E-E-E 3'-wing motif;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment;
e. wherein each E represents 2'-O-methoxyethyl sugar and each K represents a cEt sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

130. A compound having a nucleobase sequence as set forth in SEQ ID NO: 25, wherein the modified oligonucleotide consists of 20 linked nucleosides and comprises:

a. a gap segment consisting of ten linked deoxynucleosides;
b. a 5' wing segment consisting of five linked nucleosides;
c. a 3' wing segment consisting of five linked nucleosides;
d. wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment;

e. wherein each nucleoside of each wing segment comprises a 2'-O-methoxyethyl sugar;
f. wherein each internucleoside linkage is a phosphorothioate internucleoside linkage; and
g. wherein each cytosine residue is a 5-methyl cytosine.

131. The compound of any of claims 1 to 130 comprising a conjugate.

132. A composition comprising the compound of any of claims 1 to 131, and a pharmaceutically acceptable carrier or diluent.

133. A method of treating DM1 in an animal comprising administering to an animal in need thereof a compound according to any of claims 1 to 131, or a composition according to claim 132.

134. The method of claim 133, wherein the compound reduces DMPK mRNA levels.

135. The method of claim 133, wherein the compound reduces DMPK protein expression.

136. The method of claim 133, wherein the compound reduces CUGexp DMPK.

137. The method of claim 133, wherein the compound preferentially reduces CUGexp DMPK.

138. The method of claim 133, wherein the compound reduces CUGexp DMPK mRNA.

139. The method of claim 133, wherein the compound preferentially reduces CUGexp DMPK mRNA.

140. The method of claim 138 or 139, wherein the preferential reduction of CUGexp is in muscle tissue.

141. A method of reducing myotonia in an animal comprising administering to an animal in need thereof a compound according to any of claims 1 to 131, or a composition according to claim 132.

142. A method of reducing MBLN dependent spliceopathy in an animal comprising administering to an animal in need thereof a compound according to any of claims 1 to 131, or a composition according to claim 132.

143. The method of claim 142, wherein splicing of any of Serca1, m-Titin, Clcn1, and Zasp is corrected.

144. The method of any of claims 133 to 143, wherein the administering is systemic administration.

145. The method of any of claims 133 to 143, wherein the administering is parenteral administration.

146. The method of claim 144, wherein the systemic administration is any of subcutaneous administration, intravenous administration, intracerebroventricular administration, and intrathecal administration.

147. The method of any of claims 133 to 143, wherein the administration is not intramuscular administration.

148. The method of any of claims 133 to 143, wherein the animal is a human.

149. A method of reducing spliceopathy of *Serca1* in an animal in need thereof by administering a compound according to any of claims 1 to 131, or a composition according to claim 132, and thereby causing *Serca1* exon 22 inclusion.

150. A method of reducing spliceopathy of *m-Titin* in an animal in need thereof by administering a compound according to any of claims 1 to 131, or a composition according to claim 132, and thereby causing *m-Titin* exon 5 inclusion.

151. A method of reducing spliceopathy of *Clcn1* in an animal in need thereof by administering a compound according to any of claims 1 to 131, or a composition according to claim 132, and thereby causing *Clcn1* exon 7a inclusion.

152. A method of reducing spliceopathy of *Zasp* in an animal in need thereof by administering a compound according to any of claims 1 to 131, or a composition according to claim 132, and thereby causing *Zasp* exon 11 inclusion.

153. A method of reducing DMPK mRNA in a cell, comprising contacting a cell with a compound according to any of claims 1 to 131, or a composition according to claim 132.

154. A method of reducing DMPK protein in a cell, comprising contacting a cell with a compound according to any of claims 1 to 131, or a composition according to claim 132.

155. A method of reducing CUGexp mRNA in a cell, comprising contacting a cell with a compound according to any of claims 1 to 131, or a composition according to claim 132.

156. The method of any of claims 153 to 155, wherein the cell is in an animal.

157. The method of claim 156, wherein the animal is a human.

158. A method of achieving a preferential reduction of CUGexp DMPK RNA, comprising:

a. selecting a subject having type 1 myotonic dystrophy or having a CUGexp DMPK RNA; and
b. administering to said subject a compound according to any of claims 1 to 131, or a composition according to claim 132;

wherein said compound according to any of claims 1 to 131, or a composition according to claim 132, when bound to said CUGexp DMPK RNA, activates a ribonuclease, thereby achieving a preferential reduction of said CUGexp DMPK RNA.

159. A method of achieving a preferential reduction of CUGexp DMPK RNA, comprising:

a. selecting a subject having type 1 myotonic dystrophy or having a CUGexp DMPK RNA; and
b. systemically administering to said subject a compound according to any of claims 1 to 131, or a composition according to claim 132;

wherein said chemically-modified antisense oligonucleotide, when bound to said CUGexp DMPK RNA, achieves a preferential reduction of said CUGexp DMPK RNA.

160. A method of reducing spliceopathy in a subject suspected of having type 1 myotonic dystrophy or having a nuclear retained CUGexp DMPK RNA, comprising:
administering to said subject a compound according to any of claims 1 to 131, or a composition according to claim 132,
wherein the compound according to any of claims 1 to 131, or a composition according to claim 132, when bound to said mutant DMPK RNA, activates a ribonuclease, thereby reducing spliceopathy.

161. A method of preferentially reducing CUGexp DMPK RNA, reducing myotonia or reducing spliceopathy in an animal comprising administering to the animal a compound according to any of claims 1 to 131 or a pharmaceutical composition of claim 132, wherein the compound reduces

DMPK expression in the animal, thereby preferentially reducing CUGexp DMPK RNA, reducing myotonia, or reducing spliceopathy in the animal.

162. A method for treating an animal with type 1 myotonic dystrophy comprising

identifying said animal with type 1 myotonic dystrophy,

administering to said animal a therapeutically effective amount of a compound according to any of claims 1 to 131 or a pharmaceutical composition of claim 132,

wherein said animal with type 1 myotonic dystrophy is treated.

163. A method of reducing DMPK expression comprising administering to an animal a compound according to any of claims 1 to 131 or a pharmaceutical composition of claim 132, wherein expression of DMPK is reduced.

164. A compound according to any of claims 1 to 131 or a pharmaceutical composition of claim 132, for use in treating DM1 in an animal.

165. A compound according to any of claims 1 to 131 or a pharmaceutical composition of claim 132, for use in reducing myotonia in an animal.

166. A compound according to any of claims 1 to 131 or a pharmaceutical composition of claim 132, for use in reducing MBLN dependent spliceopathy in an animal.

167. Use of the compound according to any of claims 1 to 131 or the pharmaceutical composition of claim 132 for the preparation of a medicament for the treatment of type 1 myotonic dystrophy, or a symptom thereof.