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(54) **COMPOSITIONS FOR TREATING MUSCULAR DYSTROPHY**

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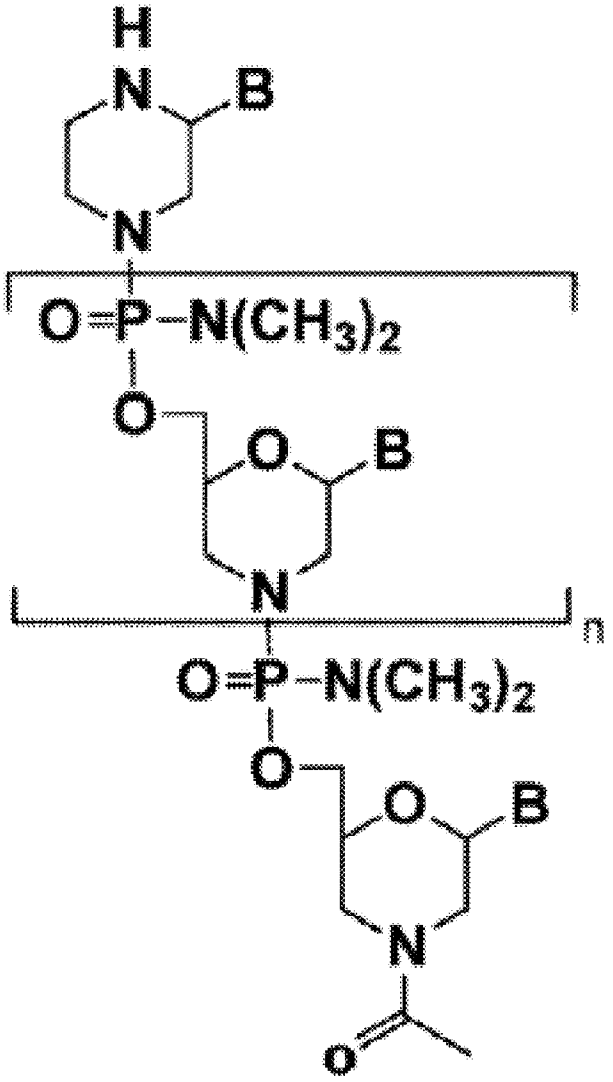
(57) **ABSTRACT**

Improved compositions and methods for treating muscular dystrophy by administering antisense molecules capable of binding to a selected target site in the human dystrophin gene to induce exon skipping are described.



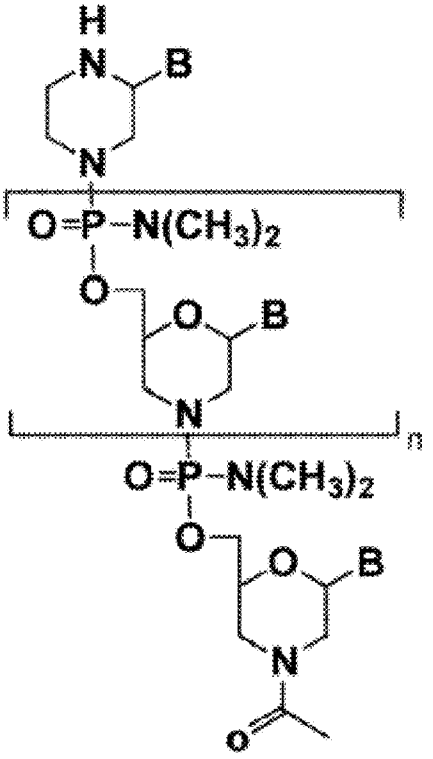


Fig. 1A

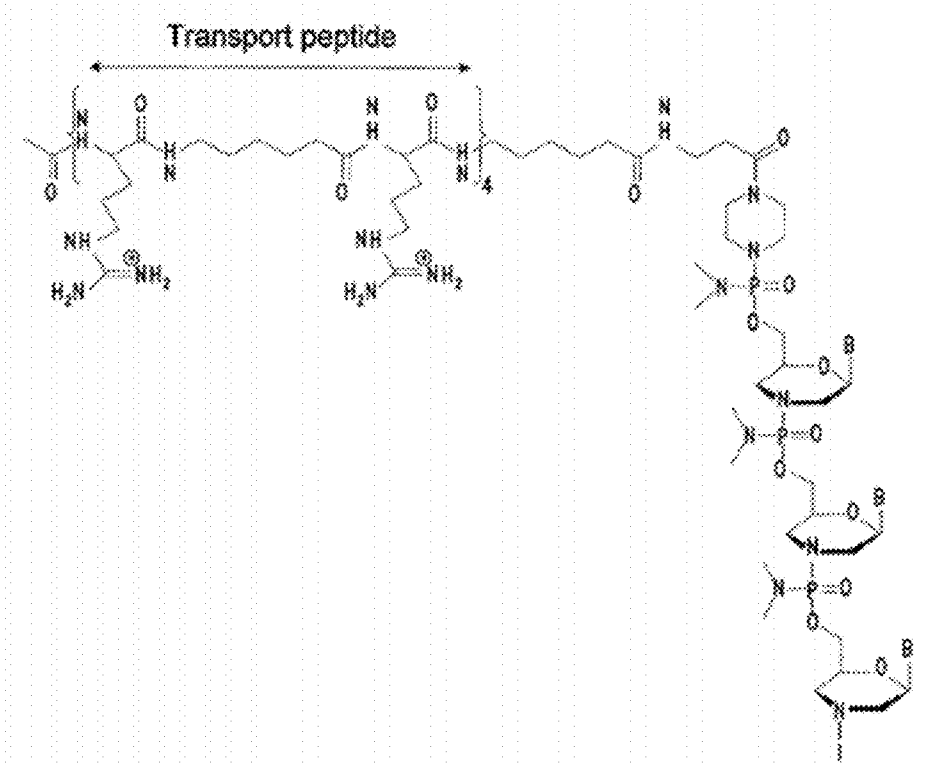


Fig. 1B

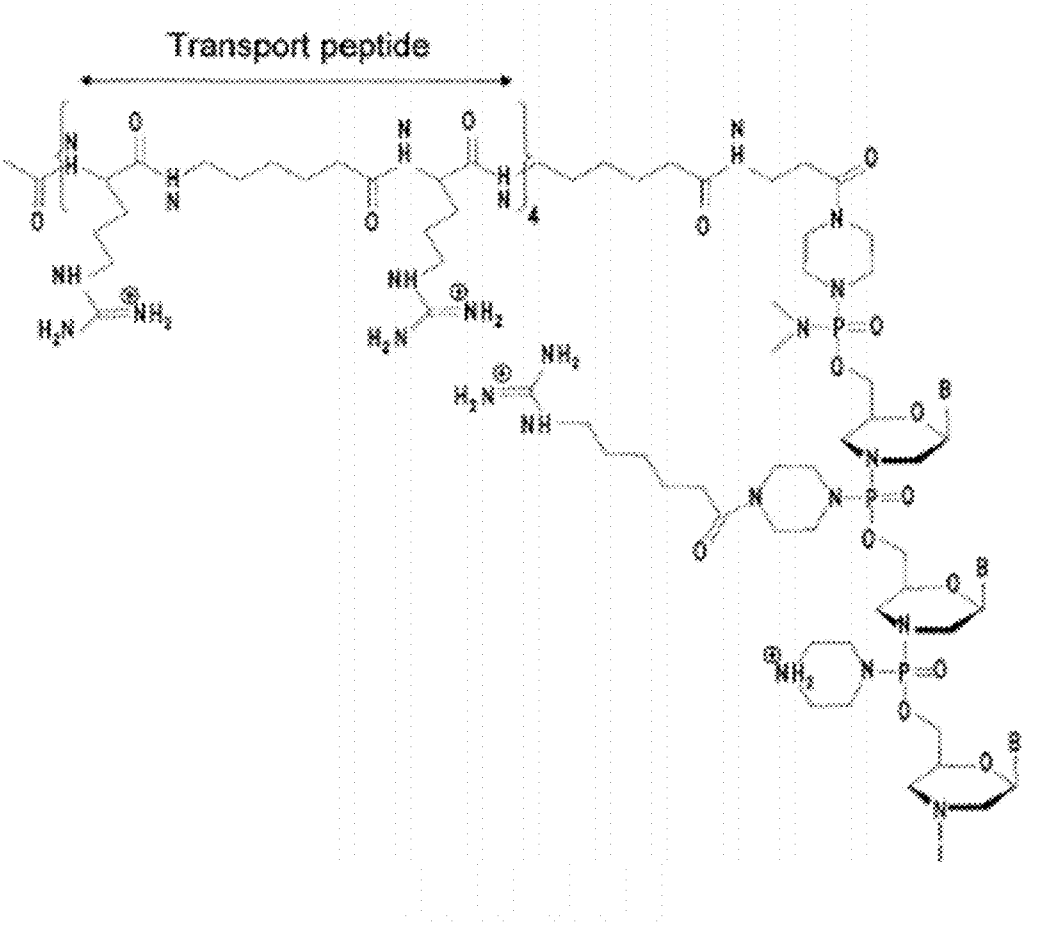


Fig. 1C

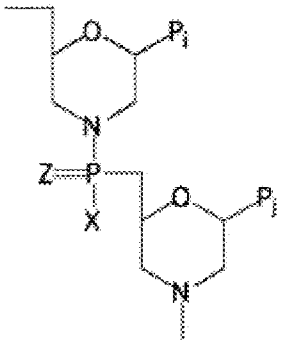


Fig. 1D

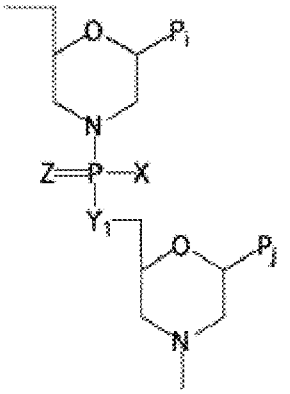


Fig. 1E

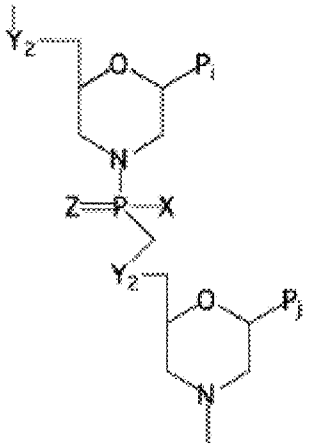


Fig. 1F

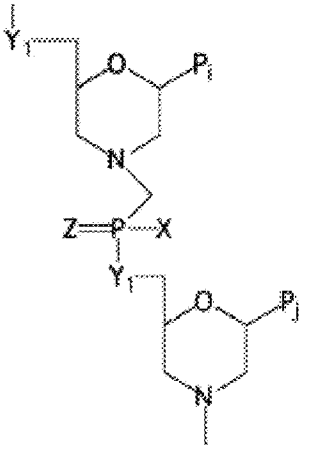


Fig. 1G

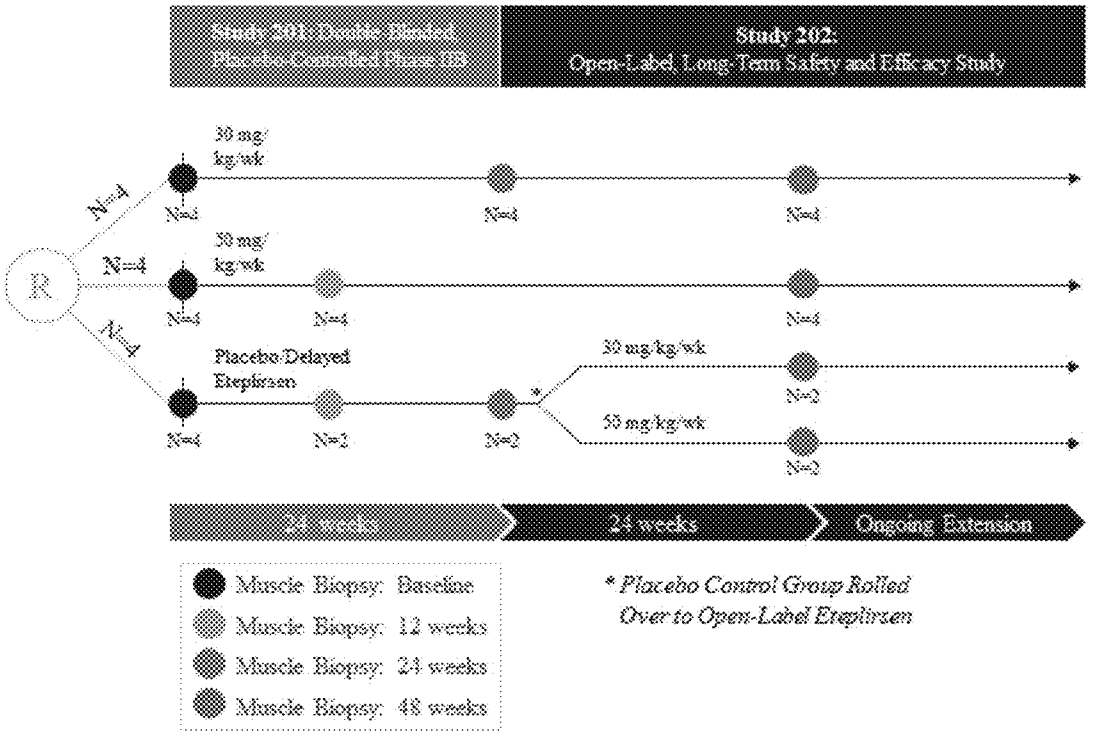

Study 201: Double-Blinded, Placebo-Controlled Phase IIB
Study 202:
Open-Label, Long-Term Safety and Efficacy Study
R
N=4
N=4
N=4
30 mg/kg/wk
30 mg/kg/wk
Placebo/Delayed Eteplirsen
N=4
N=4
N=4
N=4
N=4
N=2
N=2
N=2
N=2
30 mg/kg/wk
50 mg/kg/wk
*
24 weeks
24 weeks
Ongoing Extension
Muscle Biopsy: Baseline
Muscle Biopsy: 12 weeks
Muscle Biopsy: 24 weeks
Muscle Biopsy: 48 weeks
* Placebo Control Group Rolled Over to Open-Label Eteplirsen

Fig. 2

A

Cohort (n)	Week 12 Mean Change from BL, SE (p-value) [4]	Week 24 Mean Change from BL, SE (p-value) [4]	Week 48 Mean Change from BL, S (p-value) [5]
All Eteplirsen (8)	NA	NA	47.3, 3.89 (≤0.001)
Eteplirsen 30mg/kg (4)	ND	22.9, 2.90 (≤0.002)	51.7, 3.54 (≤0.001)
Eteplirsen 50 mg/kg (4)	0.8, 3.55 (NS)	ND	42.9, 6.72 (≤0.008)
Placebo/Delayed Eteplirsen (4) [6]	-4.0, 2.92	-4.0, 2.92	37.7, 6.30 (≤0.009) [5]
Eteplirsen 30 mg/kg (2)	ND	-7.48, 1.00	33.6, 5.23
Eteplirsen 50 mg/kg (2)	-0.6, 5.36	ND	41.8, 13.30

B

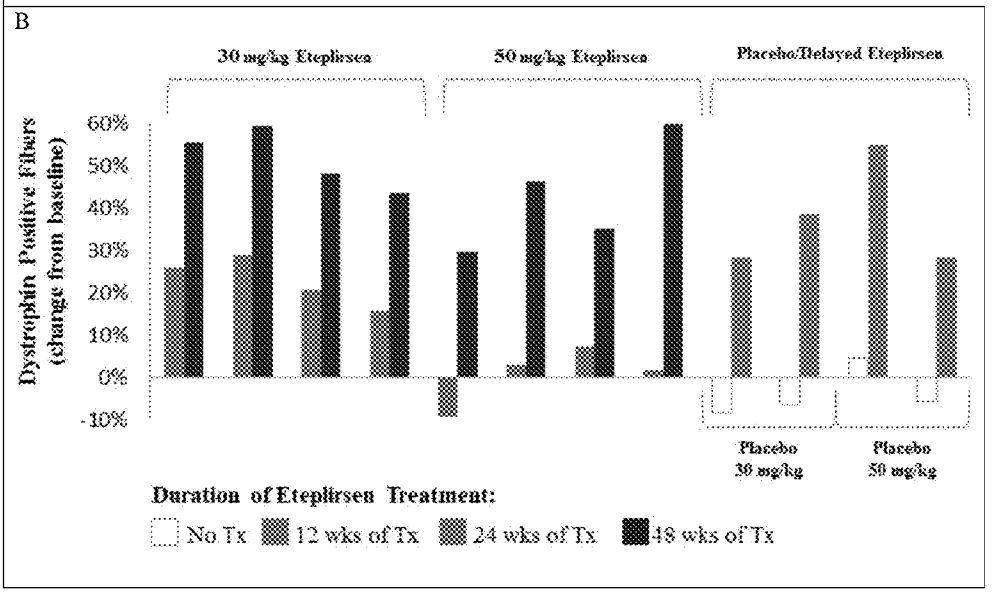


Fig. 3

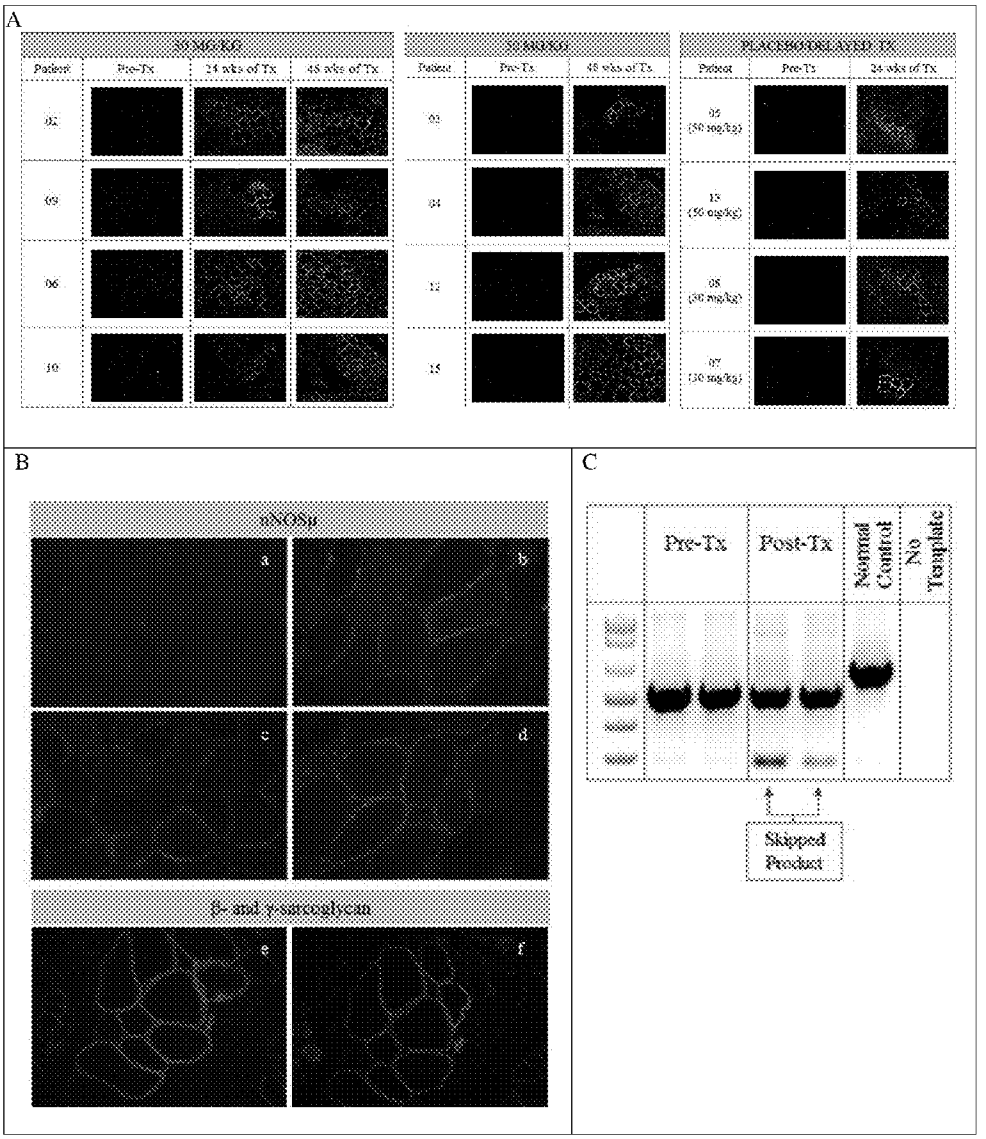

A
Patient
Pre-Tx
24 wks of Tx
48 wks of Tx
B
nNOSμ
a
b
c
d
δ- and γ-sarcoglycan
e
f
C
Pre-Tx
Post-Tx
Normal Control
No Template
Skipped Product

Fig. 4

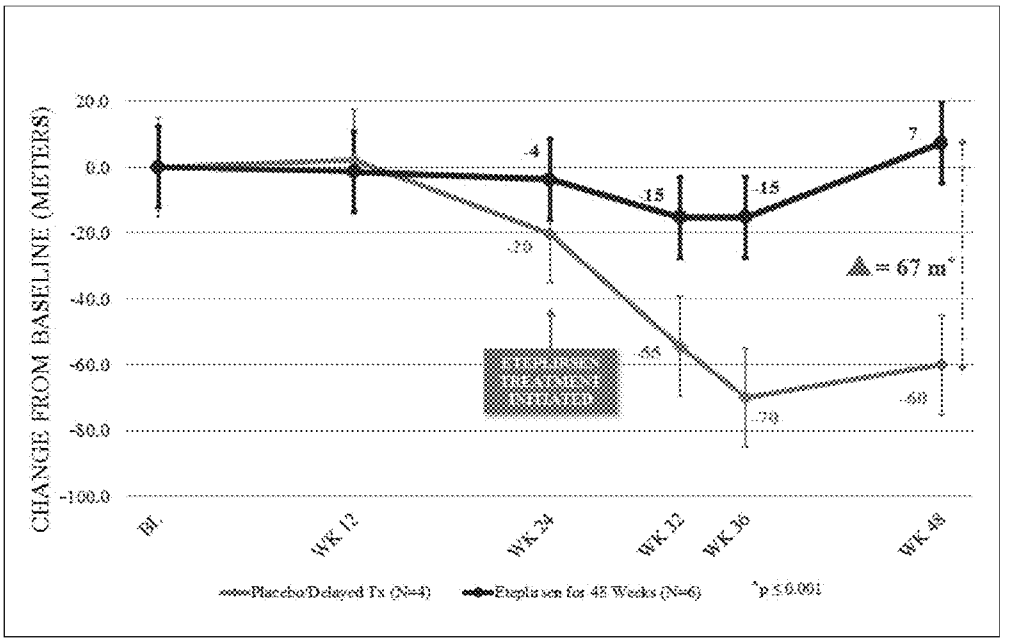

CHANGE FROM BASELINE (METERS)
20.0
0.0
-20.0
-40.0
-60.0
-80.0
-100.0
BL
WK 12
WK 24
WK 32
WK 36
WK 48
-4
-15
-15
7
-20
-52
-78
-60
Δ = 67 m*
Placebo/Delayed Tx (N=4)
Eteplirsen for 48 Weeks (N=6)
*p ≤ 0.001

Fig. 5

COMPOSITIONS FOR TREATING MUSCULAR DYSTROPHY

RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Application No. 61/793,463, filed on Mar. 15, 2013, entitled "COMPOSITIONS FOR TREATING MUSCULAR DYSTROPHY". The entire contents of the foregoing application are incorporated herein by reference.

STATEMENT REGARDING SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted in computer readable form (CRF) via EFS-Web and is hereby incorporated by reference in its entirety. Said CRF, created on Jul. 22, 2014, is named AVN_012A_Sequence_Listing.txt and is 187 Kilobytes in size. The Sequence Listing is being submitted by EFS Web and is hereby incorporated by reference into the specification.

FIELD OF THE INVENTION

[0003] The present invention relates to improved methods for treating muscular dystrophy in a patient. It also provides compositions suitable for facilitating exon skipping in the human dystrophin gene.

BACKGROUND OF THE INVENTION

[0004] Antisense technologies are being developed using a range of chemistries to affect gene expression at a variety of different levels (transcription, splicing, stability, translation). Much of that research has focused on the use of antisense compounds to correct or compensate for abnormal or disease-associated genes in a wide range of indications. Antisense molecules are able to inhibit gene expression with specificity, and because of this, many research efforts concerning oligonucleotides as modulators of gene expression have focused on inhibiting the expression of targeted genes or the function of cis-acting elements. The antisense oligonucleotides are typically directed against RNA, either the sense strand (e.g., mRNA), or minus-strand in the case of some viral RNA targets. To achieve a desired effect of specific gene down-regulation, the oligonucleotides generally either promote the decay of the targeted mRNA, block translation of the mRNA or block the function of cis-acting RNA elements, thereby effectively preventing either de novo synthesis of the target protein or replication of the viral RNA.

[0005] However, such techniques are not useful where the object is to up-regulate production of the native protein or compensate for mutations that induce premature termination of translation, such as nonsense or frame-shifting mutations. In these cases, the defective gene transcript should not be subjected to targeted degradation or steric inhibition, so the antisense oligonucleotide chemistry should not promote target mRNA decay or block translation.

[0006] In a variety of genetic diseases, the effects of mutations on the eventual expression of a gene can be modulated through a process of targeted exon skipping during the splicing process. The splicing process is directed by complex multi-component machinery that brings adjacent exon-intron junctions in pre-mRNA into close proximity and performs cleavage of phosphodiester bonds at the ends of the introns with their subsequent reformation between exons that are to be spliced together. This complex and highly precise process is mediated by sequence motifs in the pre-mRNA that are relatively short, semi-conserved RNA segments to which various nuclear splicing factors that are then involved in the splicing reactions bind. By changing the way the splicing machinery reads or recognizes the motifs involved in pre-mRNA processing, it is possible to create differentially spliced mRNA molecules. It has now been recognized that the majority of human genes are alternatively spliced during normal gene expression, although the mechanisms involved have not been identified. Bennett et al. (U.S. Pat. No. 6,210,892) describe antisense modulation of wild-type cellular mRNA processing using antisense oligonucleotide analogs that do not induce RNAse H-mediated cleavage of the target RNA. This finds utility in being able to generate alternatively spliced mRNAs that lack specific exons (e.g., as described by (Sazani, Kole, et al. 2007) for the generation of soluble TNF superfamily receptors that lack exons encoding membrane spanning domains.

[0007] In cases where a normally functional protein is prematurely terminated because of mutations therein, a means for restoring some functional protein production through antisense technology has been shown to be possible through intervention during the splicing processes, and that if exons associated with disease-causing mutations can be specifically deleted from some genes, a shortened protein product can sometimes be produced that has similar biological properties of the native protein or has sufficient biological activity to ameliorate the disease caused by mutations associated with the exon (see e.g., Sierakowska, Sambade et al. 1996; Wilton, Lloyd et al. 1999; van Deutekom, Bremmer-Bout et al. 2001; Lu, Mann et al. 2003; Aartsma-Rus, Janson et al. 2004). Kole et al. (U.S. Pat. Nos. 5,627,274; 5,916,808; 5,976,879; and 5,665,593) disclose methods of combating aberrant splicing using modified antisense oligonucleotide analogs that do not promote decay of the targeted pre-mRNA. Bennett et al. (U.S. Pat. No. 6,210,892) describe antisense modulation of wild-type cellular mRNA processing also using antisense oligonucleotide analogs that do not induce RNAse H-mediated cleavage of the target RNA.

[0008] The process of targeted exon skipping is likely to be particularly useful in long genes where there are many exons and introns, where there is redundancy in the genetic constitution of the exons or where a protein is able to function without one or more particular exons. Efforts to redirect gene processing for the treatment of genetic diseases associated with truncations caused by mutations in various genes have focused on the use of antisense oligonucleotides that either: (1) fully or partially overlap with the elements involved in the splicing process; or (2) bind to the pre-mRNA at a position sufficiently close to the element to disrupt the binding and function of the splicing factors that would normally mediate a particular splicing reaction which occurs at that element.

[0009] Duchenne muscular dystrophy (DMD) is caused by a defect in the expression of the protein dystrophin. The gene encoding the protein contains 79 exons spread out over more than 2 million nucleotides of DNA. Any exonic mutation that changes the reading frame of the exon, or introduces a stop codon, or is characterized by removal of an entire out of frame exon or exons, or duplications of one or more exons, has the potential to disrupt production of functional dystrophin, resulting in DMD.

[0010] Disease onset can be documented at birth with elevated creatine kinase levels, and significant motor deficits may be present in the first year of life. By the age of seven or

eight, most patients with DMD have an increasingly labored gait and are losing the ability to rise from the floor and climb stairs; by ages 10 to 14, most are wheelchair-dependent. DMD is uniformly fatal; affected individuals typically die of respiratory and/or cardiac failure in their late teens or early 20s. The continuous progression of DMD allows for therapeutic intervention at all stages of the disease; however, treatment is currently limited to glucocorticoids, which are associated with numerous side effects including weight gain, behavioral changes, pubertal changes, osteoporosis, Cushingoid facies, growth inhibition, and cataracts. Consequently, developing better therapies to treat the underlying cause of this disease is imperative.

[0011] A less severe form of muscular dystrophy, Becker muscular dystrophy (BMD) has been found to arise where a mutation, typically a deletion of one or more exons, results in a correct reading frame along the entire dystrophin transcript, such that translation of mRNA into protein is not prematurely terminated. If the joining of the upstream and downstream exons in the processing of a mutated dystrophin pre-mRNA maintains the correct reading frame of the gene, the result is an mRNA coding for a protein with a short internal deletion that retains some activity, resulting in a Becker phenotype.

[0012] For many years it has been known that deletions of an exon or exons which do not alter the reading frame of a dystrophin protein would give rise to a BMD phenotype, whereas an exon deletion that causes a frame-shift will give rise to DMD (Monaco, Bertelson et al. 1988). In general, dystrophin mutations including point mutations and exon deletions that change the reading frame and thus interrupt proper protein translation result in DMD. It should also be noted that some BMD and DMD patients have exon deletions covering multiple exons.

[0013] Modulation of mutant dystrophin pre-mRNA splicing with antisense oligoribonucleotides has been reported both in vitro and in vivo (see e.g., Matsuo, Masumura et al. 1991; Takeshima, Nishio et al. 1995; Pramono, Takeshima et al. 1996; Dunckley, Eperon et al. 1997; Dunckley, Manoharan et al. 1998; Errington, Mann et al. 2003).

[0014] The first example of specific and reproducible exon skipping in the mdx mouse model was reported by Wilton et al. (Wilton, Lloyd et al. 1999). By directing an antisense molecule to the donor splice site, consistent and efficient exon 23 skipping was induced in the dystrophin mRNA within 6 hours of treatment of the cultured cells. Wilton et al. also describe targeting the acceptor region of the mouse dystrophin pre-mRNA with longer antisense oligonucleotides. While the first antisense oligonucleotide directed at the intron 23 donor splice site induced consistent exon skipping in primary cultured myoblasts, this compound was found to be much less efficient in immortalized cell cultures expressing higher levels of dystrophin. However, with refined targeting and antisense oligonucleotide design, the efficiency of specific exon removal was increased by almost an order of magnitude (Mann, Honeyman et al. 2002).

[0015] Recent studies have begun to address the challenge of achieving sustained dystrophin expression accompanied by minimal adverse effects in tissues affected by the absence of dystrophin. Intramuscular injection of an antisense oligonucleotide targeted to exon 51 (PRO051) into the tibialis anterior muscle in four patients with DMD resulted in specific skipping of exon 51 without any clinically apparent adverse effects (Mann, Honeyman et al. 2002; van Deutekom, Janson et al. 2007). Studies looking at systemic delivery of an antisense phosphorodiamidate morpholino oligomer conjugated to a cell-penetrating peptide (PPMO) targeted to exon 23 in mdx mice produced high and sustained dystrophin protein production in skeletal and cardiac muscles without detectable toxicity (Jearawiriyapaisarn, Moulton et al. 2008; Wu, Moulton et al. 2008; Yin, Moulton et al. 2008).

[0016] Recent clinical trials testing the safety and efficacy of splice switching oligonucleotides (SSOs) for the treatment of DMD are based on SSO technology to induce alternative splicing of pre-mRNAs by steric blockade of the spliceosome (Cirak et al., 2011; Goemans et al., 2011; Kinali et al., 2009; van Deutekom et al., 2007). However, despite these successes, the pharmacological options available for treating DMD are limited. Notably, an antisense oligonucleotide (drisapersen), which utilizes a negatively charged phosphorothioate backbone, has been associated in clinical trials with proteinuria, increased urinary al-microglobulin, thrombocytopenia and injection site reactions, such as erythema and inflammation.

[0017] Thus, there remains a need for improved compositions and methods for treating muscular dystrophy, such as DMD and BMD in patients.

SUMMARY OF THE INVENTION

[0018] The present invention is based, at least in part, on compelling evidence of a therapeutic effect of an exon skipping antisense oligonucleotide, eteplirsen, which represents a major advance in the treatment of DMD by addressing the underlying cause of the disease. The novel finding that treatment with an exon 51 skipping antisense oligonucleotide, eteplirsen, produced reliable increases in novel dystrophin and stabilized walking ability (e.g., stabilization of ambulation), as measured by the 6 Minute Walk Test (6MWT), underscores the potential alter the course of the disease. Significantly, no drug-related adverse events were seen in 576 infusions administered over one year. When applied to other exons, the use of exon skipping antisense oligonucleotides could treat an estimated 70% to 80% of patients who have DMD due to a deletion in the dystrophin gene.

[0019] Accordingly, the present invention relates to methods of treating Duchenne muscular dystrophy (DMD) or Becker muscular dystrophy (BMD) in patients by administering an effective amount of a composition comprising an antisense oligonucleotide of 20 to 50 nucleotides in length comprising at least 10 consecutive nucleotides complementary to a target region in an exon of the human dystrophin gene to specifically hybridize to the target region, induce exon skipping, and thereby treat the disease. In one embodiment, an effective amount is at least 20 mg/kg for a period of time sufficient to increase the number of dystrophin-positive fibers in a subject to at least 20% of normal, and stabilize, maintain, or improve walking distance from a 20% deficit, for example in a 6 MWT, in the patient, relative to a healthy peer. In another embodiment, an effective amount is at least 20 mg/kg to about 30 mg/kg, about 25 mg/kg to about 30 mg/kg, or about 30 mg/kg to about 50 mg/kg. In yet another embodiment, an effective amount is about 30 mg/kg or about 50 mg/kg.

[0020] In another aspect, an effective amount is at least 20 mg/kg, about 25 mg/kg, about 30 mg/kg, or about 30 mg/kg to about 50 mg/kg, for at least 24 weeks, at least 36 weeks, or at least 48 weeks, to thereby increase the number of dystrophin-positive fibers in a subject to at least 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about

90%, about 95% of normal, and stabilize or improve walking distance from a 20% deficit, for example in a 6 MWT, in the patient relative to a healthy peer. In one embodiment, treatment increases the number of dystrophin-positive fibers to 20-60%, or 30-50% of normal in the patient. In some embodiments, treatment is by systemic administration, such as once weekly by infusion. In other embodiments, treatment includes administering another therapeutic agent, such as a steroid to the subject.

[0021] In another aspect, the present invention provides a method of treating DMD or BMD in a patient by administering about 30 mg/kg to about 50 mg/kg of a composition comprising an antisense oligonucleotide of 20 to 50 nucleotides in length comprising at least 10 consecutive nucleotides complementary to a target region in an exon of the human dystrophin gene, wherein the antisense oligonucleotide specifically hybridizes to the target region inducing exon skipping, thereby treating the subject. In one embodiment, the antisense oligonucleotide is substantially uncharged. In another embodiment, the antisense oligonucleotide comprises morpholino subunits linked by phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit. In yet another embodiment, the antisense oligonucleotide comprises morpholino subunits linked by substantially uncharged phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit. In other aspects, the antisense oligonucleotide comprises morpholino subunits and phosphorodiamidate intersubunit linkages.

[0022] In some embodiments, the antisense oligonucleotide is 20 to 50, 30 to 50, or 20 to 30 nucleotides in length comprising at least 10, 12, 15, 17, or 20 consecutive nucleotides complementary to a target region in an exon of the human dystrophin gene selected from the group consisting of exon 51, exon 50, exon 53, exon 45, exon 46, exon 44, exon 52, exon 55 and exon 8. In one embodiment, the antisense is 20 to 50, 30 to 50, or 20 to 30 nucleotides in length and includes at least 20 consecutive nucleotides eteplirsen (SEQ ID NO: 1). In another embodiment, the antisense oligonucleotide is 20 to 50, 30 to 50, or 20 to 30 nucleotides in length and includes at least 10, 12, 15, 17, or 20 consecutive nucleotides of the antisense oligonucleotide set forth as SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, or SEQ ID NO: 9. In yet another embodiment, the antisense oligonucleotide is 20 to 50, 30 to 50, or 20 to 30 nucleotides in length and includes at least 10, 12, 15, 17, or 20 consecutive nucleotides of a nucleotide sequences set forth in Tables 3 and 4, wherein uracil bases in the antisense oligonucleotide are optionally thymine bases.

[0023] In one embodiment, the composition includes eteplirsen (SEQ ID NO: 1), and, optionally, a pharmaceutically acceptable carrier. In another embodiment, the composition includes an antisense oligonucleotide selected from the group consisting of SEQ ID NOS: 1-9, such as SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, and SEQ ID NO: 9. In yet another embodiment, the antisense oligonucleotide is any one or a combination of the nucleotide sequences set forth in Tables 3 and 4, wherein uracil bases in the antisense oligonucleotide are optionally thymine bases. In some aspects, the antisense oligonucleotide is chemically linked to one or more moieties or conjugates that enhance the activity, cellular distribution, or cellular uptake of the antisense oligonucleotide, such as an arginine-rich peptide.

[0024] In another aspect, the present invention provides a method of treating DMD or BMD in a patient by administering at least 20 mg/kg of a composition comprising eteplirsen (SEQ ID NO: 1) for a period of time sufficient to increase the number of dystrophin-positive fibers in a subject to at least about 20% of normal, and stabilize or improve walking distance from a 20% deficit, for example in a 6 MWT, in the patient, relative to a healthy peer. In another embodiment, an effective amount is at least 20 mg/kg to about 30 mg/kg, about 25 mg/kg to about 30 mg/kg, or about 30 mg/kg to about 50 mg/kg of a composition comprising eteplirsen (SEQ ID NO: 1), and, optionally, a pharmaceutically acceptable carrier, such as phosphate-buffered saline.

[0025] In another aspect, an effective amount of a composition comprising eteplirsen (SEQ ID NO: 1) is at least 20 mg/kg, about 25 mg/kg, about 30 mg/kg, or about 30 mg/kg to about 50 mg/kg, for at least 24 weeks, at least 36 weeks, or at least 48 weeks, to thereby increase the number of dystrophin-positive fibers in a subject to at least about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, about 95% of normal, and stabilize or improve walking distance from a 20% deficit, for example in a 6 MWT, in the patient relative to a healthy peer. In some embodiments, treatment with antisense oligonucleotides of the present invention slows or reduces the loss of ambulation that would be expected without treatment. In some embodiments, treatment with the antisense oligonucleotides of the present invention stabilizes, maintains, or increases a stable walking distance in a patient. For example, treatment may increase the stable walking distance in the patient from baseline to greater than 3, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30 or 50 meters (including all integers in between).

BRIEF DESCRIPTION OF THE FIGURES

[0026] The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

[0027] FIG. **1**A shows an exemplary morpholino oligomer structure with a phosphorodiamidate linkage.

[0028] FIG. **1**B shows a conjugate of an arginine-rich peptide and an antisense oligomer, in accordance with an embodiment of the invention.

[0029] FIG. **1**C shows a conjugate as in FIG. **1**B, wherein the backbone linkages contain one or more positively charged groups.

[0030] FIGS. **1**D-G show the repeating subunit segment of exemplary morpholino oligonucleotides, designated D through G.

[0031] FIG. **2** is a schematic representation of the study design for treating DMD patients. Twelve DMD patients were randomized to one of three cohorts in the double-blind, placebo-controlled study, 201: Cohort 1, eteplirsen 30 mg/kg/wk; Cohort 2, eteplirsen 50 mg/kg/wk; and Cohort 3, placebo/delayed eteplirsen. At week 25, placebo-treated patients in Cohort 3 switched to open-label treatment with 30 or 50 mg/kg/week eteplirsen. Patients were maintained on their same dose of eteplirsen under the open-label extension study, 202. Muscle Biopsies. Patients underwent biceps biopsies at baseline and deltoid biopsies at week 48 for analysis of dystrophin. Additional biceps biopsies were obtained at week 12

(from patients in Cohort 2 and two patients in Cohort 3) or week 24 (from patients in Cohort 1 and two patients in Cohort 3). Efficacy Evaluations. The 6MWT was used as a functional outcome measure and was performed pre-treatment and every 12 weeks post treatment through week 48.

[0032] FIG. **3** depicts dystrophin-positive muscle fibers after 12, 24, and 48 weeks of eteplirsen. Panels A and B show the mean absolute change from baseline in the percentage of dystrophin-positive fibers at weeks 12, 24, and week 48 by treatment group. In Panel A: *P-value is for comparison between eteplirsen and placebo using the pooled results from weeks 12 and 24, and is based on an analysis of covariance model for ranked data with treatment as a fixed effect and baseline value and time since DMD diagnosis as covariates. Mean changes shown are based on descriptive statistics. †P-value is from a paired t-test comparing the week 48 value to baseline. ‡Results from the placebo-treated patients biopsied at weeks 12 and 24 are pooled. §Placebo/delayed eteplirsen patients began receiving eteplirsen at week 25 and had received a total of 24 doses at week 48. Abbreviations: BL=baseline; NA=not applicable; ND=not done; NS=not significant; SE=standard error.

[0033] FIG. **4** shows the effects of eteplirsen on the dystrophin-associated glycoprotein complex. (A) Representative examples of time-dependent increases in dystrophin-positive fibers in relation to treatment for all participating study patients. (B) nNOS μ staining in muscle from DMD (a) and normal (c) control patients (not in study), and from patient 6 at baseline (b) and week 48 (d), demonstrates restoration of nNOSμ binding with eteplirsen. β-sarcoglycan (e) and γ-sarcoglycan (f) staining in patient 6 at week 48 demonstrate restoration of the sarcoglycan complex with eteplirsen. (C) RT-PCR shows skipped product (289 bp) post-treatment in the muscle of patient 12.

[0034] FIG. **5** graphically depicts the functional efficacy of eteplirsen. The dark purple line shows the change from baseline in distance walked on the 6MWT over time for the 6 evaluable patients who received eteplirsen from the start of 201 (two boys were unable to at or beyond week 24 were excluded from this analysis). The gray line shows change from baseline in distance walked on the 6MWT for the 4 patients who received placebo for the first 24 weeks and eteplirsen for the last 24 weeks.

DETAILED DESCRIPTION

[0035] Embodiments of the present invention relate to improved methods for treating muscular dystrophy, such as DMD and BMD, by administering antisense compounds that are specifically designed to induce exon skipping in the human dystrophin gene. Dystrophin plays a vital role in muscle function, and various muscle-related diseases are characterized by mutated forms of this gene. Hence, in certain embodiments, the improved methods described herein may be used for inducing exon skipping in mutated forms of the human dystrophin gene, such as the mutated dystrophin genes found in DMD and BMD.

[0036] Due to aberrant mRNA splicing events caused by mutations, these mutated human dystrophin genes either express defective dystrophin protein or express no measurable dystrophin at all, a condition that leads to various forms of muscular dystrophy. To remedy this condition, the antisense compounds of the present invention hybridize to selected regions of a pre-processed RNA of a mutated human dystrophin gene, induce exon skipping and differential splicing in that otherwise aberrantly spliced dystrophin mRNA, and thereby allow muscle cells to produce an mRNA transcript that encodes a functional dystrophin protein. In certain embodiments, the resulting dystrophin protein is not necessarily the "wild-type" form of dystrophin, but is rather a truncated, yet functional or semi-functional, form of dystrophin.

[0037] By increasing the levels of functional dystrophin protein in muscle cells, these and related embodiments are useful in the prophylaxis and treatment of muscular dystrophy, especially those forms of muscular dystrophy, such as DMD and BMD, that are characterized by the expression of defective dystrophin proteins due to aberrant mRNA splicing. The methods described herein further provide improved treatment options for patients with muscular dystrophy and offer significant and practical advantages over alternate methods of treating relevant forms of muscular dystrophy. For example, in some embodiments, the improved methods relate to the administration of an antisense compound for inducing exon skipping in the human dystrophin gene at a higher dose and/or for a longer duration than prior approaches.

[0038] Thus, the invention relates to improved methods for treating muscular dystrophy such as DMD and BMD, by inducing exon skipping in a patient. In some embodiments, exon skipping is induced by administering an effective amount of a composition which includes a charge-neutral, phosphorodiamidate morpholino oligomer (PMO), such as eteplirsen, which selectively binds to a target sequence in an exon of dystrophin pre-mRNA. In some embodiments, the invention relates to methods of treating DMD or BMD in which an effective amount of a composition e.g., at least 20 mg/kg, about 25 mg/kg, about 30 mg/kg or about 30 mg/kg to about 50 mg/kg, which includes an antisense as described herein, such as eteplirsen, over a period of time sufficient to treat the disease.

[0039] Some embodiments of the present invention relate to the use of eteplirsen as a disease-modifying therapy for treating DMD. In a clinical study described in the Examples, no drug-related adverse events were seen in 576 infusions of eteplirsen administered over one year, nor were there any infusion-associated reactions, cardiac abnormalities, or any other organ system involvement. There was also no evidence of glomerular or renal tubular dysfunction in eteplirsen-treated patients over the course of the study (e.g., no proteinuria, elevations in serum cytstatin C, or urine cystatin C or KIM-1). Without being bound by theory, the safety profile of eteplirsen and other exon-skipping antisense oligonucleotides described herein may be attributed to its unique chemical composition, which is characterized by nucleotides bound to morpholine rings linked through charge-neutral phosphorodiamidate moieties.

[0040] In DMD patients treated with eteplirsen for one year, the mean percentage of dystrophin-positive fibers was increased to 47% of normal, relative to baseline. The magnitude of the increase was dependent upon treatment duration. Significant increases in dystrophin levels were observed in the 24-week biopsies taken from patients in Cohort 1 (30 mg/kg) and in the 48-week biopsies from patients in Cohort 3 (who started eteplirsen at week 25).

[0041] Eteplirsen's clinical benefit mirrored its ability to induce exon skipping and restore functional dystrophin production. Clinical effect was assessed with the 6MWT, a measure of endurance and muscular capacity that goes beyond the assessment of strength in individual muscle groups. Patients

who received 30 or 50 mg/kg eteplirsen from the beginning maintained a stable walking distance over 48 weeks, consistent with eteplirsen-induced increases in novel dystrophin expression between weeks 12 and 24. In contrast, patients in the placebo/delayed eteplirsen cohort lost 70 meters by week 36, but appeared to stabilize by week 48 (24 weeks after initiating eteplirsen). This is the same timeframe in which a clinical impact was seen in patients who received 30 or 50 mg/kg eteplirsen once a week from the start of the study.

[0042] The present invention is based, at least in part, on the evidence of a therapeutic effect of eteplirsen, which represents a major advance in the treatment of DMD by addressing the underlying cause of the disease. Accordingly, the invention relates to methods of treating DMD or BMD in patients by administering an effective amount of a composition which includes an antisense oligonucleotide, such as eteplirsen, which is complementary to a target region in an exon of the human dystrophin gene to specifically hybridize to the target region, induce exon skipping, and treat the disease. In one embodiment, treatment is by administering one or more antisense oligonucleotides of the present invention (e.g., a nucleotide sequence shown in Tables 3 and 4), optionally as part of a pharmaceutical formulation or dosage form, to a subject in need thereof. Treatment includes inducing exon-skipping in a subject by administering an effective amount of one or more antisense oligonucleotides, in which the exon is any one or more of exons 1-79 from the dystrophin gene. Preferably, the exon is exon 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56 or 8 from the human dystrophin gene.

[0043] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by those of ordinary skill in the art to which the invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, preferred methods and materials are described. For the purposes of the present invention, the following terms are defined below.

I. DEFINITIONS

[0044] By "about" is meant a quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length that varies by as much as 30, 25, 20, 15, 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1% to a reference quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length.

[0045] The terms "complementary" and "complementarity" refer to polynucleotides (i.e., a sequence of nucleotides) related by base-pairing rules. For example, the sequence "T-G-A (5'-3')," is complementary to the sequence "T-C-A (5'-3')." Complementarity may be "partial," in which only some of the nucleic acids' bases are matched according to base pairing rules. Or, there may be "complete" or "total" complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands. While perfect complementarity is often desired, some embodiments can include one or more but preferably 6, 5, 4, 3, 2, or 1 mismatches with respect to the target RNA. Variations at any location within the oligomer are included. In certain embodiments, variations in sequence near the termini of an oligomer are generally preferable to variations in the interior, and if present are typically within about 6, 5, 4, 3, 2, or 1 nucleotides of the 5' and/or 3' terminus.

[0046] The terms "cell penetrating peptide" and "CPP" are used interchangeably and refer to cationic cell penetrating peptides, also called transport peptides, carrier peptides, or peptide transduction domains. The peptides, as shown herein, have the capability of inducing cell penetration within 100% of cells of a given cell culture population and allow macromolecular translocation within multiple tissues in vivo upon systemic administration. A preferred CPP embodiment is an arginine-rich peptide as described further below.

[0047] The terms "antisense oligomer" and "antisense compound" and "antisense oligonucleotide" are used interchangeably and refer to a sequence of cyclic subunits, each bearing a base-pairing moiety, linked by intersubunit linkages that allow the base-pairing moieties to hybridize to a target sequence in a nucleic acid (typically an RNA) by Watson-Crick base pairing, to form a nucleic acid:oligomer heteroduplex within the target sequence. The cyclic subunits are based on ribose or another pentose sugar or, in a preferred embodiment, a morpholino group (see description of morpholino oligomers below). The oligomer may have exact or near sequence complementarity to the target sequence; variations in sequence near the termini of an oligomer are generally preferable to variations in the interior.

[0048] Such an antisense oligomer can be designed to block or inhibit translation of mRNA or to inhibit natural pre-mRNA splice processing, and may be said to be "directed to" or "targeted against" a target sequence with which it hybridizes. The target sequence is typically a region including an AUG start codon of an mRNA, a Translation Suppressing Oligomer, or splice site of a pre-processed mRNA, a Splice Suppressing Oligomer (SSO). The target sequence for a splice site may include an mRNA sequence having its 5' end 1 to about 25 base pairs downstream of a normal splice acceptor junction in a preprocessed mRNA. A preferred target sequence is any region of a preprocessed mRNA that includes a splice site or is contained entirely within an exon coding sequence or spans a splice acceptor or donor site. An oligomer is more generally said to be "targeted against" a biologically relevant target, such as a protein, virus, or bacteria, when it is targeted against the nucleic acid of the target in the manner described above.

[0049] The terms "morpholino oligomer" or "PMO" (phosphoramidate- or phosphorodiamidate morpholino oligomer) refer to an oligonucleotide analog composed of morpholino subunit structures, where (i) the structures are linked together by phosphorus-containing linkages, one to three atoms long, preferably two atoms long, and preferably uncharged or cationic, joining the morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, and (ii) each morpholino ring bears a purine or pyrimidine base-pairing moiety effective to bind, by base specific hydrogen bonding, to a base in a polynucleotide. See, for example, the structure in FIG. **1**A, which shows a preferred phosphorodiamidate linkage type. Variations can be made to this linkage as long as they do not interfere with binding or activity. For example, the oxygen attached to phosphorus may be substituted with sulfur (thiophosphorodiamidate). The 5' oxygen may be substituted with amino or lower alkyl substituted amino. The pendant nitrogen attached to phosphorus may be unsubstituted, monosubstituted, or disubstituted with (optionally substituted) lower alkyl. The purine or pyrimidine base pairing moiety is typically adenine, cytosine, guanine, uracil, thymine or inosine. The synthesis, structures, and binding characteristics of morpholino oligomers are detailed in U.S. Pat. Nos. 5,698,685,

5,217,866, 5,142,047, 5,034,506, 5,166,315, 5,521,063, 5,506,337, 8,076,476, 8,299,206 and 7,943,762 (cationic linkages), all of which are incorporated herein by reference. Modified intersubunit linkages and terminal groups are detailed in PCT application US2011/038459 and publication WO/2011/150408 which are incorporated herein by reference in their entirety.

[0050] An "amino acid subunit" or "amino acid residue" can refer to an α-amino acid residue (—CO—CHR—NH—) or a β- or other amino acid residue (e.g. —CO—(CH_2)$_n$CHR—NH—), where R is a side chain (which may include hydrogen) and n is 1 to 6, preferably 1 to 4.

[0051] The term "naturally occurring amino acid" refers to an amino acid present in proteins found in nature. The term "non-natural amino acids" refers to those amino acids not present in proteins found in nature, examples include beta-alanine (β-Ala), 6-aminohexanoic acid (Ahx) and 6-amino-pentanoic acid.

[0052] An "exon" refers to a defined section of nucleic acid that encodes for a protein, or a nucleic acid sequence that is represented in the mature form of an RNA molecule after either portions of a pre-processed (or precursor) RNA have been removed by splicing. The mature RNA molecule can be a messenger RNA (mRNA) or a functional form of a non-coding RNA, such as rRNA or tRNA. The human dystrophin gene has about 79 exons.

[0053] An "intron" refers to a nucleic acid region (within a gene) that is not translated into a protein. An intron is a non-coding section that is transcribed into a precursor mRNA (pre-mRNA), and subsequently removed by splicing during formation of the mature RNA.

[0054] An "effective amount" or "therapeutically effective amount" refers to an amount of therapeutic compound, such as an antisense oligonucleotide, administered to a human subject, either as a single dose or as part of a series of doses, which is effective to produce a desired therapeutic effect. For an antisense oligonucleotide, this effect is typically brought about by inhibiting translation or natural splice-processing of a selected target sequence. In some embodiments, an effective amount is at least 20 mg/kg of a composition including an antisense oligonucleotide for a period of time to treat the subject. In one embodiment, an effective amount is at least 20 mg/kg of a composition including an antisense oligonucleotide to increase the number of dystrophin-positive fibers in a subject to at least 20% of normal. In another embodiment, an effective amount is at least 20 mg/kg of a composition including an antisense oligonucleotide to stabilize, maintain, or improve walking distance from a 20% deficit, for example in a 6 MWT, in a patient, relative to a healthy peer. In another embodiment, an effective amount is at least 20 mg/kg to about 30 mg/kg, about 25 mg/kg to about 30 mg/kg, or about 30 mg/kg to about 50 mg/kg. In yet another embodiment, an effective amount is about 30 mg/kg or about 50 mg/kg. In another aspect, an effective amount is at least 20 mg/kg, about 25 mg/kg, about 30 mg/kg, or about 30 mg/kg to about 50 mg/kg, for at least 24 weeks, at least 36 weeks, or at least 48 weeks, to thereby increase the number of dystrophin-positive fibers in a subject to at least 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, about 95% of normal, and stabilize or improve walking distance from a 20% deficit, for example in a 6 MWT, in the patient relative to a healthy peer. In one embodiment, treatment increases the number of dystrophin-positive fibers to 20-60%, or 30-50% of normal in the patient.

[0055] "Exon skipping" refers generally to the process by which an entire exon, or a portion thereof, is removed from a given pre-processed RNA, and is thereby excluded from being present in the mature RNA, such as the mature mRNA that is translated into a protein. Hence, the portion of the protein that is otherwise encoded by the skipped exon is not present in the expressed form of the protein, typically creating an altered, though still functional, form of the protein. In certain embodiments, the exon being skipped is an aberrant exon from the human dystrophin gene, which may contain a mutation or other alteration in its sequence that otherwise causes aberrant splicing. In certain embodiments, the exon being skipped is any one or more of exons 1-79 of the human dystrophin gene, such as 3-8, 10-16, 19-40, 42-47, and 50-55, though exons 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56 and 8 of the human dystrophin gene are preferred.

[0056] "Dystrophin" is a rod-shaped cytoplasmic protein, and a vital part of the protein complex that connects the cytoskeleton of a muscle fiber to the surrounding extracellular matrix through the cell membrane. Dystrophin contains multiple functional domains. For instance, dystrophin contains an actin binding domain at about amino acids 14-240 and a central rod domain at about amino acids 253-3040. This large central domain is formed by 24 spectrin-like triple-helical elements of about 109 amino acids, which have homology to alpha-actinin and spectrin. The repeats are typically interrupted by four proline-rich non-repeat segments, also referred to as hinge regions. Repeats 15 and 16 are separated by an 18 amino acid stretch that appears to provide a major site for proteolytic cleavage of dystrophin. The sequence identity between most repeats ranges from 10-25%. One repeat contains three alpha-helices: 1, 2 and 3. Alpha-helices 1 and 3 are each formed by 7 helix turns, probably interacting as a coiled-coil through a hydrophobic interface. Alpha-helix 2 has a more complex structure and is formed by segments of four and three helix turns, separated by a Glycine or Proline residue. Each repeat is encoded by two exons, typically interrupted by an intron between amino acids 47 and 48 in the first part of alpha-helix 2. The other intron is found at different positions in the repeat, usually scattered over helix-3. Dystrophin also contains a cysteine-rich domain at about amino acids 3080-3360), including a cysteine-rich segment (i.e., 15 Cysteines in 280 amino acids) showing homology to the C-terminal domain of the slime mold (Dictyostelium discoideum) alpha-actinin. The carboxy-terminal domain is at about amino acids 3361-3685.

[0057] The amino-terminus of dystrophin binds to F-actin and the carboxy-terminus binds to the dystrophin-associated protein complex (DAPC) at the sarcolemma. The DAPC includes the dystroglycans, sarcoglycans, integrins and caveolin, and mutations in any of these components cause autosomally inherited muscular dystrophies. The DAPC is destabilized when dystrophin is absent, which results in diminished levels of the member proteins, and in turn leads to progressive fibre damage and membrane leakage. In various forms of muscular dystrophy, such as Duchenne's muscular dystrophy (DMD) and Becker's muscular dystrophy (BMD), muscle cells produce an altered and functionally defective form of dystrophin, or no dystrophin at all, mainly due to mutations in the gene sequence that lead to incorrect splicing. The predominant expression of the defective dystrophin protein, or the complete lack of dystrophin or a dystrophin-like protein, leads to rapid progression of muscle degeneration, as noted above. In this regard, a "defective" dystrophin protein

may be characterized by the forms of dystrophin that are produced in certain subjects with DMD or BMD, as known in the art, or by the absence of detectable dystrophin.

[0058] As used herein, the terms "function" and "functional" and the like refer to a biological, enzymatic, or therapeutic function.

[0059] A "functional" dystrophin protein refers generally to a dystrophin protein having sufficient biological activity to reduce the progressive degradation of muscle tissue that is otherwise characteristic of muscular dystrophy, typically as compared to the altered or "defective" form of dystrophin protein that is present in certain subjects with DMD or BMD. In certain embodiments, a functional dystrophin protein may have about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% (including all integers in between) of the in vitro or in vivo biological activity of wild-type dystrophin, as measured according to routine techniques in the art. As one example, dystrophin-related activity in muscle cultures in vitro can be measured according to myotube size, myofibril organization (or disorganization), contractile activity, and spontaneous clustering of acetylcholine receptors (see, e.g., Brown et al., Journal of Cell Science. 112:209-216, 1999). Animal models are also valuable resources for studying the pathogenesis of disease, and provide a means to test dystrophin-related activity. Two of the most widely used animal models for DMD research are the mdx mouse and the golden retriever muscular dystrophy (GRMD) dog, both of which are dystrophin negative (see, e.g., Collins & Morgan, Int J Exp Pathol 84: 165-172, 2003). These and other animal models can be used to measure the functional activity of various dystrophin proteins. Included are truncated forms of dystrophin, such as those forms that are produced by certain of the exon-skipping antisense compounds of the present invention.

[0060] The term "restoration" of dystrophin synthesis or production refers generally to the production of a dystrophin protein including truncated forms of dystrophin in a patient with muscular dystrophy following treatment with an antisense oligonucleotide as described herein. In some embodiments, treatment results in an increase in novel dystrophin production in a patient by 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100% (including all integers in between). In some embodiments, treatment increases the number of dystrophin-positive fibers to at least 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90% or about 95% to 100% of normal in the subject. In other embodiments, treatment increases the number of dystrophin-positive fibers to about 20% to about 60%, or about 30% to about 50% of normal in the subject. The percent of dystrophin-positive fibers in a patient following treatment can be determined by a muscle biopsy using known techniques. For example, a muscle biopsy may be taken from a suitable muscle, such as the biceps brachii muscle in a patient.

[0061] Analysis of the percentage of positive dystrophin fibers may be performed pre-treatment and/or post-treatment or at time points throughout the course of treatment. In some embodiments, a post-treatment biopsy is taken from the contralateral muscle from the pre-treatment biopsy. Pre- and post-treatment dystrophin expression studies may be performed using any suitable assay for dystrophin. In one embodiment, immunohistochemical detection is performed on tissue sections from the muscle biopsy using an antibody that is a marker for dystrophin, such as a monoclonal or a polyclonal antibody. For example, the MANDYS106 antibody can be used which is a highly sensitive marker for dystrophin. Any suitable secondary antibody may be used.

[0062] In some embodiments, the percent dystrophin-positive fibers are calculated by dividing the number of positive fibers by the total fibers counted. Normal muscle samples have 100% dystrophin-positive fibers. Therefore, the percent dystrophin-positive fibers can be expressed as a percentage of normal. To control for the presence of trace levels of dystrophin in the pretreatment muscle as well as revertant fibers a baseline can be set using sections of pre-treatment muscles from each patient when counting dystrophin-positive fibers in post-treatment muscles. This may be used as a threshold for counting dystrophin-positive fibers in sections of post-treatment muscle in that patient. In other embodiments, antibody-stained tissue sections can also be used for dystrophin quantification using Bioquant image analysis software (Bioquant Image Analysis Corporation, Nashville, Tenn.). The total dystrophin fluorescence signal intensity can be reported as a percentage of normal. In addition, Western blot analysis with monoclonal or polyclonal anti-dystrophin antibodies can be used to determine the percentage of dystrophin positive fibers. For example, the anti-dystrophin antibody NCL-Dysl from Novacastra may be used. The percentage of dystrophin-positive fibers can also be analyzed by determining the expression of the components of the sarcoglycan complex (β,γ) and/or neuronal NOS.

[0063] By "isolated" is meant material that is substantially or essentially free from components that normally accompany it in its native state. For example, an "isolated polynucleotide," as used herein, may refer to a polynucleotide that has been purified or removed from the sequences that flank it in a naturally-occurring state, e.g., a DNA fragment that has been removed from the sequences that are normally adjacent to the fragment.

[0064] As used herein, "sufficient length" refers to an antisense oligonucleotide that is complementary to at least 8, more typically 8-30, contiguous nucleobases in a target dystrophin pre-mRNA. In some embodiments, an antisense of sufficient length includes at least 8, 9, 10, 11, 12, 13, 14, or 15 contiguous nucleobases in the target dystrophin pre-mRNA. In other embodiments an antisense of sufficient length includes at least 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 contiguous nucleobases in the target dystrophin pre-mRNA. An antisense oligonucleotide of sufficient length has at least a minimal number of nucleotides to be capable of specifically hybridizing to any one or more of exons 1-79 of the dystrophin gene. Preferably, the antisense oligonucleotide of the invention has a minimal number of nucleotides to be capable of specifically hybridizing to any one or more of exons 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56 or 8 of the human dystrophin gene. Preferably an oligonucleotide of sufficient length is from about 10 to about 50 nucleotides in length, including oligonucleotides of 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 and 40 or more nucleotides. In one embodiment, an oligonucleotide of sufficient length is from 10 to about 30 nucleotides in length. In another embodiment, an oligonucleotide of sufficient length is from 15 to about 25 nucleotides in length. In yet another embodiment, an oligonucleotide of sufficient length is from 20 to 30, or 20 to 50, nucleotides in length. In yet another embodiment, an oligonucleotide of sufficient length is from 25 to 28 nucleotides in length.

[0065] By "enhance" or "enhancing," or "increase" or "increasing," or "stimulate" or "stimulating," refers generally to the ability of one or antisense compounds or compositions to produce or cause a greater physiological response (i.e., downstream effects) in a cell or a subject, as compared to the response caused by either no antisense compound or a control compound. A measurable physiological response may include increased expression of a functional form of a dystrophin protein, or increased dystrophin-related biological activity in muscle tissue, among other responses apparent from the understanding in the art and the description herein. Increased muscle function can also be measured, including increases or improvements in muscle function by about 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100%. The percentage of muscle fibers that express a functional dystrophin can also be measured, including increased dystrophin expression in about 1%, 2%, %, 15%, 16%, 17%, 18%, 19%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of muscle fibers. For instance, it has been shown that around 40% of muscle function improvement can occur if 25-30% of fibers express dystrophin (see, e.g., DelloRusso et al, Proc Natl Acad Sci USA 99: 12979-12984, 2002). An "increased" or "enhanced" amount is typically a "statistically significant" amount, and may include an increase that is 1.1, 1.2, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30, 40, 50 or more times (e.g., 500, 1000 times) (including all integers and decimal points in between and above 1), e.g., 1.5, 1.6, 1.7, 1.8, etc.) the amount produced by no antisense compound (the absence of an agent) or a control compound.

[0066] The term "reduce" or "inhibit" may relate generally to the ability of one or more antisense compounds of the invention to "decrease" a relevant physiological or cellular response, such as a symptom of a disease or condition described herein, as measured according to routine techniques in the diagnostic art. Relevant physiological or cellular responses (in vivo or in vitro) will be apparent to persons skilled in the art, and may include reductions in the symptoms or pathology of muscular dystrophy, or reductions in the expression of defective forms of dystrophin, such as the altered forms of dystrophin that are expressed in individuals with DMD or BMD. A "decrease" in a response may be statistically significant as compared to the response produced by no antisense compound or a control composition, and may include a 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% decrease, including all integers in between.

[0067] Also included are vector delivery systems that are capable of expressing the oligomeric, dystrophin-targeting sequences of the present invention, such as vectors that express a polynucleotide sequence comprising any one or more of the sequences shown in Tables 3 and 4, and variants thereof, as described herein. By "vector" or "nucleic acid construct" is meant a polynucleotide molecule, preferably a DNA molecule derived, for example, from a plasmid, bacteriophage, yeast or virus, into which a polynucleotide can be inserted or cloned. A vector preferably contains one or more unique restriction sites and can be capable of autonomous replication in a defined host cell including a target cell or tissue or a progenitor cell or tissue thereof, or be integrated with the genome of the defined host such that the cloned sequence is reproducible. Accordingly, the vector can be an autonomously replicating vector, i.e., a vector that exists as an extra-chromosomal entity, the replication of which is independent of chromosomal replication, e.g., a linear or closed circular plasmid, an extra-chromosomal element, a minichromosome, or an artificial chromosome. The vector can contain any means for assuring self-replication. Alternatively, the vector can be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated.

[0068] "Treatment" of an individual (e.g. a mammal, such as a human) or a cell is any type of intervention used in an attempt to alter the natural course of the individual or cell. Treatment includes, but is not limited to, administration of a pharmaceutical composition, and may be performed either prophylactically or subsequent to the initiation of a pathologic event or contact with an etiologic agent. Treatment includes any desirable effect on the symptoms or pathology of a disease or condition associated with the dystrophin protein, as in certain forms of muscular dystrophy, and may include, for example, minimal changes or improvements in one or more measurable markers of the disease or condition being treated. Also included are "prophylactic" treatments, which can be directed to reducing the rate of progression of the disease or condition being treated, delaying the onset of that disease or condition, or reducing the severity of its onset. "Treatment" or "prophylaxis" does not necessarily indicate complete eradication, cure, or prevention of the disease or condition, or associated symptoms thereof.

[0069] In one embodiment, treatment with an antisense oligonucleotide of the invention increases novel dystrophin production and slows or reduces the loss of ambulation that would be expected without treatment. For example, treatment may stabilize, maintain, improve or increase walking ability (e.g., stabilization of ambulation) in the subject. In some embodiments, treatment maintains or increases a stable walking distance in a patient, as measured by, for example, the 6 Minute Walk Test (6MWT), described by McDonald, et al. (Muscle Nerve, 2010; 42:966-74, herein incorporated by reference). A change in the 6 Minute Walk Distance (6MWD) may be expressed as an absolute value, a percentage change or a change in the %-predicted value. In some embodiments, treatment maintains or improves a stable walking distance in a 6MWT from a 20% deficit in the subject relative to a healthy peer. The performance of a DMD patient in the 6MWT relative to the typical performance of a healthy peer can be determined by calculating a %-predicted value. For example, the %-predicted 6MWD may be calculated using the following equation for males: $196.72+(39.81\times age)-(1.36\times age^2)+(132.28\times height\ in\ meters)$. For females, the %-predicted 6MWD may be calculated using the following equation: $188.61+(51.50\times age)-(1.86\times age^2)+(86.10\times height\ in\ meters)$ (Henricson et al. PLoS Curr., 2012, version 2, herein incorporated by reference). In some embodiments, treatment with an antisense oligonucleotide increases the stable walking distance in the patient from baseline to greater than 3, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30 or 50 meters (including all integers in between).

[0070] Loss of muscle function in patients with DMD may occur against the background of normal childhood growth and development. Indeed, younger children with DMD may show an increase in distance walked during 6MWT over the course of about 1 year despite progressive muscular impairment. In some embodiments, the 6MWD from patients with

DMD is compared to typically developing control subjects and to existing normative data from age and sex matched subjects. In some embodiments, normal growth and development can be accounted for using an age and height based equation fitted to normative data. Such an equation can be used to convert 6MWD to a percent-predicted (%-predicted) value in subjects with DMD. In certain embodiments, analysis of %-predicted 6MWD data represents a method to account for normal growth and development, and may show that gains in function at early ages (e.g., less than or equal to age 7) represent stable rather than improving abilities in patients with DMD (Henricson et al. PLoS Curr., 2012, version 2, herein incorporated by reference).

[0071] A "subject," as used herein, includes any animal that exhibits a symptom, or is at risk for exhibiting a symptom, which can be treated with an antisense compound of the invention, such as a subject that has or is at risk for having DMD or BMD, or any of the symptoms associated with these conditions (e.g., muscle fibre loss). Suitable subjects (patients) include laboratory animals (such as mouse, rat, rabbit, or guinea pig), farm animals, and domestic animals or pets (such as a cat or dog). Non-human primates and, preferably, human patients, are included.

[0072] "Alkyl" or "alkylene" both refer to a saturated straight or branched chain hydrocarbon radical containing from 1 to 18 carbons. Examples include without limitation methyl, ethyl, propyl, iso-propyl, butyl, iso-butyl, tert-butyl, n-pentyl and n-hexyl. The term "lower alkyl" refers to an alkyl group, as defined herein, containing between 1 and 8 carbons.

[0073] "Alkenyl" refers to an unsaturated straight or branched chain hydrocarbon radical containing from 2 to 18 carbons and comprising at least one carbon to carbon double bond. Examples include without limitation ethenyl, propenyl, iso-propenyl, butenyl, iso-butenyl, tert-butenyl, n-pentenyl and n-hexenyl. The term "lower alkenyl" refers to an alkenyl group, as defined herein, containing between 2 and 8 carbons.

[0074] "Alkynyl" refers to an unsaturated straight or branched chain hydrocarbon radical containing from 2 to 18 carbons comprising at least one carbon to carbon triple bond. Examples include without limitation ethynyl, propynyl, iso-propynyl, butynyl, iso-butynyl, tert-butynyl, pentynyl and hexynyl. The term "lower alkynyl" refers to an alkynyl group, as defined herein, containing between 2 and 8 carbons.

[0075] "Cycloalkyl" refers to a mono- or poly-cyclic alkyl radical. Examples include without limitation cyclobutyl, cyclopentyl, cyclohexyl, cycloheptyl and cyclooctyl.

[0076] "Aryl" refers to a cyclic aromatic hydrocarbon moiety containing from to 18 carbons having one or more closed ring(s). Examples include without limitation phenyl, benzyl, naphthyl, anthracenyl, phenanthracenyl and biphenyl.

[0077] "Aralkyl" refers to a radical of the formula RaRb where Ra is an alkylene chain as defined above and Rb is one or more aryl radicals as defined above, for example, benzyl, diphenylmethyl and the like.

[0078] "Thioalkoxy" refers to a radical of the formula —SRc where Rc is an alkyl radical as defined herein. The term "lower thioalkoxy" refers to an alkoxy group, as defined herein, containing between 1 and 8 carbons.

[0079] "Alkoxy" refers to a radical of the formula —ORda where Rd is an alkyl radical as defined herein. The term "lower alkoxy" refers to an alkoxy group, as defined herein, containing between 1 and 8 carbons. Examples of alkoxy groups include, without limitation, methoxy and ethoxy.

[0080] "Alkoxyalkyl" refers to an alkyl group substituted with an alkoxy group.

[0081] "Carbonyl" refers to the C(═O)— radical.

[0082] "Guanidynyl" refers to the $H_2N(C{=}NH_2)$—NH— radical.

[0083] "Amidinyl" refers to the $H_2N(C{=}NH_2)CH$— radical.

[0084] "Amino" refers to the NH_2 radical.

[0085] "Alkylamino" refers to a radical of the formula —NHRd or —NRdRd where each Rd is, independently, an alkyl radical as defined herein. The term "lower alkylamino" refers to an alkylamino group, as defined herein, containing between 1 and 8 carbons.

[0086] "Heterocycle" means a 5- to 7-membered monocyclic, or 7- to 10-membered bicyclic, heterocyclic ring which is either saturated, unsaturated, or aromatic, and which contains from 1 to 4 heteroatoms independently selected from nitrogen, oxygen and sulfur, and wherein the nitrogen and sulfur heteroatoms may be optionally oxidized, and the nitrogen heteroatom may be optionally quaternized, including bicyclic rings in which any of the above heterocycles are fused to a benzene ring. The heterocycle may be attached via any heteroatom or carbon atom. Heterocycles include heteroaryls as defined below. Thus, in addition to the heteroaryls listed below, heterocycles also include morpholinyl, pyrrolidinonyl, pyrrolidinyl, piperidinyl, piperizinyl, hydantoinyl, valerolactamyl, oxiranyl, oxetanyl, tetrahydrofuranyl, tetrahydropyranyl, tetrahydropyridinyl, tetrahydrothiophenyl, tetrahydrothiopyranyl, tetrahydropyrimidinyl, tetrahydrothiopyranyl, and the like.

[0087] "Heteroaryl" means an aromatic heterocycle ring of 5- to 10 members and having at least one heteroatom selected from nitrogen, oxygen and sulfur, and containing at least 1 carbon atom, including both mono- and bicyclic ring systems. Representative heteroaryls are pyridyl, furyl, benzofuranyl, thiophenyl, benzothiophenyl, quinolinyl, pyrrolyl, indolyl, oxazolyl, benzoxazolyl, imidazolyl, benzimidazolyl, thiazolyl, benzothiazolyl, isoxazolyl, pyrazolyl, isothiazolyl, pyridazinyl, pyrimidinyl, pyrazinyl, triazinyl, cinnolinyl, phthalazinyl, and quinazolinyl.

[0088] The terms "optionally substituted alkyl", "optionally substituted alkenyl", "optionally substituted alkoxy", "optionally substituted thioalkoxy", "optionally substituted alkyl amino", "optionally substituted lower alkyl", "optionally substituted lower alkenyl", "optionally substituted lower alkoxy", "optionally substituted lower thioalkoxy", "optionally substituted lower alkyl amino" and "optionally substituted heterocyclyl" mean that, when substituted, at least one hydrogen atom is replaced with a substituent. In the case of an oxo substituent (═O) two hydrogen atoms are replaced. In this regard, substituents include: deuterium, optionally substituted alkyl, optionally substituted alkenyl, optionally substituted alkynyl, optionally substituted aryl, optionally substituted heterocycle, optionally substituted cycloalkyl, oxo, halogen, —CN, —ORx, NRxRy, NRxC(═O)Ry, NRxSO2Ry, —NRxC(═O)NRxRy, C(═O)Rx, C(═O)ORx, C(═O)NRxRy, —SOmRx and —SOmNRxRy, wherein m is 0, 1 or 2, Rx and Ry are the same or different and independently hydrogen, optionally substituted alkyl, optionally substituted alkenyl, optionally substituted alkynyl, optionally substituted aryl, optionally substituted heterocycle or optionally substituted cycloalkyl and each of said optionally substituted alkyl, optionally substituted alkenyl, optionally substituted alkynyl, optionally substituted aryl, option-

ally substituted heterocycle and optionally substituted cycloalkyl substituents may be further substituted with one or more of oxo, halogen, —CN, —ORx, NRxRy, NRxC(═O)Ry, NRxSO2Ry, —NRxC(═O)NRxRy, C(═O)Rx, C(═O)ORx, C(═O)NRxRy, —SOmRx and —SOmNRxRy.

[0089] An antisense molecule nomenclature system was proposed and published to distinguish between the different antisense molecules (see Mann et al., (2002) J Gen Med 4, 644-654). This nomenclature became especially relevant when testing several slightly different antisense molecules, all directed at the same target region, as shown below:

H#A/D(x:y).

[0090] The first letter designates the species (e.g. H: human, M: murine, C: canine). "#" designates target dystrophin exon number. "A/D" indicates acceptor or donor splice site at the beginning and end of the exon, respectively. (x y) represents the annealing coordinates where "−" or "+" indicate intronic or exonic sequences respectively. For example, A(−6+18) would indicate the last 6 bases of the intron preceding the target exon and the first 18 bases of the target exon. The closest splice site would be the acceptor so these coordinates would be preceded with an "A". Describing annealing coordinates at the donor splice site could be D(+2-18) where the last 2 exonic bases and the first 18 intronic bases correspond to the annealing site of the antisense molecule. Entirely exonic annealing coordinates that would be represented by A(+65+85), that is the site between the 65th and 85th nucleotide from the start of that exon.

II. CONSTRUCTING THE ANTISENSE OLIGONUCLEOTIDE

[0091] Exemplary embodiments of the invention relate to morpholino oligonucleotides having phosphorus-containing backbone linkages are illustrated in FIGS. **1**A-**1**C. Preferred is a phosphorodiamidate-linked morpholino oligonucleotide such as shown in FIG. **1**C, which is modified, in accordance with one aspect of the present invention, to contain positively charged groups at preferably 10%-50% of its backbone linkages. Morpholino oligonucleotides with uncharged backbone linkages, including antisense oligonucleotides, are detailed, for example, in (Summerton and Weller 1997) and in co-owned U.S. Pat. Nos. 5,698,685, 5,217,866, 5,142,047, 5,034,506, 5,166,315, 5,185, 444, 5,521,063, 5,506,337, 8,076,476, 8,299,206 and 7,943,762 all of which are expressly incorporated by reference herein.

[0092] Important properties of the morpholino-based subunits include: 1) the ability to be linked in a oligomeric form by stable, uncharged or positively charged backbone linkages; 2) the ability to support a nucleotide base (e.g. adenine, cytosine, guanine, thymidine, uracil and inosine) such that the polymer formed can hybridize with a complementary-base target nucleic acid, including target RNA, Tm values above about 45° C. in relatively short oligonucleotides (e.g., 10-15 bases); 3) the ability of the oligonucleotide to be actively or passively transported into mammalian cells; and 4) the ability of the antisense oligonucleotide:RNA heteroduplex to resist RNAse and RNase H degradation, respectively.

[0093] Exemplary backbone structures for antisense oligonucleotides of the claimed subject matter include the morpholino subunit types shown in FIGS. **1**D-G, each linked by an uncharged or positively charged, phosphorus-containing subunit linkage. FIG. **1**D shows a phosphorus-containing linkage which forms the five atom repeating-unit backbone, where the morpholino rings are linked by a 1-atom phosphoamide linkage. FIG. **1**E shows a linkage which produces a 6-atom repeating-unit backbone. In this structure, the atom Y linking the 5' morpholino carbon to the phosphorus group may be sulfur, nitrogen, carbon or, preferably, oxygen. The X moiety pendant from the phosphorus may be fluorine, an alkyl or substituted alkyl, an alkoxy or substituted alkoxy, a thioalkoxy or substituted thioalkoxy, or unsubstituted, monosubstituted, or disubstituted nitrogen, including cyclic structures, such as morpholines or piperidines. Alkyl, alkoxy and thioalkoxy preferably include 1-6 carbon atoms. The Z moieties are sulfur or oxygen, and are preferably oxygen.

[0094] The linkages shown in FIGS. **1**F and **1**G are designed for 7-atom unit-length backbones. In structure **1**F, the X moiety is as in Structure **1**E, and the Y moiety may be methylene, sulfur, or, preferably, oxygen. In Structure **1**G, the X and Y moieties are as in Structure **1**E. Particularly preferred morpholino oligonucleotides include those composed of morpholino subunit structures of the form shown in FIG. **1**E, where X═NH_2, $N(CH_3)_2$, or 1-piperazine or other charged group, Y═O, and Z═O.

[0095] A substantially uncharged oligonucleotide may be modified, in accordance with an aspect of the invention, to include charged linkages, e.g., up to about 1 per every 2-5 uncharged linkages, such as about 4-5 per every 10 uncharged linkages. In certain embodiments, optimal improvement in antisense activity may be seen when about 25% of the backbone linkages are cationic. In certain embodiments, enhancement may be seen with a small number e.g., 10-20% cationic linkages, or where the number of cationic linkages are in the range 50-80%, such as about 60%.

[0096] Oligomers having any number of cationic linkages are provided, including fully cationic-linked oligomers. Preferably, however, the oligomers are partially charged, having, for example, 10%-80%. In preferred embodiments, about 10% to 60%, and preferably 20% to 50% of the linkages are cationic.

[0097] In one embodiment, the cationic linkages are interspersed along the backbone. The partially charged oligomers preferably contain at least two consecutive uncharged linkages; that is, the oligomer preferably does not have a strictly alternating pattern along its entire length.

[0098] Also considered are oligomers having blocks of cationic linkages and blocks of uncharged linkages; for example, a central block of uncharged linkages may be flanked by blocks of cationic linkages, or vice versa. In one embodiment, the oligomer has approximately equal-length 5', 3' and center regions, and the percentage of cationic linkages in the center region is greater than about 50%, preferably greater than about 70%.

[0099] In certain embodiments, the antisense compounds can be prepared by stepwise solid-phase synthesis, employing methods detailed in the references cited above, and below with respect to the synthesis of oligonucleotides having a mixture or uncharged and cationic backbone linkages. In some cases, it may be desirable to add additional chemical moieties to the antisense compound, e.g., to enhance pharmacokinetics or to facilitate capture or detection of the compound. Such a moiety may be covalently attached, according to standard synthetic methods. For example, addition of a polyethylene glycol moiety or other hydrophilic polymer, e.g., one having 1-100 monomeric subunits, may be useful in enhancing solubility.

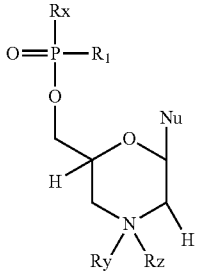
[0100] A reporter moiety, such as fluorescein or a radiolabeled group, may be attached for purposes of detection. Alternatively, the reporter label attached to the oligomer may be a ligand, such as an antigen or biotin, capable of binding a labeled antibody or streptavidin. In selecting a moiety for attachment or modification of an antisense compound, it is generally of course desirable to select chemical compounds of groups that are biocompatible and likely to be tolerated by a subject without undesirable side effects.

[0101] Oligomers for use in antisense applications generally range in length from about 10 to about 50 subunits, more preferably about 10 to 30 subunits, and typically 15-25 bases. For example, an oligomer of the invention having 19-20 subunits, a useful length for an antisense compound, may ideally have two to ten, e.g., four to eight, cationic linkages, and the remainder uncharged linkages. An oligomer having 14-15 subunits may ideally have two to seven, e.g., 3, 4, or 5, cationic linkages and the remainder uncharged linkages. In a preferred embodiment, the oligomers have 25 to 28 subunits.

[0102] Each morpholino ring structure supports a base pairing moiety, to form a sequence of base pairing moieties which is typically designed to hybridize to a selected antisense target in a cell or in a subject being treated. The base pairing moiety may be a purine or pyrimidine found in native DNA or RNA (e.g., A, G, C, T or U) or an analog, such as hypoxanthine (the base component of the nucleoside inosine) or 5-methyl cytosine.

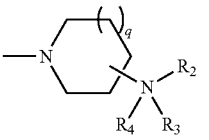
[0103] As noted above, certain embodiments are directed to oligomers comprising novel intersubunit linkages, including PMO-X oligomers and those having modified terminal groups. In some embodiments, these oligomers have higher affinity for DNA and RNA than do the corresponding unmodified oligomers and demonstrate improved cell delivery, potency, and/or tissue distribution properties compared to oligomers having other intersubunit linkages. The structural features and properties of the various linkage types and oligomers are described in more detail in the following discussion. The synthesis of these and related oligomers is described in co-owned U.S. application Ser. No. 13/118,298, which is incorporated by reference in its entirety.

[0104] In certain embodiments, the invention provides for an oligonucleotide having a sequence complementary to the target sequence which is associated with a human disease, and comprises a sequence of nucleotides having a formula:



[0105] wherein Nu is a nucleobase;

[0106] R_1 has the formula



[0107] q is 0, 1, or 2;

[0108] R_2 is selected from the group consisting of hydrogen, C_1-C_5 alkyl, C_1-C_5 aralkyl, and a formamidinyl group, and

[0109] R_3 is selected from the group consisting of hydrogen, C_1-C_{10} acyl, C_1-C_{10} aminoacyl, acyl moiety of a natural or unnatural alpha or beta amino acid, C_1-C_{10} aralkyl, and C_1-C_{10} alkyl, or

[0110] R_2 and R_3 are joined to form a 5-7 membered ring where the ring may be optionally substituted with a substituent selected from the group consisting of C_1-C_{10} alkyl, phenyl, halogen, and C_1-C_{10} aralkyl;

[0111] R_4 is selected from the group consisting of an electron pair, hydrogen, a C_1-C_6 alkyl and C_1-C_6 aralkyl;

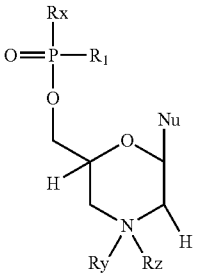
[0112] Rx is selected from the group consisting of sarcosinamide, hydroxyl, a nucleotide, a cell penetrating peptide moiety, and piperazinyl;

[0113] Ry is selected from the group consisting of hydrogen, a C_1-C_6 alkyl, a nucleotide a cell penetrating peptide moiety, an amino acid, a formamidinyl group, and C_1-C_6 acyl; and,

[0114] Rz is selected from the group consisting of an electron pair, hydrogen, a C_1-C_6 alkyl, and C_1-C_6 acyl pharmaceutically acceptable salts thereof.

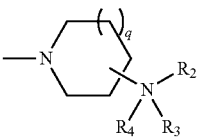
[0115] Nu may be selected from the group consisting of adenine, guanine, thymine, uracil, cytosine, and hypoxanthine. More preferably Nu is thymine or uracil.

[0116] In preferred embodiments, the invention provides an oligonucleotide having a sequence of nucleotides having a formula:



[0117] wherein Nu is a nucleobase;

[0118] R_1 is selected from the group consisting of R_1' and R_1" wherein R_1' is dimethylamino and R_1" has the formula



[0119] wherein at least one R_1 is R_1";

[0120] q is 0, 1, or 2; with the proviso that at least one of R_1 is a piperidinyl moiety;

[0121] R_2 is selected from the group consisting of hydrogen, C_1-C_5 alkyl, C_1-C_5 aralkyl, and a formamidinyl group, and

[0122] R_3 is selected from the group consisting of hydrogen, C_1-C_{10} acyl, C_1-C_{10} aminoacyl, acyl moiety of a natural or unnatural alpha or beta amino acid, C_1-C_{10} aralkyl, and C_1-C_{10} alkyl, or

[0123] R_2 and R_3 are joined to form a 5-7 membered ring where the ring may be optionally substituted with a substituent selected from the group consisting of C_1-C_{10} alkyl, phenyl, halogen, and C_1-C_{10} aralkyl;

[0124] R_4 is selected from the group consisting of an electron pair, hydrogen, a C_1-C_6 alkyl and aralkyl;

[0125] Rx is selected from the group consisting of sarcosinamide, hydroxyl, a nucleotide, a cell penetrating peptide moiety, and piperazinyl;

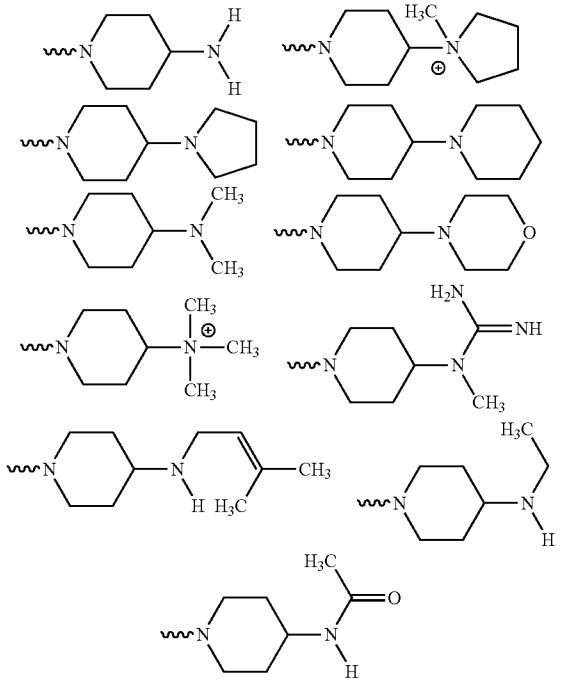
[0126] Ry is selected from the group consisting of hydrogen, a C_1-C_6 alkyl, a nucleotide a cell penetrating peptide moiety, an amino acid, a formamidinyl group, and C_1-C_6 acyl; and,

[0127] Rz is selected from the group consisting of an electron pair, hydrogen, a C_1-C_6 alkyl, and C_1-C_6 acyl pharmaceutically acceptable salts thereof.

[0128] Nu may be selected from the group consisting of adenine, guanine, thymine, uracil, cytosine, and hypoxanthine. More preferably Nu is thymine or uracil.

[0129] About 90-50% of the R_1 groups are dimethylamino (i.e. R_1'). More, preferably, 90-50% of the R_1 groups are dimethylamino. Most, preferably about 66% of the R_1 groups are dimethylamino.

[0130] R_1" may be selected from the group consisting of



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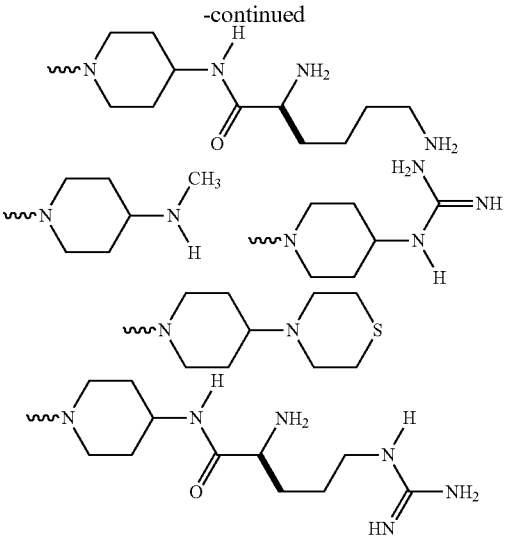
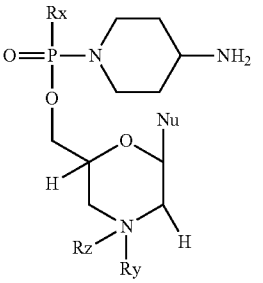


[0131] Preferably, at least one nucleotide of the oligonucleotide has the formula:



[0132] wherein Rx, Ry, Rz, and Nu are as stated above. Most preferably, Nu is thymine or uracil.

[0133] Although thymine (T) is the preferred base pairing moiety (Nu or Pi) containing the chemical modifications described above, any base subunit known to a person of skill in the art can be used as the base pairing moiety.

[0134] The oligonucleotide and the DNA or RNA are complementary to each other when a sufficient number of corresponding positions in each molecule are occupied by nucleotides which can hydrogen bond with each other. Thus, "specifically hybridizable" and "complementary" are terms which are used to indicate a sufficient degree of complementarity or precise pairing such that stable and specific binding occurs between the oligonucleotide and the DNA or RNA target. It is understood in the art that the sequence of an antisense molecule need not be 100% complementary to that of its target sequence to be specifically hybridizable. An antisense molecule is specifically hybridizable when binding of the compound to the target DNA or RNA molecule interferes with the normal function of the target DNA or RNA to cause a loss of utility, and there is a sufficient degree of complementarity to avoid non-specific binding of the antisense compound to non-target sequences under conditions in which specific binding is desired, i.e., under physiological condi-

tions in the case of in vivo assays or therapeutic treatment, and in the case of in vitro assays, under conditions in which the assays are performed.

[0135] While the above method may be used to select antisense molecules capable of deleting any exon from within a protein that is capable of being shortened without affecting its biological function, the exon deletion should not lead to a reading frame shift in the shortened transcribed mRNA. Thus, if in a linear sequence of three exons the end of the first exon encodes two of three nucleotides in a codon and the next exon is deleted then the third exon in the linear sequence must start with a single nucleotide that is capable of completing the nucleotide triplet for a codon. If the third exon does not commence with a single nucleotide there will be a reading frame shift that would lead to the generation of truncated or a non-functional protein.

[0136] It will be appreciated that the codon arrangements at the end of exons in structural proteins may not always break at the end of a codon, consequently there may be a need to delete more than one exon from the pre-mRNA to ensure in-frame reading of the mRNA. In such circumstances, a plurality of antisense oligonucleotides may need to be selected by the method of the invention wherein each is directed to a different region responsible for inducing splicing in the exons that are to be deleted.

[0137] The length of an antisense molecule may vary so long as it is capable of binding selectively to the intended location within the pre-mRNA molecule. The length of such sequences can be determined in accordance with selection procedures described herein. Generally, the antisense molecule will be from about 10 nucleotides in length up to about 50 nucleotides in length. It will be appreciated however that any length of nucleotides within this range may be used in the method. Preferably, the length of the antisense molecule is between 10-30 nucleotides in length.

[0138] The most common method for producing antisense molecules is the methylation of the 2' hydroxyribose position and the incorporation of a phosphorothioate backbone produces molecules that superficially resemble RNA but that are much more resistant to nuclease degradation.

[0139] To avoid degradation of pre-mRNA during duplex formation with the antisense molecules, the antisense molecules used in the method may be adapted to minimize or prevent cleavage by endogenous RNase H. This property is highly preferred as the treatment of the RNA with the unmethylated oligonucleotides either intracellularly or in crude extracts that contain RNase H leads to degradation of the pre-mRNA: antisense oligonucleotide duplexes. Any form of modified antisense molecules that is capable of by-passing or not inducing such degradation may be used in the present method. An example of antisense molecules which when duplexed with RNA are not cleaved by cellular RNase H is 2'-O-methyl derivatives. 2'-O-methyl-oligoribonucleotides are very stable in a cellular environment and in animal tissues, and their duplexes with RNA have higher Tm values than their ribo- or deoxyribo-counterparts.

[0140] Antisense molecules that do not activate RNase H can be made in accordance with known techniques (see, e.g., U.S. Pat. No. 5,149,797). Such antisense molecules, which may be deoxyribonucleotide or ribonucleotide sequences, simply contain any structural modification which sterically hinders or prevents binding of RNase H to a duplex molecule containing the oligonucleotide as one member thereof, which structural modification does not substantially hinder or disrupt duplex formation. Because the portions of the oligonucleotide involved in duplex formation are substantially different from those portions involved in RNase H binding thereto, numerous antisense molecules that do not activate RNase H are available. For example, such antisense molecules may be oligonucleotides wherein at least one, or all, of the inter-nucleotide bridging phosphate residues are modified phosphates, such as methyl phosphonates, methyl phosphorothioates, phosphoromorpholidates, phosphoropiperazidates and phosphoramidates. For example, every other one of the internucleotide bridging phosphate residues may be modified as described. In another non-limiting example, such antisense molecules are molecules wherein at least one, or all, of the nucleotides contain a 2' lower alkyl moiety (e.g., C_1-C_4, linear or branched, saturated or unsaturated alkyl, such as methyl, ethyl, ethenyl, propyl, 1-propenyl, 2-propenyl, and isopropyl). For example, every other one of the nucleotides may be modified as described.

[0141] While antisense oligonucleotides are a preferred form of the antisense molecules, the present invention comprehends other oligomeric antisense molecules, including but not limited to oligonucleotide mimetics such as are described below.

[0142] Specific examples of preferred antisense compounds useful in this invention include oligonucleotides containing modified backbones or non-natural inter-nucleoside linkages. As defined in this specification, oligonucleotides having modified backbones include those that retain a phosphorus atom in the backbone and those that do not have a phosphorus atom in the backbone. For the purposes of this specification, and as sometimes referenced in the art, modified oligonucleotides that do not have a phosphorus atom in their inter-nucleoside backbone can also be considered to be oligonucleosides.

[0143] In other preferred oligonucleotide mimetics, both the sugar and the inter-nucleoside linkage, i.e., the backbone, of the nucleotide units are replaced with novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound, an oligonucleotide mimetic that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleo-bases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone.

[0144] Modified oligonucleotides may also contain one or more substituted sugar moieties. Oligonucleotides may also include nucleobase (often referred to in the art simply as "base") modifications or substitutions. Certain nucleo-bases are particularly useful for increasing the binding affinity of the oligomeric compounds of the invention. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2° C. and are presently preferred base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications.

[0145] Another modification of the oligonucleotides of the invention involves chemically linking to the oligonucleotide one or more moieties or conjugates that enhance the activity, cellular distribution or cellular uptake of the oligonucleotide.

Such moieties include but are not limited to lipid moieties such as a cholesterol moiety, cholic acid, a thioether, e.g., hexyl-5-tritylthiol, a thiocholesterol, an aliphatic chain, e.g., dodecandiol or undecyl residues, a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate, a polyamine or a polyethylene glycol chain, or adamantane acetic acid, a palmityl moiety, or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety.

[0146] It is not necessary for all positions in a given compound to be uniformly modified, and in fact more than one of the aforementioned modifications may be incorporated in a single compound or even at a single nucleoside within an oligonucleotide. The present invention also includes antisense compounds that are chimeric compounds. "Chimeric" antisense compounds or "chimeras," in the context of this invention, are antisense molecules, particularly oligonucleotides, which contain two or more chemically distinct regions, each made up of at least one monomer unit, i.e., a nucleotide in the case of an oligonucleotide compound. These oligonucleotides typically contain at least one region wherein the oligonucleotide is modified so as to confer upon the increased resistance to nuclease degradation, increased cellular uptake, and an additional region for increased binding affinity for the target nucleic acid.

III. PEPTIDE TRANSPORTERS

[0147] The antisense compounds of the invention may include an oligonucleotide moiety conjugated to a CPP, preferably an arginine-rich peptide transport moiety effective to enhance transport of the compound into cells. The transport moiety is preferably attached to a terminus of the oligomer, as shown, for example, in FIGS. **1**B and **1**C. The peptides have the capability of inducing cell penetration within 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100% of cells of a given cell culture population, including all integers in between, and allow macromolecular translocation within multiple tissues in vivo upon systemic administration. In one embodiment, the cell-penetrating peptide may be an arginine-rich peptide transporter. In another embodiment, the cell-penetrating peptide may be Penetratin or the Tat peptide. These peptides are well known in the art and are disclosed, for example, in US Publication No. 2010-0016215 A1, incorporated by reference in its entirety. A particularly preferred approach to conjugation of peptides to antisense oligonucleotides can be found in PCT publication WO2012/150960, which is incorporated by reference in its entirety. A preferred embodiment of a peptide conjugated oligonucleotide of the present invention utilizes glycine as the linker between the CPP and the antisense oligonucleotide. For example, a preferred peptide conjugated PMO consists of R_6-G-PMO.

[0148] The transport moieties as described above have been shown to greatly enhance cell entry of attached oligomers, relative to uptake of the oligomer in the absence of the attached transport moiety. Uptake is preferably enhanced at least ten fold, and more preferably twenty fold, relative to the unconjugated compound.

[0149] The use of arginine-rich peptide transporters (i.e., cell-penetrating peptides) are particularly useful in practicing the present invention. Certain peptide transporters have been shown to be highly effective at delivery of antisense compounds into primary cells including muscle cells (Marshall, Oda et al. 2007; Jearawiriyapaisarn, Moulton et al. 2008; Wu, Moulton et al. 2008). Furthermore, compared to other known peptide transporters such as Penetratin and the Tat peptide, the peptide transporters described herein, when conjugated to an antisense PMO, demonstrate an enhanced ability to alter splicing of several gene transcripts (Marshall, Oda et al. 2007).

[0150] Exemplary peptide transporters, excluding linkers are given below in Table 1.

TABLE 1

Exemplary peptide transporters

NAME (DESIGNATION)	SEQUENCE	SEQ ID NO[A]
rTAT	RRRQRRKKR	876
Tat	RKKRRQRRR	877
R_9F_2	RRRRRRRRRFF	878
$R_5F_2R_4$	RRRRRFFRRRR	879
R_4	RRRR	880
R_5	RRRRR	881
R_6	RRRRRR	882
R_7	RRRRRRR	883
R_8	RRRRRRRR	884
R_9	RRRRRRRRR	885
$(RX)_8$	RXRXRXRXRXRXRXRX	886
$(RAhxR)_4$; (P007)	RAhxRRAhxRRAhxRRAhxR	887
$(RAhxR)_5$; (CP04057)	RAhxRRAhxRRAhxRRAhxRRAhxR	888
$(RAhxRRBR)_2$; (CP06062)	RAhxRRBRRAhxRRBR	889
$(RAR)_4F_2$	RARRARRARRARFF	890
$(RGR)_4F_2$	RGRRGRRGRRGRFF	891

[A]Sequences assigned to SEQ ID NOs do not include the linkage portion (e.g., C, G, P, Ahx, B, AhxB where Ahx and B refer to 6-aminohexanoic acid and beta-alanine, respectively).

IV. FORMULATIONS AND TREATMENT

[0151] In certain embodiments, the present invention provides formulations or compositions suitable for the therapeutic delivery of antisense oligomers, as described herein. Hence, in certain embodiments, the present invention provides pharmaceutically acceptable compositions that comprise a therapeutically-effective amount of one or more of the oligomers described herein, formulated together with one or more pharmaceutically acceptable carriers (additives) and/or diluents. While it is possible for an oligomer of the present invention to be administered alone, it is preferable to administer the compound as a pharmaceutical formulation (composition).

[0152] The compositions of the present invention may be administered alone or in combination with another therapeutic. The additional therapeutic may be administered prior, concurrently or subsequently to the administration of the composition of the present invention. For example, the compositions may be administered in combination with a steroid and/or an antibiotic. The steroid may be a glucocorticoid or

prednisone. Other agents which can be administered include an antagonist of the ryanodine receptor, such as dantrolene, which has been shown to enhance antisense-mediated exon skipping in patient cells and a mouse model of DMD (G. Kendall et al. Sci Tranl Med 4 164ra160 (2012), incorporated herein by reference).

[0153] Methods for the delivery of nucleic acid molecules are described, for example, in Akhtar et al., 1992, Trends Cell Bio., 2:139; and Delivery Strategies for Antisense Oligonucleotide Therapeutics, ed. Akhtar; Sullivan et al., PCT WO 94/02595. These and other protocols can be utilized for the delivery of virtually any nucleic acid molecule, including the isolated oligomers of the present invention.

[0154] As detailed below, the pharmaceutical compositions of the present invention may be specially formulated for administration in solid or liquid form, including those adapted for the following: (1) oral administration, for example, drenches (aqueous or non-aqueous solutions or suspensions), tablets, e.g., those targeted for buccal, sublingual, and systemic absorption, boluses, powders, granules, pastes for application to the tongue; (2) parenteral administration, for example, by subcutaneous, intramuscular, intravenous or epidural injection as, for example, a sterile solution or suspension, or sustained-release formulation; (3) topical application, for example, as a cream, ointment, or a controlled-release patch or spray applied to the skin; (4) intravaginally or intrarectally, for example, as a pessary, cream or foam; (5) sublingually; (6) ocularly; (7) transdermally; or (8) nasally.

[0155] The phrase "pharmaceutically acceptable" is employed herein to refer to those compounds, materials, compositions, and/or dosage forms which are, within the scope of sound medical judgment, suitable for use in contact with the tissues of human beings and animals without excessive toxicity, irritation, allergic response, or other problem or complication, commensurate with a reasonable benefit/risk ratio.

[0156] The phrase "pharmaceutically-acceptable carrier" as used herein means a pharmaceutically-acceptable material, composition or vehicle, such as a liquid or solid filler, diluent, excipient, manufacturing aid (e.g., lubricant, talc magnesium, calcium or zinc stearate, or steric acid), or solvent encapsulating material, involved in carrying or transporting the subject compound from one organ, or portion of the body, to another organ, or portion of the body. Each carrier must be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not injurious to the patient.

[0157] Some examples of materials that can serve as pharmaceutically-acceptable carriers include, without limitation: (1) sugars, such as lactose, glucose and sucrose; (2) starches, such as corn starch and potato starch; (3) cellulose, and its derivatives, such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; (4) powdered tragacanth; (5) malt; (6) gelatin; (7) talc; (8) excipients, such as cocoa butter and suppository waxes; (9) oils, such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; (10) glycols, such as propylene glycol; (11) polyols, such as glycerin, sorbitol, mannitol and polyethylene glycol; (12) esters, such as ethyl oleate and ethyl laurate; (13) agar; (14) buffering agents, such as magnesium hydroxide and aluminum hydroxide; (15) alginic acid; (16) pyrogen-free water; (17) isotonic saline; (18) Ringer's solution; (19) ethyl alcohol; (20) pH buffered solutions; (21) polyesters, polycarbonates and/or polyanhydrides; and (22) other non-toxic compatible substances employed in pharmaceutical formulations.

[0158] Additional non-limiting examples of agents suitable for formulation with the antisense oligomers of the instant invention include: PEG conjugated nucleic acids, phospholipid conjugated nucleic acids, nucleic acids containing lipophilic moieties, phosphorothioates, P-glycoprotein inhibitors (such as Pluronic P85) which can enhance entry of drugs into various tissues; biodegradable polymers, such as poly (DL-lactide-coglycolide) microspheres for sustained release delivery after implantation (Emerich, D F et al., 1999, Cell Transplant, 8, 47-58) Alkermes, Inc. Cambridge, Mass.; and loaded nanoparticles, such as those made of polybutylcyanoacrylate, which can deliver drugs across the blood brain barrier and can alter neuronal uptake mechanisms (Prog Neuropsychopharmacol Biol Psychiatry, 23, 941-949, 1999).

[0159] The invention also features the use of the composition comprising surface-modified liposomes containing poly (ethylene glycol) lipids (PEG-modified, branched and unbranched or combinations thereof, or long-circulating liposomes or stealth liposomes). Oligomers of the invention can also comprise covalently attached PEG molecules of various molecular weights. These formulations offer a method for increasing the accumulation of drugs in target tissues. This class of drug carriers resists opsonization and elimination by the mononuclear phagocytic system (MPS or RES), thereby enabling longer blood circulation times and enhanced tissue exposure for the encapsulated drug (Lasic et al. Chem. Rev. 1995, 95, 2601-2627; Ishiwata et al., Chem. Pharm. Bull. 1995, 43, 1005-1011). Such liposomes have been shown to accumulate selectively in tumors, presumably by extravasation and capture in the neovascularized target tissues (Lasic et al., Science 1995, 267, 1275-1276; Oku et al., 1995, Biochim. Biophys. Acta, 1238, 86-90). The long-circulating liposomes enhance the pharmacokinetics and pharmacodynamics of DNA and RNA, particularly compared to conventional cationic liposomes which are known to accumulate in tissues of the MPS (Liu et al., J. Biol. Chem. 1995, 42, 24864-24870; Choi et al., International PCT Publication No. WO 96/10391; Ansell et al., International PCT Publication No. WO 96/10390; Holland et al., International PCT Publication No. WO 96/10392). Long-circulating liposomes are also likely to protect drugs from nuclease degradation to a greater extent compared to cationic liposomes, based on their ability to avoid accumulation in metabolically aggressive MPS tissues such as the liver and spleen.

[0160] In a further embodiment, the present invention includes oligomer compositions prepared for delivery as described in U.S. Pat. Nos. 6,692,911, 7,163,695 and 7,070,807. In this regard, in one embodiment, the present invention provides an oligomer of the present invention in a composition comprising copolymers of lysine and histidine (HK) (as described in U.S. Pat. Nos. 7,163,695, 7,070,807, and 6,692,911) either alone or in combination with PEG (e.g., branched or unbranched PEG or a mixture of both), in combination with PEG and a targeting moiety or any of the foregoing in combination with a crosslinking agent. In certain embodiments, the present invention provides antisense oligomers in compositions comprising gluconic-acid-modified polyhistidine or gluconylated-polyhistidine/transferrin-polylysine. One skilled in the art will also recognize that amino acids with properties similar to His and Lys may be substituted within the composition.

[0161] Certain embodiments of the oligomers described herein may contain a basic functional group, such as amino or alkylamino, and are, thus, capable of forming pharmaceutically-acceptable salts with pharmaceutically-acceptable acids. The term "pharmaceutically-acceptable salts" in this respect, refers to the relatively non-toxic, inorganic and organic acid addition salts of compounds of the present invention. These salts can be prepared in situ in the administration vehicle or the dosage form manufacturing process, or by separately reacting a purified compound of the invention in its free base form with a suitable organic or inorganic acid, and isolating the salt thus formed during subsequent purification. Representative salts include the hydrobromide, hydrochloride, sulfate, bisulfate, phosphate, nitrate, acetate, valerate, oleate, palmitate, stearate, laurate, benzoate, lactate, phosphate, tosylate, citrate, maleate, fumarate, succinate, tartrate, napthylate, mesylate, glucoheptonate, lactobionate, and laurylsulphonate salts and the like. (See, e.g., Berge et al. (1977) "Pharmaceutical Salts", J. Pharm. Sci. 66:1-19).

[0162] The pharmaceutically acceptable salts of the subject oligomers include the conventional nontoxic salts or quaternary ammonium salts of the compounds, e.g., from non-toxic organic or inorganic acids. For example, such conventional nontoxic salts include those derived from inorganic acids such as hydrochloride, hydrobromic, sulfuric, sulfamic, phosphoric, nitric, and the like; and the salts prepared from organic acids such as acetic, propionic, succinic, glycolic, stearic, lactic, malic, tartaric, citric, ascorbic, palmitic, maleic, hydroxymaleic, phenylacetic, glutamic, benzoic, salicyclic, sulfanilic, 2-acetoxybenzoic, fumaric, toluenesulfonic, methanesulfonic, ethane disulfonic, oxalic, isothionic, and the like.

[0163] In certain embodiments, the oligomers of the present invention may contain one or more acidic functional groups and, thus, are capable of forming pharmaceutically-acceptable salts with pharmaceutically-acceptable bases. The term "pharmaceutically-acceptable salts" in these instances refers to the relatively non-toxic, inorganic and organic base addition salts of compounds of the present invention. These salts can likewise be prepared in situ in the administration vehicle or the dosage form manufacturing process, or by separately reacting the purified compound in its free acid form with a suitable base, such as the hydroxide, carbonate or bicarbonate of a pharmaceutically-acceptable metal cation, with ammonia, or with a pharmaceutically-acceptable organic primary, secondary or tertiary amine. Representative alkali or alkaline earth salts include the lithium, sodium, potassium, calcium, magnesium, and aluminum salts and the like. Representative organic amines useful for the formation of base addition salts include ethylamine, diethylamine, ethylenediamine, ethanolamine, diethanolamine, piperazine and the like. (See, e.g., Berge et al., supra).

[0164] Wetting agents, emulsifiers and lubricants, such as sodium lauryl sulfate and magnesium stearate, as well as coloring agents, release agents, coating agents, sweetening, flavoring and perfuming agents, preservatives and antioxidants can also be present in the compositions.

[0165] Examples of pharmaceutically-acceptable antioxidants include: (1) water soluble antioxidants, such as ascorbic acid, cysteine hydrochloride, sodium bisulfate, sodium metabisulfite, sodium sulfite and the like; (2) oil-soluble antioxidants, such as ascorbyl palmitate, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), lecithin, propyl gallate, alpha-tocopherol, and the like; and (3) metal chelating agents, such as citric acid, ethylenediamine tetraacetic acid (EDTA), sorbitol, tartaric acid, phosphoric acid, and the like.

[0166] Formulations of the present invention include those suitable for oral, nasal, topical (including buccal and sublingual), rectal, vaginal and/or parenteral administration. The formulations may conveniently be presented in unit dosage form and may be prepared by any methods well known in the art of pharmacy. The amount of active ingredient that can be combined with a carrier material to produce a single dosage form will vary depending upon the host being treated, the particular mode of administration. The amount of active ingredient which can be combined with a carrier material to produce a single dosage form will generally be that amount of the compound which produces a therapeutic effect. Generally, out of one hundred percent, this amount will range from about 0.1 percent to about ninety-nine percent of active ingredient, preferably from about 5 percent to about 70 percent, most preferably from about 10 percent to about 30 percent.

[0167] In certain embodiments, a formulation of the present invention comprises an excipient selected from cyclodextrins, celluloses, liposomes, micelle forming agents, e.g., bile acids, and polymeric carriers, e.g., polyesters and polyanhydrides; and an oligomer of the present invention. In certain embodiments, an aforementioned formulation renders orally bioavailable an oligomer of the present invention.

[0168] Methods of preparing these formulations or compositions include the step of bringing into association an oligomer of the present invention with the carrier and, optionally, one or more accessory ingredients. In general, the formulations are prepared by uniformly and intimately bringing into association a compound of the present invention with liquid carriers, or finely divided solid carriers, or both, and then, if necessary, shaping the product.

[0169] Formulations of the invention suitable for oral administration may be in the form of capsules, cachets, pills, tablets, lozenges (using a flavored basis, usually sucrose and acacia or tragacanth), powders, granules, or as a solution or a suspension in an aqueous or non-aqueous liquid, or as an oil-in-water or water-in-oil liquid emulsion, or as an elixir or syrup, or as pastilles (using an inert base, such as gelatin and glycerin, or sucrose and acacia) and/or as mouth washes and the like, each containing a predetermined amount of a compound of the present invention as an active ingredient. An oligomer of the present invention may also be administered as a bolus, electuary or paste.

[0170] In solid dosage forms of the invention for oral administration (capsules, tablets, pills, dragees, powders, granules, trouches and the like), the active ingredient may be mixed with one or more pharmaceutically-acceptable carriers, such as sodium citrate or dicalcium phosphate, and/or any of the following: (1) fillers or extenders, such as starches, lactose, sucrose, glucose, mannitol, and/or silicic acid; (2) binders, such as, for example, carboxymethylcellulose, alginates, gelatin, polyvinyl pyrrolidone, sucrose and/or acacia; (3) humectants, such as glycerol; (4) disintegrating agents, such as agar-agar, calcium carbonate, potato or tapioca starch, alginic acid, certain silicates, and sodium carbonate; (5) solution retarding agents, such as paraffin; (6) absorption accelerators, such as quaternary ammonium compounds and surfactants, such as poloxamer and sodium lauryl sulfate; (7) wetting agents, such as, for example, cetyl alcohol, glycerol monostearate, and non-ionic surfactants; (8) absorbents, such as kaolin and bentonite clay; (9) lubricants, such as talc,

calcium stearate, magnesium stearate, solid polyethylene glycols, sodium lauryl sulfate, zinc stearate, sodium stearate, stearic acid, and mixtures thereof; (10) coloring agents; and (11) controlled release agents such as crospovidone or ethyl cellulose. In the case of capsules, tablets and pills, the pharmaceutical compositions may also comprise buffering agents. Solid compositions of a similar type may also be employed as fillers in soft and hard-shelled gelatin capsules using such excipients as lactose or milk sugars, as well as high molecular weight polyethylene glycols and the like.

[0171] A tablet may be made by compression or molding, optionally with one or more accessory ingredients. Compressed tablets may be prepared using binder (e.g., gelatin or hydroxypropylmethyl cellulose), lubricant, inert diluent, preservative, disintegrant (for example, sodium starch glycolate or cross-linked sodium carboxymethyl cellulose), surface-active or dispersing agent. Molded tablets may be made by molding in a suitable machine a mixture of the powdered compound moistened with an inert liquid diluent.

[0172] The tablets, and other solid dosage forms of the pharmaceutical compositions of the present invention, such as dragees, capsules, pills and granules, may optionally be scored or prepared with coatings and shells, such as enteric coatings and other coatings well known in the pharmaceutical-formulating art. They may also be formulated so as to provide slow or controlled release of the active ingredient therein using, for example, hydroxypropylmethyl cellulose in varying proportions to provide the desired release profile, other polymer matrices, liposomes and/or microspheres. They may be formulated for rapid release, e.g., freeze-dried. They may be sterilized by, for example, filtration through a bacteria-retaining filter, or by incorporating sterilizing agents in the form of sterile solid compositions which can be dissolved in sterile water, or some other sterile injectable medium immediately before use. These compositions may also optionally contain opacifying agents and may be of a composition that they release the active ingredient(s) only, or preferentially, in a certain portion of the gastrointestinal tract, optionally, in a delayed manner. Examples of embedding compositions which can be used include polymeric substances and waxes. The active ingredient can also be in micro-encapsulated form, if appropriate, with one or more of the above-described excipients.

[0173] Liquid dosage forms for oral administration of the compounds of the invention include pharmaceutically acceptable emulsions, microemulsions, solutions, suspensions, syrups and elixirs. In addition to the active ingredient, the liquid dosage forms may contain inert diluents commonly used in the art, such as, for example, water or other solvents, solubilizing agents and emulsifiers, such as ethyl alcohol, isopropyl alcohol, ethyl carbonate, ethyl acetate, benzyl alcohol, benzyl benzoate, propylene glycol, 1,3-butylene glycol, oils (in particular, cottonseed, groundnut, corn, germ, olive, castor and sesame oils), glycerol, tetrahydrofuryl alcohol, polyethylene glycols and fatty acid esters of sorbitan, and mixtures thereof.

[0174] Besides inert diluents, the oral compositions can also include adjuvants such as wetting agents, emulsifying and suspending agents, sweetening, flavoring, coloring, perfuming and preservative agents.

[0175] Suspensions, in addition to the active compounds, may contain suspending agents as, for example, ethoxylated isostearyl alcohols, polyoxyethylene sorbitol and sorbitan esters, microcrystalline cellulose, aluminum metahydroxide, bentonite, agar-agar and tragacanth, and mixtures thereof.

[0176] Formulations for rectal or vaginal administration may be presented as a suppository, which may be prepared by mixing one or more compounds of the invention with one or more suitable nonirritating excipients or carriers comprising, for example, cocoa butter, polyethylene glycol, a suppository wax or a salicylate, and which is solid at room temperature, but liquid at body temperature and, therefore, will melt in the rectum or vaginal cavity and release the active compound.

[0177] Formulations or dosage forms for the topical or transdermal administration of an oligomer as provided herein include powders, sprays, ointments, pastes, creams, lotions, gels, solutions, patches and inhalants. The active oligomers may be mixed under sterile conditions with a pharmaceutically-acceptable carrier, and with any preservatives, buffers, or propellants which may be required. The ointments, pastes, creams and gels may contain, in addition to an active compound of this invention, excipients, such as animal and vegetable fats, oils, waxes, paraffins, starch, tragacanth, cellulose derivatives, polyethylene glycols, silicones, bentonites, silicic acid, talc and zinc oxide, or mixtures thereof.

[0178] Powders and sprays can contain, in addition to an oligomer of the present invention, excipients such as lactose, talc, silicic acid, aluminum hydroxide, calcium silicates and polyamide powder, or mixtures of these substances. Sprays can additionally contain customary propellants, such as chlorofluorohydrocarbons and volatile unsubstituted hydrocarbons, such as butane and propane.

[0179] Transdermal patches have the added advantage of providing controlled delivery of an oligomer of the present invention to the body. Such dosage forms can be made by dissolving or dispersing the oligomer in the proper medium. Absorption enhancers can also be used to increase the flux of the agent across the skin. The rate of such flux can be controlled by either providing a rate controlling membrane or dispersing the agent in a polymer matrix or gel, among other methods known in the art.

[0180] Pharmaceutical compositions suitable for parenteral administration may comprise one or more oligomers of the invention in combination with one or more pharmaceutically-acceptable sterile isotonic aqueous or nonaqueous solutions, dispersions, suspensions or emulsions, or sterile powders which may be reconstituted into sterile injectable solutions or dispersions just prior to use, which may contain sugars, alcohols, antioxidants, buffers, bacteriostats, solutes which render the formulation isotonic with the blood of the intended recipient or suspending or thickening agents. Examples of suitable aqueous and nonaqueous carriers which may be employed in the pharmaceutical compositions of the invention include water, ethanol, polyols (such as glycerol, propylene glycol, polyethylene glycol, and the like), and suitable mixtures thereof, vegetable oils, such as olive oil, and injectable organic esters, such as ethyl oleate. Proper fluidity can be maintained, for example, by the use of coating materials, such as lecithin, by the maintenance of the required particle size in the case of dispersions, and by the use of surfactants.

[0181] These compositions may also contain adjuvants such as preservatives, wetting agents, emulsifying agents and dispersing agents. Prevention of the action of microorganisms upon the subject oligomers may be ensured by the inclusion of various antibacterial and antifungal agents, for example, paraben, chlorobutanol, phenol sorbic acid, and the

like. It may also be desirable to include isotonic agents, such as sugars, sodium chloride, and the like into the compositions. In addition, prolonged absorption of the injectable pharmaceutical form may be brought about by the inclusion of agents which delay absorption such as aluminum monostearate and gelatin.

[0182] In some cases, in order to prolong the effect of a drug, it is desirable to slow the absorption of the drug from subcutaneous or intramuscular injection. This may be accomplished by the use of a liquid suspension of crystalline or amorphous material having poor water solubility, among other methods known in the art. The rate of absorption of the drug then depends upon its rate of dissolution which, in turn, may depend upon crystal size and crystalline form. Alternatively, delayed absorption of a parenterally-administered drug form is accomplished by dissolving or suspending the drug in an oil vehicle.

[0183] Injectable depot forms may be made by forming microencapsule matrices of the subject oligomers in biodegradable polymers such as polylactide-polyglycolide. Depending on the ratio of oligomer to polymer, and the nature of the particular polymer employed, the rate of oligomer release can be controlled. Examples of other biodegradable polymers include poly(orthoesters) and poly(anhydrides). Depot injectable formulations may also prepared by entrapping the drug in liposomes or microemulsions that are compatible with body tissues.

[0184] When the oligomers of the present invention are administered as pharmaceuticals, to humans and animals, they can be given per se or as a pharmaceutical composition containing, for example, 0.1 to 99% (more preferably, 10 to 30%) of active ingredient in combination with a pharmaceutically acceptable carrier.

[0185] As noted above, the formulations or preparations of the present invention may be given orally, parenterally, systemically, topically, rectally or intramuscular administartion. They are typically given in forms suitable for each administration route. For example, they are administered in tablets or capsule form, by injection, inhalation, eye lotion, ointment, suppository, etc. administration by injection, infusion or inhalation; topical by lotion or ointment; and rectal by suppositories.

[0186] The phrases "parenteral administration" and "administered parenterally" as used herein means modes of administration other than enteral and topical administration, usually by injection, and includes, without limitation, intravenous, intramuscular, intraarterial, intrathecal, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal and intrasternal injection and infusion.

[0187] The phrases "systemic administration," "administered systemically," "peripheral administration" and "administered peripherally" as used herein mean the administration of a compound, drug or other material other than directly into the central nervous system, such that it enters the patient's system and, thus, is subject to metabolism and other like processes, for example, subcutaneous administration.

[0188] Regardless of the route of administration selected, the oligomers of the present invention, which may be used in a suitable hydrated form, and/or the pharmaceutical compositions of the present invention, may be formulated into pharmaceutically-acceptable dosage forms by conventional methods known to those of skill in the art. Actual dosage levels of the active ingredients in the pharmaceutical compositions of this invention may be varied so as to obtain an amount of the active ingredient which is effective to achieve the desired therapeutic response for a particular patient, composition, and mode of administration, without being unacceptably toxic to the patient.

[0189] The selected dosage level will depend upon a variety of factors including the activity of the particular oligomer of the present invention employed, or the ester, salt or amide thereof, the route of administration, the time of administration, the rate of excretion or metabolism of the particular oligomer being employed, the rate and extent of absorption, the duration of the treatment, other drugs, compounds and/or materials used in combination with the particular oligomer employed, the age, sex, weight, condition, general health and prior medical history of the patient being treated, and like factors well known in the medical arts.

[0190] A physician or veterinarian having ordinary skill in the art can readily determine and prescribe the effective amount of the pharmaceutical composition required. For example, the physician or veterinarian could start doses of the compounds of the invention employed in the pharmaceutical composition at levels lower than that required in order to achieve the desired therapeutic effect and gradually increase the dosage until the desired effect is achieved. In general, a suitable daily dose of a compound of the invention will be that amount of the compound which is the lowest dose effective to produce a therapeutic effect. Such an effective dose will generally depend upon the factors described above. Generally, oral, intravenous, intracerebroventricular, intramuscular and subcutaneous doses of the compounds of this invention for a patient, when used for the indicated effects, will range from about 0.0001 to about 100 mg per kilogram of body weight per day.

[0191] Preferred doses of the oligomers of the present invention (e.g., phosphorodiamidate morpholino oligomers; eteplirsen) are administered generally from about 20-100 mg/kg. In some cases, doses of greater than 100 mg/kg may be necessary. For i.v. administration, preferred doses are from about 0.5 mg to 100 mg/kg. In some embodiments, the oligomers are administered at doses of about 20 mg/kg, 21 mg/kg, 25 mg/kg, 26 mg/kg, 27 mg/kg, 28 mg/kg, 29 mg/kg, 30 mg/kg, 31 mg/kg, 32 mg/kg, 33 mg/kg, 34 mg/kg, 35 mg/kg, 36 mg/kg, 37 mg/kg, 38 mg/kg, 39 mg/kg, 40 mg/kg, 41 mg/kg, 42 mg/kg, 43 mg/kg, 44 mg/kg, 45 mg/kg, 46 mg/kg, 47 mg/kg, 48 mg/kg, 49 mg/kg 50 mg/kg, 51 mg/kg, 52 mg/kg, 53 mg/kg, 54 mg/kg, 55 mg/kg, 56 mg/kg, 57 mg/kg, 58 mg/kg, 59 mg/kg, 60 mg/kg, 65 mg/kg, 70 mg/kg, 75 mg/kg, 80 mg/kg, 85 mg/kg, 90 mg/kg, 95 mg/kg, 100 mg/kg, including all integers in between. In a preferred embodiment, the oligomer is administered at 30 mg/kg. In another preferred embodiment, the oligomer is administered at 50 mg/kg.

[0192] If desired, the effective daily dose of the active compound may be administered as two, three, four, five, six or more sub-doses administered separately at appropriate intervals throughout the day, optionally, in unit dosage forms. In certain situations, dosing is one administration per day. In certain embodiments, dosing is one or more administration per every 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 days, or every 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 weeks, or every 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 months, as needed, to maintain the desired expression of a functional dystrophin protein.

[0193] In some embodiments, the oligomers of the present invention (e.g., phosphorodiamidate morpholino oligomers; eteplirsen) are administered, generally at regular intervals (e.g., daily, weekly, biweekly, monthly, bimonthly). The oligomers may be administered at regular intervals, e.g., daily; once every two days; once every three days; once every 3 to 7 days; once every 3 to 10 days; once every 7 to 10 days; once every week; once every two weeks; once monthly. For example, the oligomers may be administered once weekly by intravenous infusion. The oligomers may be administered intermittently over a longer period of time, e.g., for several weeks, months or years. For example, the oligomers may be administered once every one, two, three, four, five, six, seven, eight, nine, ten, eleven or twelve months. In addition, the oligomers may be administered once every one, two, three, four or five years. Administration may be followed by, or concurrent with, administration of an antibiotic, steroid or other therapeutic agent. The treatment regimen may be adjusted (dose, frequency, route, etc.) as indicated, based on the results of immunoassays, other biochemical tests and physiological examination of the subject under treatment.

[0194] Nucleic acid molecules can be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres, as described herein and known in the art. In certain embodiments, microemulsification technology may be utilized to improve bioavailability of lipophilic (water insoluble) pharmaceutical agents. Examples include Trimetrine (Dordunoo, S. K., et al., Drug Development and Industrial Pharmacy, 17(12), 1685-1713, 1991 and REV 5901 (Sheen, P. C., et al., J Pharm Sci 80(7), 712-714, 1991). Among other benefits, microemulsification provides enhanced bioavailability by preferentially directing absorption to the lymphatic system instead of the circulatory system, which thereby bypasses the liver, and prevents destruction of the compounds in the hepatobiliary circulation.

[0195] In one aspect of invention, the formulations contain micelles formed from an oligomer as provided herein and at least one amphiphilic carrier, in which the micelles have an average diameter of less than about 100 nm. More preferred embodiments provide micelles having an average diameter less than about 50 nm, and even more preferred embodiments provide micelles having an average diameter less than about 30 nm, or even less than about 20 nm.

[0196] While all suitable amphiphilic carriers are contemplated, the presently preferred carriers are generally those that have Generally-Recognized-as-Safe (GRAS) status, and that can both solubilize the compound of the present invention and microemulsify it at a later stage when the solution comes into a contact with a complex water phase (such as one found in human gastro-intestinal tract). Usually, amphiphilic ingredients that satisfy these requirements have HLB (hydrophilic to lipophilic balance) values of 2-20, and their structures contain straight chain aliphatic radicals in the range of C-6 to C-20. Examples are polyethylene-glycolized fatty glycerides and polyethylene glycols.

[0197] Examples of amphiphilic carriers include saturated and monounsaturated polyethyleneglycolyzed fatty acid glycerides, such as those obtained from fully or partially hydrogenated various vegetable oils. Such oils may advantageously consist of tri-, di-, and mono-fatty acid glycerides and di- and mono-polyethyleneglycol esters of the corresponding fatty acids, with a particularly preferred fatty acid composition including capric acid 4-10, capric acid 3-9, lauric acid 40-50, myristic acid 14-24, palmitic acid 4-14 and stearic acid 5-15%. Another useful class of amphiphilic carriers includes partially esterified sorbitan and/or sorbitol, with saturated or mono-unsaturated fatty acids (SPAN-series) or corresponding ethoxylated analogs (TWEEN-series).

[0198] Commercially available amphiphilic carriers may be particularly useful, including Gelucire-series, Labrafil, Labrasol, or Lauroglycol (all manufactured and distributed by Gattefosse Corporation, Saint Priest, France), PEG-monooleate, PEG-di-oleate, PEG-mono-laurate and di-laurate, Lecithin, Polysorbate 80, etc (produced and distributed by a number of companies in USA and worldwide).

[0199] In certain embodiments, the delivery may occur by use of liposomes, nanocapsules, microparticles, microspheres, lipid particles, vesicles, and the like, for the introduction of the compositions of the present invention into suitable host cells. In particular, the compositions of the present invention may be formulated for delivery either encapsulated in a lipid particle, a liposome, a vesicle, a nanosphere, a nanoparticle or the like. The formulation and use of such delivery vehicles can be carried out using known and conventional techniques.

[0200] Hydrophilic polymers suitable for use in the present invention are those which are readily water-soluble, can be covalently attached to a vesicle-forming lipid, and which are tolerated in vivo without toxic effects (i.e., are biocompatible). Suitable polymers include polyethylene glycol (PEG), polylactic (also termed polylactide), polyglycolic acid (also termed polyglycolide), a polylactic-polyglycolic acid copolymer, and polyvinyl alcohol. In certain embodiments, polymers have a molecular weight of from about 100 or 120 daltons up to about 5,000 or 10,000 daltons, or from about 300 daltons to about 5,000 daltons. In other embodiments, the polymer is polyethyleneglycol having a molecular weight of from about 100 to about 5,000 daltons, or having a molecular weight of from about 300 to about 5,000 daltons. In certain embodiments, the polymer is polyethyleneglycol of 750 daltons (PEG(750)). Polymers may also be defined by the number of monomers therein; a preferred embodiment of the present invention utilizes polymers of at least about three monomers, such PEG polymers consisting of three monomers (approximately 150 daltons).

[0201] Other hydrophilic polymers which may be suitable for use in the present invention include polyvinylpyrrolidone, polymethoxazoline, polyethyloxazoline, polyhydroxypropyl methacrylamide, polymethacrylamide, polydimethylacrylamide, and derivatized celluloses such as hydroxymethylcellulose or hydroxyethylcellulose.

[0202] In certain embodiments, a formulation of the present invention comprises a biocompatible polymer selected from the group consisting of polyamides, polycarbonates, polyalkylenes, polymers of acrylic and methacrylic esters, polyvinyl polymers, polyglycolides, polysiloxanes, polyurethanes and co-polymers thereof, celluloses, polypropylene, polyethylenes, polystyrene, polymers of lactic acid and glycolic acid, polyanhydrides, poly(ortho)esters, poly (butic acid), poly(valeric acid), poly(lactide-co-caprolactone), polysaccharides, proteins, polyhyaluronic acids, polycyanoacrylates, and blends, mixtures, or copolymers thereof.

[0203] Cyclodextrins are cyclic oligosaccharides, consisting of 6, 7 or 8 glucose units, designated by the Greek letter α, β, or γ, respectively. The glucose units are linked by α-1,4-

glucosidic bonds. As a consequence of the chair conformation of the sugar units, all secondary hydroxyl groups (at C-2, C-3) are located on one side of the ring, while all the primary hydroxyl groups at C-6 are situated on the other side. As a result, the external faces are hydrophilic, making the cyclodextrins water-soluble. In contrast, the cavities of the cyclodextrins are hydrophobic, since they are lined by the hydrogen of atoms C-3 and C-5, and by ether-like oxygens. These matrices allow complexation with a variety of relatively hydrophobic compounds, including, for instance, steroid compounds such as 17α-estradiol (see, e.g., van Uden et al. Plant Cell Tiss. Org. Cult. 38:1-3-113 (1994)). The complexation takes place by Van der Waals interactions and by hydrogen bond formation. For a general review of the chemistry of cyclodextrins, see, Wenz, Agnew. Chem. Int. Ed. Engl., 33:803-822 (1994).

[0204] The physico-chemical properties of the cyclodextrin derivatives depend strongly on the kind and the degree of substitution. For example, their solubility in water ranges from insoluble (e.g., triacetyl-beta-cyclodextrin) to 147% soluble (w/v) (G-2-beta-cyclodextrin). In addition, they are soluble in many organic solvents. The properties of the cyclodextrins enable the control over solubility of various formulation components by increasing or decreasing their solubility.

[0205] Numerous cyclodextrins and methods for their preparation have been described. For example, Parmeter (I), et al. (U.S. Pat. No. 3,453,259) and Gramera, et al. (U.S. Pat. No. 3,459,731) described electroneutral cyclodextrins. Other derivatives include cyclodextrins with cationic properties [Parmeter (II), U.S. Pat. No. 3,453,257], insoluble crosslinked cyclodextrins (Solms, U.S. Pat. No. 3,420,788), and cyclodextrins with anionic properties [Parmeter (III), U.S. Pat. No. 3,426,011]. Among the cyclodextrin derivatives with anionic properties, carboxylic acids, phosphorous acids, phosphinous acids, phosphonic acids, phosphoric acids, thiophosphonic acids, thiosulphinic acids, and sulfonic acids have been appended to the parent cyclodextrin [see, Parmeter (III), supra]. Furthermore, sulfoalkyl ether cyclodextrin derivatives have been described by Stella, et al. (U.S. Pat. No. 5,134,127).

[0206] Liposomes consist of at least one lipid bilayer membrane enclosing an aqueous internal compartment. Liposomes may be characterized by membrane type and by size. Small unilamellar vesicles (SUVs) have a single membrane and typically range between 0.02 and 0.05 μm in diameter; large unilamellar vesicles (LUVS) are typically larger than 0.05 μm. Oligolamellar large vesicles and multilamellar vesicles have multiple, usually concentric, membrane layers and are typically larger than 0.1 μm. Liposomes with several nonconcentric membranes, i.e., several smaller vesicles contained within a larger vesicle, are termed multivesicular vesicles.

[0207] One aspect of the present invention relates to formulations comprising liposomes containing an oligomer of the present invention, where the liposome membrane is formulated to provide a liposome with increased carrying capacity. Alternatively or in addition, the compound of the present invention may be contained within, or adsorbed onto, the liposome bilayer of the liposome. An oligomer of the present invention may be aggregated with a lipid surfactant and carried within the liposome's internal space; in these cases, the liposome membrane is formulated to resist the disruptive effects of the active agent-surfactant aggregate.

[0208] According to one embodiment of the present invention, the lipid bilayer of a liposome contains lipids derivatized with polyethylene glycol (PEG), such that the PEG chains extend from the inner surface of the lipid bilayer into the interior space encapsulated by the liposome, and extend from the exterior of the lipid bilayer into the surrounding environment.

[0209] Active agents contained within liposomes of the present invention are in solubilized form. Aggregates of surfactant and active agent (such as emulsions or micelles containing the active agent of interest) may be entrapped within the interior space of liposomes according to the present invention. A surfactant acts to disperse and solubilize the active agent, and may be selected from any suitable aliphatic, cycloaliphatic or aromatic surfactant, including but not limited to biocompatible lysophosphatidylcholines (LPGs) of varying chain lengths (for example, from about C14 to about C20). Polymer-derivatized lipids such as PEG-lipids may also be utilized for micelle formation as they will act to inhibit micelle/membrane fusion, and as the addition of a polymer to surfactant molecules decreases the CMC of the surfactant and aids in micelle formation. Preferred are surfactants with CMOs in the micromolar range; higher CMC surfactants may be utilized to prepare micelles entrapped within liposomes of the present invention.

[0210] Liposomes according to the present invention may be prepared by any of a variety of techniques that are known in the art. See, e.g., U.S. Pat. No. 4,235,871; Published PCT applications WO 96/14057; New RRC, Liposomes: A practical approach, IRL Press, Oxford (1990), pages 33-104; Lasic D D, Liposomes from physics to applications, Elsevier Science Publishers BV, Amsterdam, 1993. For example, liposomes of the present invention may be prepared by diffusing a lipid derivatized with a hydrophilic polymer into preformed liposomes, such as by exposing preformed liposomes to micelles composed of lipid-grafted polymers, at lipid concentrations corresponding to the final mole percent of derivatized lipid which is desired in the liposome. Liposomes containing a hydrophilic polymer can also be formed by homogenization, lipid-field hydration, or extrusion techniques, as are known in the art.

[0211] In another exemplary formulation procedure, the active agent is first dispersed by sonication in a lysophosphatidylcholine or other low CMC surfactant (including polymer grafted lipids) that readily solubilizes hydrophobic molecules. The resulting micellar suspension of active agent is then used to rehydrate a dried lipid sample that contains a suitable mole percent of polymer-grafted lipid, or cholesterol. The lipid and active agent suspension is then formed into liposomes using extrusion techniques as are known in the art, and the resulting liposomes separated from the unencapsulated solution by standard column separation.

[0212] In one aspect of the present invention, the liposomes are prepared to have substantially homogeneous sizes in a selected size range. One effective sizing method involves extruding an aqueous suspension of the liposomes through a series of polycarbonate membranes having a selected uniform pore size; the pore size of the membrane will correspond roughly with the largest sizes of liposomes produced by extrusion through that membrane. See e.g., U.S. Pat. No. 4,737,323 (Apr. 12, 1988). In certain embodiments, reagents such as DharmaFECT® and Lipofectamine® may be utilized to introduce polynucleotides or proteins into cells.

[0213] The release characteristics of a formulation of the present invention depend on the encapsulating material, the concentration of encapsulated drug, and the presence of release modifiers. For example, release can be manipulated to be pH dependent, for example, using a pH sensitive coating that releases only at a low pH, as in the stomach, or a higher pH, as in the intestine. An enteric coating can be used to prevent release from occurring until after passage through the stomach. Multiple coatings or mixtures of cyanamide encapsulated in different materials can be used to obtain an initial release in the stomach, followed by later release in the intestine. Release can also be manipulated by inclusion of salts or pore forming agents, which can increase water uptake or release of drug by diffusion from the capsule. Excipients which modify the solubility of the drug can also be used to control the release rate. Agents which enhance degradation of the matrix or release from the matrix can also be incorporated. They can be added to the drug, added as a separate phase (i.e., as particulates), or can be co-dissolved in the polymer phase depending on the compound. In most cases the amount should be between 0.1 and thirty percent (w/w polymer). Types of degradation enhancers include inorganic salts such as ammonium sulfate and ammonium chloride, organic acids such as citric acid, benzoic acid, and ascorbic acid, inorganic bases such as sodium carbonate, potassium carbonate, calcium carbonate, zinc carbonate, and zinc hydroxide, and organic bases such as protamine sulfate, spermine, choline, ethanolamine, diethanolamine, and triethanolamine and surfactants such as Tween® and Pluronic®. Pore forming agents which add microstructure to the matrices (i.e., water soluble compounds such as inorganic salts and sugars) are added as particulates. The range is typically between one and thirty percent (w/w polymer).

[0214] Uptake can also be manipulated by altering residence time of the particles in the gut. This can be achieved, for example, by coating the particle with, or selecting as the encapsulating material, a mucosal adhesive polymer. Examples include most polymers with free carboxyl groups, such as chitosan, celluloses, and especially polyacrylates (as used herein, polyacrylates refers to polymers including acrylate groups and modified acrylate groups such as cyanoacrylates and methacrylates).

[0215] An oligomer may be formulated to be contained within, or, adapted to release by a surgical or medical device or implant. In certain aspects, an implant may be coated or otherwise treated with an oligomer. For example, hydrogels, or other polymers, such as biocompatible and/or biodegradable polymers, may be used to coat an implant with the compositions of the present invention (i.e., the composition may be adapted for use with a medical device by using a hydrogel or other polymer). Polymers and copolymers for coating medical devices with an agent are well-known in the art. Examples of implants include, but are not limited to, stents, drug-eluting stents, sutures, prosthesis, vascular catheters, dialysis catheters, vascular grafts, prosthetic heart valves, cardiac pacemakers, implantable cardioverter defibrillators, IV needles, devices for bone setting and formation, such as pins, screws, plates, and other devices, and artificial tissue matrices for wound healing.

[0216] In addition to the methods provided herein, the oligomers for use according to the invention may be formulated for administration in any convenient way for use in human or veterinary medicine, by analogy with other pharmaceuticals. The antisense oligomers and their corresponding formulations may be administered alone or in combination with other therapeutic strategies in the treatment of muscular dystrophy, such as myoblast transplantation, stem cell therapies, administration of aminoglycoside antibiotics, proteasome inhibitors, and up-regulation therapies (e.g., upregulation of utrophin, an autosomal paralogue of dystrophin).

[0217] The routes of administration described are intended only as a guide since a skilled practitioner will be able to determine readily the optimum route of administration and any dosage for any particular animal and condition. Multiple approaches for introducing functional new genetic material into cells, both in vitro and in vivo have been attempted (Friedmann (1989) Science, 244:1275-1280). These approaches include integration of the gene to be expressed into modified retroviruses (Friedmann (1989) supra; Rosenberg (1991) Cancer Research 51(18), suppl.: 5074S-5079S); integration into non-retrovirus vectors (e.g., adeno-associated viral vectors) (Rosenfeld, et al. (1992) Cell, 68:143-155; Rosenfeld, et al. (1991) Science, 252:431-434); or delivery of a transgene linked to a heterologous promoter-enhancer element via liposomes (Friedmann (1989), supra; Brigham, et al. (1989) Am. J. Med. Sci., 298:278-281; Nabel, et al. (1990) Science, 249:1285-1288; Hazinski, et al. (1991) Am. J. Resp. Cell Molec. Biol., 4:206-209; and Wang and Huang (1987) Proc. Natl. Acad. Sci. (USA), 84:7851-7855); coupled to ligand-specific, cation-based transport systems (Wu and Wu (1988) J. Biol. Chem., 263:14621-14624) or the use of naked DNA, expression vectors (Nabel et al. (1990), supra); Wolff et al. (1990) Science, 247:1465-1468). Direct injection of transgenes into tissue produces only localized expression (Rosenfeld (1992) supra); Rosenfeld et al. (1991) supra; Brigham et al. (1989) supra; Nabel (1990) supra; and Hazinski et al. (1991) supra). The Brigham et al. group (Am. J. Med. Sci. (1989) 298:278-281 and Clinical Research (1991) 39 (abstract)) have reported in vivo transfection only of lungs of mice following either intravenous or intratracheal administration of a DNA liposome complex. An example of a review article of human gene therapy procedures is: Anderson, Science (1992) 256:808-813.

V. KITS

[0218] The invention also provides kits for treatment of a patient with a genetic disease which kit comprises at least an antisense molecule (e.g., one or more antisense oligonucleotides capable of specifically hybridizing to any one or more of exons 1-79 of the dystrophin gene; for example, Exon 51 as set forth in Tables 3 and 4 herein), packaged in a suitable container, together with instructions for its use. The kits may also contain peripheral reagents such as buffers, stabilizers, etc. Those of ordinary skill in the field should appreciate that applications of the above method has wide application for identifying antisense molecules suitable for use in the treatment of many other diseases.

VII. EXAMPLES

Materials and Methods

Patients

[0219] Eligible patients were between 7 and 13 years of age (inclusive), with out-of-frame deletions of the DMD gene that could be corrected by skipping exon 51. Patients were confirmed to have stable cardiac and pulmonary function and a stable dose of glucocorticoids for at least 24 weeks prior to

enrollment. Only patients who could walk between 200 and 400 meters (±10%) on the 6-Minute Walk Test (6MWT) at baseline were enrolled.

Study Design

[0220] This one-year trial was conducted in two phases: (1) treatment was double-blind through week 24 and (2) open-label thereafter. Primary endpoints were change in percent dystrophin fibers and ambulation as measured by the 6-Minute Walk Test (6MWT).

[0221] Study 201 was a single-site, randomized, double-blind, placebo-controlled, multiple-dose efficacy, safety and tolerability trial of eteplirsen. Twelve patients with DMD were randomized to one of three groups: eteplirsen 30 mg/kg/week (Cohort 1); eteplirsen 50 mg/kg/week (Cohort 2); or placebo/delayed eteplirsen (Cohort 3). All patients received weekly intravenous eteplirsen or placebo/delayed eteplirsen dosing. Placebo-treated patients crossed over to weekly eteplirsen 30 (n=2) or 50 mg/kg (n=2) at week 25. Efficacy and safety were assessed at scheduled visits, and an independent Data Safety Monitoring Board ensured the welfare of all patients. All patients had bicep biopsies at baseline. Follow-up biopsies were performed in the opposite arm (biceps) at week 12 for the 50 mg/kg group and two placebo-treated patients and at week 24 for the 30 mg/kg group and two placebo-treated patients.

[0222] Patients continued weekly dosing with 30 or 50 mg/kg eteplirsen under Study 202, a long-term, open-label extension study. All efficacy assessments continued to be performed during Study 202, including a third biopsy (in the left deltoid muscle) in all patients at week 48. Monitoring of adverse events continued throughout the study. A schematic of the study design is shown in FIG. **1**.

Study Drug

[0223] Eteplirsen [sequence 5'-CTCCAACATCAAGGAAGATGGCATTTCTAG-3'] (SEQ ID NO:1) was supplied by Sarepta Therapeutics, Inc. in single-use vials of phosphate-buffered saline (100 mg/ml). Eteplirsen was reconstituted with 150 ml normal saline and infused over 60 minutes. Placebo, administered during the first 24 weeks of Study 201, was supplied as identical vials of phosphate-buffered saline and was administered in the same manner as eteplirsen.

Safety and Tolerability Monitoring

[0224] Safety was assessed by evaluation of adverse events, vital signs, physical examinations, electrocardiograms, echocardiograms, and clinical laboratory testing. In addition, kidney function was monitored via regular assessments of serum cystatin C and urine cystatin C and KIM-1.

Pharmacokinetic and Immune Assessments

[0225] Pharmacokinetic parameters of eteplirsen were established from plasma and urine taken after the twelfth dose using a validated and sensitive anion exchange high-performance liquid chromatography with fluorescence detection bioanalytical method. Single samples for analysis of plasma concentrations were taken at weeks 24, 25, and 36. Immune response to novel dystrophin protein was measured every six weeks through week 24 with ELISPOT following methods previously published.

Biochemical Efficacy Assessments

[0226] Pre- and post-treatment dystrophin expression studies were based on MANDYS106 [a gift from Glen Morris, MDA Monoclonal Antibody Library], a highly sensitive marker for dystrophin used in prior studies of eteplirsen and other exon skipping candidates. Three 10 μm frozen sections, separated by at least 200 μm, were stained with MANDYS106, followed by a secondary antibody (Alexa Fluor 594 goat antimouse antibody). Percent dystrophin-positive fibers were calculated by dividing the number of positive fibers by the total fibers counted. As normal muscle samples have 100% dystrophin-positive fibers, percent dystrophin-positive fibers is expressed as a percentage of normal. The same antibody-stained sections were used for dystrophin quantification using Bioquant image analysis software. The total dystrophin fluorescence signal intensity was reported as a percentage of normal.

[0227] Supportive measurements included expression of the components of the sarcoglycan complex (β,γ), neuronal NOS, and Western blot (with the anti-dystrophin antibody NCL-Dysl from Novacastra). RT-PCR analysis, for confirmation of exon skipping, was performed on 400 ng of total RNA using dystrophin-specific reverse primers as previously described.

Clinical Efficacy Assessments

[0228] The 6MWT was administered using the protocol established for patients with DMD by McDonald, et al. (Muscle Nerve, 2010; 42:966-74, herein incorporated by reference). Exploratory functional outcomes included the North Star Ambulatory Assessment, quantitative muscle testing, the 9-Hole Peg Test, pulmonary function testing (PFT), timed function tests, and assessment of quality of life.

Statistical Analysis

[0229] SAS version 9.3 (Cary, N.C.) was used for all statistical analyses. Mixed model with treatment as fixed effect, subject nested within treatment as random effect, with the baseline value and time since DMD diagnosis as covariates for the analysis of muscle biopsy data was used. Mixed model repeated measures (MMRM) with treatment, time, and treatment-by-time interaction terms as fixed effect, subject nested within treatment as random effect, and with the baseline value and time since DMD diagnosis as covariates for analysis of the 6MWT data was used. Safety and muscle biopsy analyses were performed on the intent-to-treat population; analysis of ambulation-related outcomes, including the 6MWT, used a modified intent-to-treat (mITT) population that excluded two patients in Cohort 1 who showed signs of disease progression and significant decline on the 6MWT within weeks of enrollment and could not perform measures of ambulation at week 24 or beyond.

Example 1

Subject Characteristics

[0230] Baseline characteristics of the 12 patients in this study are summarized in Table 2. Five different genotypes amenable to exon 51 skipping were represented in the study population. Mean distances on the 6-Minute Walk Test (6MWT) at baseline were similar to those in other studies of children with DMD, and as expected, were well below the 600 plus meters typically observed in age-matched healthy

children. Due to the stochastic nature of the sampling, the 30 mg/kg cohort was slightly older, heavier, and taller, relative to the other cohorts, and had a lower mean 6MWT distance at baseline. All patients received all infusions of study medication as planned and completed all assessments.

TABLE 2

Baseline Demography and Disease Characteristics

Treatment Arm	Placebo/ Delayed Eteplirsen N = 4	Eteplirsen 30 mg/kg N = 4	Eteplirsen 50 mg/kg N = 4
Mutation			
45-50 n (%)	0	2 (50)	1 (25)
48-50 n (%)	0	1 (25)	0
49-50 n (%)	3 (75)	0	2 (50)
50 n (%)	1 (25)	0	0
52 n (%)	0	1 (25)	1 (25)
Gender n (%)			
Male	4 (100)	4 (100)	4 (100)
Age, years			
Mean	8.5	9.3	8.5
SD	1.73	0.50	1.29
Min, Max	7, 10	9, 10	7, 10
Height, cm			
Mean	119.3	130.5	121.3
SD	3.40	9.47	7.85
Min, Max	116, 124	117, 138	117, 133
Weight, kg			
Mean	30.6	34.8	29.0
SD	6.04	7.05	6.38
Min, Max	22.1, 36.2	24.8, 39.8	23.7, 38.3
Race, n (%)			
Asian	0	1 (25)	0
White	4 (100)	3 (75)	4 (100)
6MWT*, meters			
Mean	394.5	355.3	396.0
SD	42.25	74.78	26.61
Min, Max	364, 456	261, 442	365, 429

Example 2

Safety and Lack of Adverse Events

[0231] Eteplirsen was well tolerated with no treatment-related adverse events, serious adverse events, discontinuations or missed doses through 48 weeks of treatment. Moreover, no clinically significant changes were observed on physical examination or in vital signs. Electrocardiograms, echocardiograms, and PFTs remained stable, and chemistries showed no clinically significant changes in hematologic, renal, coagulation or liver functions. Mild and transient proteinuria was observed in a single placebo-treated subject.

Example 3

Pharmacokinetic Profile

[0232] Analysis of PK parameters at week 12 revealed rapid absorption. Plasma clearance averaged 339±75.8 mL/hr/kg for 30 mg/kg and 319±125 mL/hr/kg for 50 mg/kg. Half-life averaged 3.30±0.341 hr for 30 mg/kg and 3.17±0.249 hr for 50 mg/kg, with renal clearance accounting for approximately 65-70% of total systemic clearance.

Example 4

Efficacy

[0233] At week 48, eteplirsen produced robust increases in the number and intensity of dystrophin-positive fibers. As shown in FIG. **3**, patients who received 30 or 50 mg/kg eteplirsen without interruption for 48 weeks showed a mean increase in the percentage of dystrophin-positive fibers to 47% of normal ($p \leq 0.001$), relative to baseline. Increases were similar when the 30 (52%; $p \leq 0.001$) and 50 (43%; $p \leq 0.008$) mg/kg cohorts were analyzed separately, suggesting that eteplirsen's effect on the production of novel dystrophin is independent of dose within this range of doses.

[0234] Biopsies were taken at staggered time points (see FIG. **2**) to evaluate the impact of treatment duration on novel dystrophin production. At week 12, the 50 mg/kg cohort had undetectable levels of novel dystrophin. At week 24, the 30 mg/kg cohort demonstrated an increase in the percentage of dystrophin-positive fibers to 23% of normal ($p \leq 0.002$), and at week 48, after 24 weeks of treatment with 30 or 50 mg/kg eteplirsen, the 4 patients in the placebo/delayed eteplirsen cohort showed an increase to 38% of normal, relative to baseline ($p \leq 0.009$). Together these data suggest that treatment duration plays an important role in eteplirsen's ability to uniformly restore novel dystrophin production. Consistent with these findings, eteplirsen also significantly increased mean fluorescence signal intensity at week 48 in all three treatment groups (all p-values≤ 0.023).

[0235] FIG. **4** illustrates eteplirsen's time-dependent effect on the percentage of dystrophin-positive fibers (Panel A), which was accompanied by restoration of β- and γ-sarcoglycan and nNOSμ at the sarcolemma (Panel B). Dystrophin expression and exon skipping were confirmed by Western blot and RT-PCR in all patients. RT-PCR results from a representative patient are shown in Panel C. These data confirmed the increase in functional dystrophin in the patients.

Example 5

Functional Outcomes

[0236] The progressive loss of walking ability is a universal hallmark of DMD, with most patients showing functional compromise by 7 or 8 years of age and becoming wheelchair dependent by 10 to 14 years of age. Consistent with this, boys assigned to the placebo/delayed eteplirsen cohort in this study showed a decline in walking ability after week 12 at a rate predicted by prior studies, culminating in a loss of approximately 60 meters by week 48 (FIG. **5**). In marked contrast, eteplirsen-treated patients maintained a stable walking distance over the duration of the study, with a mean increase from baseline of about 7 meters by week 48. The difference between the eteplirsen-treated patients and those in the placebo/delayed eteplirsen cohort first became statistically significant at week 32 (39-meter difference; $p \leq 0.05$). Interestingly, patients in the placebo/delayed eteplirsen cohort appeared to stabilize after week 36, i.e., between 12 and 24 weeks after initiating treatment with eteplirsen at week 25. As previously noted, two boys who showed signs of rapid disease progression and significant decline on the 6MWT within weeks of enrollment and were unable to perform measures of ambulation at 24 weeks or beyond, were excluded from this

analysis. However, both remained on eteplirsen through week 48 with no treatment-related adverse events and maintained stable pulmonary and upper limb function as measured by PFT and the 9-Hole Peg Test, respectively.

[0237] Notably, patients receiving eteplirsen for 48 weeks, evaluable on the 6MWT (n=6), significantly ($p \leq 0.001$) improved on the 6MWT (67.3 m) compared to the placebo/delayed cohort.

Example 6

Immune Response

[0238] There were no differences between the eteplirsen- and placebo-treated patients in the number of interferon-γ-induced spot forming colonies to dystrophin peptide pools (extended over the entire protein) at any time point assessed, including week 24, indicating that the newly expressed dystrophin in the eteplirsen-treated patients did not elicit a T-cell response.

[0239] All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

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SEQUENCE LISTING

[0272] With respect to the nucleic acid sequences provided in the application, persons skilled in the art will appreciate that depending on the use of the oligomers, Ts and Us are interchangeable.

TABLE 3

EXON	SEQ ID	SEQUENCE	NUCLEOTIDE SEQUENCE (5'-3')
51	1	eteplirsen H51A(+66 + 95)	CTC CAA CAT CAA GGA AGA TGG CAT TTC TAG
51	2	H51A(+66 + 90)	ACA UCA AGG AAG AUG GCA UUU CUA G
51	3	H51A(+61 + 90)	ACA UCA AGG AAG AUG GCA UUU CUA GUU UGG
51	4	Hu.DMD.exon51.25.001.2	GAG CAG GTA CCT CCA ACA TCA AGG AA
50	5	H50D(+07 - 18)	GGG AUC CAG UAU ACU UAC AGG CUC C
50	6	AVI-4038/5038	CTT ACA GGC TCC AAT AGT GGT CAG T
53	7	H53A27(+30 + 56)	CCT CCG GTT CTG AAG GTG TTC TTG TAC
53	8	H53A(+36 + 60)	GTT GCC TCC GGT TCT GAA GGT GTT C
45	9	H45A (-03 + 19)	CAA TGC CAT CCT GGA GTT CCT G

TABLE 4

SEQ ID	SEQUENCE	NUCLEOTIDE SEQUENCE (5' - 3')
10	H8A(-06 + 18)	GAU AGG UGG UAU CAA CAU CUG UAA
11	H8A (-04 + 18)	GAU AGG UGG UAU CAA CAU CUG
12	H8A(-07 + 18)	GAU AGG UGG UAU CAA CAU CUG UAA G
13	H8A(-06 + 14)	GGU GGU AUC AAC AUC UGU AA
14	H8A(-10 + 10)	GUA UCA ACA UCU GUA AGC AC
15	H7A(+45 + 67)	UGC AUG UUC CAG UCG UUG UGU GG
16	H7A(+02 + 26)	CAC UAU UCC AGU CAA AUA GGU CUG G
17	H7D(+15-10)	AUU UAC CAA CCU UCA GGA UCG AGU A
18	H7A(-18 + 03)	GGC CUA AAA CAC AUA CAC AUA
19	C6A(-10 + 10)	CAU UUU UGA CCU ACA UGU GG
20	C6A(-14 + 06)	UUU GAC CUA CAU GUG GAA AG
21	C6A(-14 + 12)	UAC AUU UUU GAC CUA CAU GUG GAA AG
22	C6A(-14 + 09)	AUU UUU GAC CUA CAU GGG AAA G
23	CH6A(+69 + 91)	UAC GAG UUG AUU GUC GGA CCC AG
24	C6D(+12 - 13)	GUG GUC UCC UUA CCU AUG ACU GUG G
25	C6D(+06 - 11)	GGU CUC CUU ACC UAU GA
26	H6D(+04 - 21)	UGU CUC AGU AAU CUU CUU ACC UAU
27	H6D(+18 - 04)	UCU UAC CUA UGA CUA UGG AUG AGA
28	H4A(+13 + 32)	GCA UGA ACU CUU GUG GAU CC

TABLE 4-continued

29	H4D(+04 - 16)	CCA GGG UAC UAC UUA CAU UA
30	H4D(-24 - 44)	AUC GUG UGU CAC AGC AUC CAG
31	H4A(+11 + 40)	UGU UCA GGG CAU GAA CUC UUG UGG AUC CUU
32	H3A(+30 + 60)	UAG GAG GCG CCU CCC AUC CUG UAG GUC ACU G
33	H3A(+35 + 65)	AGG UCU AGG AGG CGC CUC CCA UCC UGU AGG U
34	H3A(+30 + 54)	GCG CCU CCC AUC CUG UAG GUC ACU G
35	H3D(+46 - 21)	CUU CGA GGA GGU CUA GGA GGC GCC UC
36	H3A(+30 + 50)	CUC CCA UCC UGU AGG UCA CUG
37	H3D(+19 - 03)	UAC CAG UUU UUG CCC UGU CAG G
38	H3A(-06 + 20)	UCA AUA UGC UGC UUC CCA AAC UGA AA
39	H3A(+37 + 61)	CUA GGA GGC GCC UCC CAU CCU GUA G
40	H5A(+20 + 50)	UUA UGA UUU CCA UCU ACG AUG UCA GUA CUU C
41	H5D(+25 - 05)	CUU ACC UGC CAG UGG AGG AUU AUA UUC CAA A
42	H5D(+10 - 15)	CAU CAG GAU UCU UAC CUG CCA GUG G
43	H5A(+10 + 34)	CGA UGU CAG UAC UUC CAA UAU UCA C
44	H5D(-04 - 21)	ACC AUU CAU CAG GAU UCU
45	H5D(+16 - 02)	ACC UGC CAG UGG AGG AUU
46	H5A(-07 + 20)	CCA AUA UUC ACU AAA UCA ACC UGU UAA
47	H5D(+18 - 12)	CAG GAU UGU UAC CUG CCA GUG GAG GAU UAU
48	H5A(+05 + 35)	ACG AUG UCA GUA CUU CCA AUA UUC ACU AAA U
49	H5A(+15 + 45)	AUU UCC AUC UAC GAU GUC AGU ACU UCC AAU A
50	H10A(-05 + 16)	CAG GAG CUU CCA AAU GCU GCA
51	H10A(-05 + 24)	CUU GUC UUC AGG AGC UUC CAA AUG CUG CA
52	H10A(+98 + 119)	UCC UCA GCA GAA AGA AGC CAC G
53	H10A(+130 + 149)	UUA GAA AUC UCU CCU UGU GC
54	H10A(-33 - 14)	UAA AUU GGG UGU UAC ACA AU
55	H11D(+26 + 49)	CCC UGA GGC AUU CCC AUC UUG AAU
56	H11D(+11 - 09)	AGG ACU UAC UUG CUU UGU UU
57	H11A(+118 + 140)	CUU GAA UUU AGG AGA UUC AUC UG
58	H11A(+75 + 97)	CAU CUU CUG AUA AUU UUC CUG UU
59	H12A(+52 + 75)	UCU UCU GUU UUU GUU AGC CAG UCA
60	H12A(-10 + 10)	UCU AUG UAA ACU GAA AAU UU
61	H12A(+11 + 30)	UUC UGG AGA UCC AUU AAA AC
62	H13A(+77 + 100)	CAG CAG UUG CGU GAU CUC CAC UAG
63	H13A(+55 + 75)	UUC AUC AAC UAC CAC CAC CAU
64	H13D(+06 - 19)	CUA AGC AAA AUA AUC UGA CCU UAA G
65	H14A(+37 + 64)	CUU GUA AAA GAA CCC AGC GGU CUU CUG U
66	H14A(+14 + 35)	CAU CUA CAG AUG UUU GCC CAU C
67	H14A(+51 + 73)	GAA GGA UGU CUU GUA AAA GAA CC
68	H14D(-02 + 18)	ACC UGU UCU UCA GUA AGA CG
69	H14D(+14 - 10)	CAU GAC ACA CCU GUU CUU CAG UAA
70	H14A(+61 + 80)	CAU UUG AGA AGG AUG UCU UG
71	H14A(-12 + 12)	AUC UCC CAA UAC CUG GAG AAG AGA
72	H15A(-12 + 19)	GCC AUG CAC UAA AAA GGC ACU GCA AGA CAU U
73	H15A(+48 + 71)	UCU UUA AAG CCA GUU GUG UGA AUC
74	H15A(+08 + 28)	UUU CUG AAA GCC AUG CAC UAA
75	H15D(+17 - 08)	GUA CAU ACG GCC AGU UUU UGA AGA C
76	H16A(-12 + 19)	CUA GAU CCG CUU UUA AAA CCU GUU AAA ACA A
77	H16A(-06 + 25)	UCU UUU CUA GAU CCG CUU UUA AAA CCU GUU A
78	H16A(-06 + 19)	CUA GAU CCG CUU UUA AAA CCU GUU A
79	H16A(+87 + 109)	CCG UCU UCU GGG UCA CUG ACU UA
80	H16A(-07 + 19)	CUA GAU CCG CUU UUA AAA CCU GUU AA
81	H16A(-07 + 13)	CCG CUU UUA AAA CCU GUU AA
82	H16A(+12 + 37)	UGG AUU GCU UUU UCU UUU CUA GAU CC
83	H16A(+92 + 116)	CAU GCU UCC GUC UUC UGG GUC ACU G
84	H16A(+45 + 67)	G AUC UUG UUU GAG UGA AUA CAG U
85	H16A(+105 + 126)	GUU AUC CAG CCA UGC UUC CGU C
86	H16D(+05 - 20)	UGA UAA UUG GUA UCA CUA ACC UGU G
87	H16D(+12 - 11)	GUA UCA CUA ACC UGU GCU GUA C
88	H19A(+35 + 53)	CUG CUG GCA UCU UGC AGU U
89	H19A(+35 + 65)	GCC UGA GCU GAU CUG CUG GCA UCU UGC AGU U
90	H20A(+44 + 71)	CUG GCA GAA UUC GAU CCA CCG GCU GUU C
91	H20A(+147 + 168)	CAG CAG UAG UUG UCA UCU GCU C
92	H20A(+185 + 203)	UGA UGG GGU GGU GGG UUG G
93	H20A(-08 + 17)	AUC UGC AUU AAC ACC CUC UAG AAA G
94	H20A(+30 + 53)	CCG GCU GUU CAG UUG UUC UGA GGC
95	H20A(-11 + 17)	AUC UGC AUU AAC ACC CUC UAG AAA GAA A
96	H20D(+08 - 20)	GAA GGA GAA GAG AUU CUU ACC UUA CAA A
97	H20A(+44 + 63)	AUU CGA UCC ACC GGC UGU UC
98	H20A(+149 + 168)	CAG CAG UAG UUG UCA UCU GC
99	H21A(-06 + 16)	GCC GGU UGA CUU CAU CCU GUG C
100	H21A(+85 + 106)	CUG CAU CCA GGA ACA UGG GUC C
101	H21A(+85 + 108)	GUC UGC AUC CAG GAA CAU GGG UC
102	H21A(+08 + 31)	GUU GAA GAU CUG AUA GCC GGU UGA
103	H21D(+18 - 07)	UAC UUA CUG UCU GUA GCU CUU UCU
104	H22A(+22 + 45)	CAC UCA UGG UCU CCU GAU AGC GCA
105	H22A(+125 + 146)	CUG CAA UUC CCC GAG UCU CUG C

TABLE 4-continued

106	H22A(+47 + 69)	ACU GCU GGA CCC AUG UCC UGA UG
107	H22A(+80 + 101)	CUA AGU UGA GGU AUG GAG AGU
108	H22D(+13 - 11)	UAU UCA CAG ACC UGC AAU UCC CC
109	H23A(+34 + 59)	ACA GUG GUG CUG AGA UAG UAU AGG CC
110	H23A(+18 + 39)	UAG GCC ACU UUG UUG CUC UUG C
111	H23A(+72 + 90)	UUC AGA GGG CGC UUU CUU C
112	H24A(+48 + 70)	GGG CAG GCC AUU CCU CCU UCA GA
113	H24A(-02 + 22)	UCU UCA GGG UUU GUA UGU GAU UCU
114	H25A(+9 + 36)	CUG GGC UGA AUU GUC UGA AUA UCA CUG
115	H25A(+131 + 156)	CUG UUG GCA CAU GUG AUC CCA CUG AG
116	H25D(+16 - 08)	GUC UAU ACC UGU UGG CAC AUG UGA
117	H26A(+132 + 156)	UGC UUU CUG UAA UUC AUC UGG AGU U
118	H26A(-07 + 19)	CCU CCU UUC UGG CAU AGA CCU UCC AC
119	H26A(+68 + 92)	UGU GUC AUC CAU UCG UGC AUC UCU G
120	H27A(+82 + 106)	UUA AGG CCU CUU GUG CUA CAG GUG G
121	H27A(-4 + 19)	GGG GCU CUU CUU UAG CUC UCU GA
122	H27D(+19 - 03)	GAC UUC CAA AGU CUU GCA UUU C
123	H28A(-05 + 19)	GCC AAC AUG CCC AAA CUU CCU AAG
124	H28A(+99 + 124)	CAG AGA UUU CCU CAG CUC CGC CAG GA
125	H28D(+16 - 05)	CUU ACA UCU AGC ACC UCA GAG
126	H29A(+57 + 81)	UCC GCC AUC UGU UAG GGU CUG UGC C
127	H29A(+18 + 42)	AUU UGG GUU AUC CUC UGA AUG UCG C
128	H29D(+17 - 05)	CAU ACC UCU UCA UGU AGU UCC C
129	H30A(+122 + 147)	CAU UUG AGC UGC GUC CAC CUU GUC UG
130	H30A(+25 + 50)	UCC UGG GCA GAC UGG AUG CUC UGU UC
131	H30D(+19 - 04)	UUG CCU GGG CUU CCU GAG GCA UU
132	H31D(+06 - 18)	UUC UGA AAU AAC AUA UAC CUG UGC
133	H31D(+03 - 22)	UAG UUU CUG AAA UAA CAU AUA CCU G
134	H31A(+05 + 25)	GAC UUG UCA AAU CAG AUU GGA
135	H31D(+04 - 20)	GUU UCU GAA AUA ACA UAU ACC UGU
136	H32D(+04 - 16)	CAC CAG AAA UAC AUA CCA CA
137	H32A(+151 + 170)	CAA UGA UUU AGC UGU GAC UG
138	H32A(+10 + 32)	CGA AAC UUC AUG GAG ACA UCU UG
139	H32A(+49 + 73)	CUU GUA GAC GCU GCU CAA AAU UGG C
140	H33D(+09 - 11)	CAU GCA CAC ACC UUU GCU CC
141	H33A(+53 + 76)	UCU GUA CAA UCU GAC GUC CAG UCU
142	H33A(+30 + 56)	GUC UUU AUC ACC AUU UCC ACU UCA GAC
143	H33A(+64 + 88)	CCG UCU GCU UUU UCU GUA CAA UCU G
144	H34A(+83 + 104)	UCC AUA UCU GUA GCU GCC AGC C
145	H34A(+143 + 165)	CCA GGC AAC UUC AGA AUC CAA AU
146	H34A(-20 + 10)	UUU CUG UUA CCU GAA AAG AAU UAU AAU GAA
147	H34A(+46 + 70)	CAU UCA UUU CCU UUC GCA UCU UAC G
148	H34A(+95 + 120)	UGA UCU CUU UGU CAA UUC CAU AUC UG
149	H34D(+10 - 20)	UUC AGU GAU AUA GGU UUU ACC UUU CCC CAG
150	H34A(+72 + 96)	CUG UAG CUG CCA GCC AUU CUG UCA AG
151	H35A(+141 + 161)	UCU UCU GCU CGG GAG GUG ACA
152	H35A(+116 + 135)	CCA GUU ACU AUU CAG AAG AC
153	H35A(+24 + 43)	UCU UCA GGU GCA CCU UCU GU
154	H36A(+26 + 50)	UGU GAU GUG GUC CAC AUU CUG GUC A
155	H36A(-02 + 18)	CCA UGU GUU UCU GGU AUU CC
156	H37A(+26 + 50)	CGU GUA GAG UCC ACC UUU GGG CGU A
157	H37A(+82 + 105)	UAC UAA UUU CCU GCA GUG GUC ACC
158	H37A(+134 + 157)	UUC UGU GUG AAA UGG CUG CAA AUC
159	H38A(-01 + 19)	CCU UCA AAG GAA UGG AGG CC
160	H38A(+59 + 83)	UGC UGA AUU UCA GCC UCC AGU GGU U
161	H38A(+88 + 112)	UGA AGU CUU CCU CUU UCA GAU UCA C
162	H39A(+62 + 85)	CUG GCU UUC UCU CAU CUG UGA UUC
163	H39A(+39 + 58)	GUU GUA AGU UGU CUC CUC UU
164	H39A(+102 + 121)	UUG UCU GUA ACA GCU GCU GU
165	H39D(+10 - 10)	GCU CUA AUA CCU UGA GAG CA
166	H40A(-05 + 17)	CUU UGA GAC CUC AAA UCC UGU U
167	H40A(+129 + 153)	CUU UAU UUU CCU UUC AUC UCU GGG C
168	H42A(-04 + 23)	AUC GUU UCU UCA CGG ACA GUG UGC UGG
169	H42A(+86 + 109)	GGG CUU GUG AGA CAU GAG UGA UUU
170	H42D(+19 - 02)	A CCU UCA GAG GAC UCC UCU UGC
171	H43D(+10-15)	UAU GUG UUA CCU ACC CUU GUC GGU C
172	H43A(+101 + 120)	GGA GAG AGC UUC CUG UAG CU
173	H43A(+78 + 100)	UCA CCC UUU CCA CAG GCG UUG CA
174	H44A(+85 + 104)	UUU GUG UCU UUC UGA GAA AC
175	H44D(+10 - 10)	AAA GAC UUA CCU UAA GAU AC
176	H44A(-06 + 14)	AUC UGU CAA AUC GCC UGC AG
177	H46D(+16 - 04)	UUA CCU UGA CUU GCU CAA GC
178	H46A(+90 + 109)	UCC AGG UUC AAG UGG GAU AC
179	H47A(+76 + 100)	GCU CUU CUG GGC UUA UGG GAG CAC U
180	H47D(+25 - 02)	ACC UUU AUC CAC UGG AGA UUU GUC UGC
181	H47A(-9 + 12)	UUC CAC CAG UAA CUG AAA CAG
182	H50A(+02 + 30)	CCA CUC AGA GCU CAG AUC UUC UAA CUU CC

TABLE 4-continued

183	H50A(+07 + 33)	CUU CCA CUC AGA GCU CAG AUC UUC UAA
184	H51A(-01 + 25)	ACC AGA GUA ACA GUC UGA GUA GGA GC
185	H51D(+16 - 07)	CUC AUA CCU UCU GCU UGA UGA UC
186	H51A(+111 + 134)	UUC UGU CCA AGC CCG GUU GAA AUC
187	H51A(+66 + 95)	CUC CAA CAU CAA GGA AGA UGG CAU UUC UAG
188	H51D(+08 - 17)	AUC AUU UUU UCU CAU ACC UUC UGC U
189	H51A/D(+08 - 17) & (-15 +)	AUC AUU UUU UCU CAU ACC UUC UGC UAG GAG CUA AAA
190	H51A(+175 + 195)	CAC CCA CCA UCA CCC UCU GUG
191	H51A(+199 + 220)	AUC AUC UCG UUG AUA UCC UCA A
192	H52A(-07 + 14)	UCC UGC AUU GUU GCC UGU AAG
193	H52A(+12 + 41)	UCC AAC UGG GGA CGC CUC UGU UCC AAA UCC
194	H52A(+17 + 37)	ACU GGG GAC GCC UCU GUU CCA
195	H52A(+93 + 112)	CCG UAA UGA UUG UUC UAG CC
196	H52D(+05 - 15)	UGU UAA AAA ACU UAC UUC GA
197	H53A(+45 + 69)	CAU UCA ACU GUU GCC UCC GGU UCU G
198	H53A(+39 + 62)	CUG UUG CCU CCG GUU CUG AAG GUG
199	H53A(+39 + 69)	CAU UCA ACU GUU GCC UCC GGU UCU GAA GGU G
200	H53D(+14 - 07)	UAC UAA CCU UGG UUU CUG UGA
201	H53A(+23 + 47)	CUG AAG GUG UUC UUG UAC UUC AUC C
202	H53A(+150 + 176)	UGU AUA GGG ACC CUC CUU CCA UGA CUC
203	H53D(+20 - 05)	CUA ACC UUG GUU UCU GUG AUU UUC U
204	H53D(+09 - 18)	GGU AUC UUU GAU ACU AAC CUU GGU UUC
205	H53A(-12 + 10)	AUU CUU UCA ACU AGA AUA AAA G
206	H53A(-07 + 18)	GAU UCU GAA UUC UUU CAA CUA GAA U
207	H53A(+07 + 26)	AUC CCA CUG AUU CUG AAU UC
208	H53A(+124 + 145)	UUG GCU CUG GCC UGU CCU AAG A
209	H46A(+86 + 115)	CUC UUU UCC AGG UUC AAG UGG GAU ACU AGC
210	H46A(+107 + 137)	CAA GCU UUU CUU UUA GUU GCU GCU CUU UUC C
211	H46A(-10 + 20)	UAU UCU UUU GUU CUU CUA GCC UGG AGA AAG
212	H46A(+50 + 77)	CUG CUU CCU CCA ACC AUA AAA CAA AUU C
213	H45A(-06 + 20)	CCA AUG CCA UCC UGG AGU UCC UGU AA
214	H45A(+91 + 110)	UCC UGU AGA AUA CUG GCA UC
215	H45A(+125 + 151)	UGC AGA CCU CCU GCC ACC GCA GAU UCA
216	H45D(+16 - 04)	CUA CCU CUU UUU UCU GUC UG
217	H45A(+71 + 90)	UGU UUU UGA GGA UUG CUG AA

Description	Sequence	SEQ ID NO
H53A(+33 + 60)	GTTGCCTCCGGTTCTGAAGGTGTTCTTG	218
H53A(+23 + 47)	CTGAAGGTGTTCTTGTACTTCATCC	219
H53A(+33 + 62)	CTGTTGCCTCCGGTTCTGAAGGTGTTCTTG	220
H53A(+33 + 65)	CAACTGTTGCCTCCGGTTCTGAAGGTGTTCTTG	221
H53A(+31 + 55)	CTCCGGTTCTGAAGGTGTTCTTGTA	222
H53A(+46 + 73)	ATTTCATTCAACTGTTGCCTCCGGTTCT	223
H53A(+22 + 46)	TGAAGGTGTTCTTGTACTTCATCCC	224
H53A(+46 + 69)	CATTCAACTGTTGCCTCCGGTTCT	225
H53A(+40 + 61)	TGTTGCCTCCGGTTCTGAAGGT	226
H53A(+30 + 60)	GTTGCCTCCGGTTCTGAAGGTGTTC	227
H53A(+30 + 57)	GCCTCCGGTTCTGAAGGTGTTCTTGTAC	228
H53A(+30 + 56)	CCTCCGGTTCTGAAGGTGTTCTTGTAC	229
H53A(+30 + 55)	CTCCGGTTCTGAAGGTGTTCTTGTAC	230
H53A(+33 + 57)	GCCTCCGGTTCTGAAGGTGTTCTTG	231
H44A(-07 + 17)	CAGATCTGTCAAATCGCCTGCAGG	232
H44A(-07 + 20)	CAACAGATCTGTCAAATCGCCTGCAGG	233
H44A(-07 + 22)	CTCAACAGATCTGTCAAATCGCCTGCAGG	234
H44A(+77 + 101)	GTGTCTTTCTGAGAAACTGTTCAGC	235
H44A(+64 + 91)	GAGAAACTGTTCAGCTTCTGTTAGCCAC	236
H44A(+62 + 89)	GAAACTGTTCAGCTTCTGTTAGCCACTG	237
H44A(+62 + 85)	CTGTTCAGCTTCTGTTAGCCACTG	238
H44A(-06 + 14)	ATCTGTCAAATCGCCTGCAG	239
H44A(+85 + 104)	TTTGTGTCTTTCTGAGAAAC	240
H44A(+61 + 84)	TGTTCAGCTTCTGTTAGCCACTGA	241
H44A(-10 + 15)	GATCTGTCAAATCGCCTGCAGGTAA	242
H44A(+64 + 88)	AAACTGTTCAGCTTCTGTTAGCCAC	243
H44A(+79 + 103)	TTGTGTCTTTCTGAGAAACTGTTCA	244
H44A(-06 + 20)	CAACAGATCTGTCAAATCGCCTGCAG	245

TABLE 4-continued

H44A(-09 + 17)	CAGATCTGTCAAATCGCCTGCAGGTA	246
H44A(+59 + 85)	CTGTTCAGCTTCTGTTAGCCACTGATT	247
H44A(+59 + 89)	GAAACTGTTCAGCTTCTGTTAGCCACTGATT	248
H44A(+65 + 90)	AGAAACTGTTCAGCTTCTGTTAGCCA	249

Name	Sequences	SEQ ID NO.
	Oligomer Targeting Sequences (5' to 3'):	
Hu.DMD.Exon44.25.001	CTGCAGGTAAAAGCATATGGATCAA	250
Hu.DMD.Exon44.25.002	ATCGCCTGCAGGTAAAAGCATATGG	251
Hu.DMD.Exon44.25.003	GTCAAATCGCCTGCAGGTAAAAGCA	252
Hu.DMD.Exon44.25.005	CAACAGATCTGTCAAATCGCCTGCA	253
Hu.DMD.Exon44.25.006	TTTCTCAACAGATCTGTCAAATCGC	254
Hu.DMD.Exon44.25.007	CCATTTCTCAACAGATCTGTCAAAT	255
Hu.DMD.Exon44.25.008	ATAATGAAAACGCCGCCATTTCTCA	256
Hu.DMD.Exon44.25.009	AAATATCTTTATATCATAATGAAAA	257
Hu.DMD.Exon44.25.010	TGTTAGCCACTGATTAAATATCTTT	258
Hu.DMD.Exon44.25.013	CCAATTCTCAGGAATTTGTGTCTTT	259
Hu.DMD.Exon44.25.014	GTATTTAGCATGTTCCCAATTCTCA	260
Hu.DMD.Exon44.25.015	CTTAAGATACCATTTGTATTTAGCA	261
Hu.DMD.Exon44.25.016	CTTACCTTAAGATACCATTTGTATT	262
Hu.DMD.Exon44.25.017	AAAGACTTACCTTAAGATACCATTT	263
Hu.DMD.Exon44.25.018	AAATCAAAGACTTACCTTAAGATAC	264
Hu.DMD.Exon44.25.019	AAAACAAATCAAAGACTTACCTTAA	265
Hu.DMD.Exon44.25.020	TCGAAAAAACAAATCAAAGACTTAC	266
Hu.DMD.Exon45.25.001	CTGTAAGATACCAAAAAGGCAAAAC	267
Hu.DMD.Exon45.25.002	CCTGTAAGATACCAAAAAGGCAAAA	268
Hu.DMD.Exon45.25.002.2	AGTTCCTGTAAGATACCAAAAAGGC	269
Hu.DMD.Exon45.25.003	GAGTTCCTGTAAGATACCAAAAAGG	270
Hu.DMD.Exon45.25.003.2	CCTGGAGTTCCTGTAAGATACCAAA	271
Hu.DMD.Exon45.25.004	TCCTGGAGTTCCTGTAAGATACCAA	272
Hu.DMD.Exon45.25.004.2	GCCATCCTGGAGTTCCTGTAAGATA	273
Hu.DMD.Exon45.25.005	TGCCATCCTGGAGTTCCTGTAAGAT	274
Hu.DMD.Exon45.25.005.2	CCAATGCCATCCTGGAGTTCCTGTA	275
Hu.DMD.Exon45.25.006	CCCAATGCCATCCTGGAGTTCCTGT	276
Hu.DMD.Exon45.25.006.2	GCTGCCCAATGCCATCCTGGAGTTC	277
Hu.DMD.Exon45.25.007	CGCTGCCCAATGCCATCCTGGAGTT	278
Hu.DMD.Exon45.25.008	AACAGTTTGCCGCTGCCCAATGCCA	279
Hu.DMD.Exon45.25.008.2	CTGACAACAGTTTGCCGCTGCCCAA	280
Hu.DMD.Exon45.25.009	GTTGCATTCAATGTTCTGACAACAG	281
Hu.DMD.Exon45.25.010	GCTGAATTATTTCTTCCCCAGTTGC	282
Hu.DMD.Exon45.25.010.2	ATTATTTCTTCCCCAGTTGCATTCA	283
Hu.DMD.Exon45.25.011	GGCATCTGTTTTTGAGGATTGCTGA	284
Hu.DMD.Exon45.25.011.2	TTTGAGGATTGCTGAATTATTTCTT	285
Hu.DMD.Exon45.25.012	AATTTTTCCTGTAGAATACTGGCAT	286
Hu.DMD.Exon45.25.012.2	ATACTGGCATCTGTTTTTGAGGATT	287
Hu.DMD.Exon45.25.013	ACCGCAGATTCAGGCTTCCCAATTT	288
Hu.DMD.Exon45.25.014	CTGTTTGCAGACCTCCTGCCACCGC	289
Hu.DMD.Exon45.25.014.2	AGATTCAGGCTTCCCAATTTTTCCT	290
Hu.DMD.Exon45.25.015	CTCTTTTTTCTGTCTGACAGCTGTT	291
Hu.DMD.Exon45.25.015.2	ACCTCCTGCCACCGCAGATTCAGGC	292
Hu.DMD.Exon45.25.016	CCTACCTCTTTTTTCTGTCTGACAG	293
Hu.DMD.Exon45.25.016.2	GACAGCTGTTTGCAGACCTCCTGCC	294
Hu.DMD.Exon45.25.017	GTCGCCCTACCTCTTTTTTCTGTCT	295
Hu.DMD.Exon45.25.018	GATCTGTCGCCCTACCTCTTTTTTC	296
Hu.DMD.Exon45.25.019	TATTAGATCTGTCGCCCTACCTCTT	297
Hu.DMD.Exon45.25.020	ATTCCTATTAGATCTGTCGCCCTAC	298
Hu.DMD.Exon45.20.001	AGATACCAAAAAGGCAAAAC	299
Hu.DMD.Exon45.20.002	AAGATACCAAAAAGGCAAAA	300
Hu.DMD.Exon45.20.003	CCTGTAAGATACCAAAAAGG	301
Hu.DMD.Exon45.20.004	GAGTTCCTGTAAGATACCAA	302
Hu.DMD.Exon45.20.005	TCCTGGAGTTCCTGTAAGAT	303
Hu.DMD.Exon45.20.006	TGCCATCCTGGAGTTCCTGT	304
Hu.DMD.Exon45.20.007	CCCAATGCCATCCTGGAGTT	305
Hu.DMD.Exon45.20.008	CGCTGCCCAATGCCATCCTG	306
Hu.DMD.Exon45.20.009	CTGACAACAGTTTGCCGCTG	307
Hu.DMD.Exon45.20.010	GTTGCATTCAATGTTCTGAC	308
Hu.DMD.Exon45.20.011	ATTATTTCTTCCCCAGTTGC	309
Hu.DMD.Exon45.20.012	TTTGAGGATTGCTGAATTAT	310
Hu.DMD.Exon45.20.013	ATACTGGCATCTGTTTTTGA	311
Hu.DMD.Exon45.20.014	AATTTTTCCTGTAGAATACT	312
Hu.DMD.Exon45.20.015	AGATTCAGGCTTCCCAATTT	313
Hu.DMD.Exon45.20.016	ACCTCCTGCCACCGCAGATT	314
Hu.DMD.Exon45.20.017	GACAGCTGTTTGCAGACCTC	315
Hu.DMD.Exon45.20.018	CTCTTTTTTCTGTCTGACAG	316
Hu.DMD.Exon45.20.019	CCTACCTCTTTTTTCTGTCT	317

TABLE 4-continued

Hu.DMD.Exon45.20.020	GTCGCCCTACCTCTTTTTTC	318
Hu.DMD.Exon45.20.021	GATCTGTCGCCCTACCTCTT	319
Hu.DMD.Exon45.20.022	TATTAGATCTGTCGCCCTAC	320
Hu.DMD.Exon45.20.023	ATTCCTATTAGATCTGTCGC	321
Hu.DMD.Exon46.25.001	GGGGGATTTGAGAAAATAAAATTAC	322
Hu.DMD.Exon46.25.002	ATTTGAGAAAATAAAATTACCTTGA	323
Hu.DMD.Exon46.25.002.2	CTAGCCTGGAGAAAGAAGAATAAAA	324
Hu.DMD.Exon46.25.003	AGAAAATAAAATTACCTTGACTTGC	325
Hu.DMD.Exon46.25.003.2	TTCTTCTAGCCTGGAGAAAGAAGAA	326
Hu.DMD.Exon46.25.004	ATAAAATTACCTTGACTTGCTCAAG	327
Hu.DMD.Exon46.25.004.2	TTTTGTTCTTCTAGCCTGGAGAAAG	328
Hu.DMD.Exon46.25.005	ATTACCTTGACTTGCTCAAGCTTTT	329
Hu.DMD.Exon46.25.005.2	TATTCTTTTGTTCTTCTAGCCTGGA	330
Hu.DMD.Exon46.25.006	CTTGACTTGCTCAAGCTTTTCTTTT	331
Hu.DMD.Exon46.25.006.2	CAAGATATTCTTTTGTTCTTCTAGC	332
Hu.DMD.Exon46.25.007	CTTTTAGTTGCTGCTCTTTTCCAGG	333
Hu.DMD.Exon46.25.008	CCAGGTTCAAGTGGGATACTAGCAA	334
Hu.DMD.Exon46.25.008.2	ATCTCTTTGAAATTCTGACAAGATA	335
Hu.DMD.Exon46.25.009	AGCAATGTTATCTGCTTCCTCCAAC	336
Hu.DMD.Exon46.25.009.2	AACAAATTCATTTAAATCTCTTTGA	337
Hu.DMD.Exon46.25.010	CCAACCATAAAACAAATTCATTTAA	338
Hu.DMD.Exon46.25.010.2	TTCCTCCAACCATAAAACAAATTCA	339
Hu.DMD.Exon46.25.011	TTTAAATCTCTTTGAAATTCTGACA	340
Hu.DMD.Exon46.25.012	TGACAAGATATTCTTTTGTTCTTCT	341
Hu.DMD.Exon46.25.012.2	TTCAAGTGGGATACTAGCAATGTTA	342
Hu.DMD.Exon46.25.013	AGATATTCTTTTGTTCTTCTAGCCT	343
Hu.DMD.Exon46.25.013.2	CTGCTCTTTTCCAGGTTCAAGTGGG	344
Hu.DMD.Exon46.25.014	TTCTTTTGTTCTTCTAGCCTGGAGA	345
Hu.DMD.Exon46.25.014.2	CTTTTCTTTTAGTTGCTGCTCTTTT	346
Hu.DMD.Exon46.25.015	TTGTTCTTCTAGCCTGGAGAAAGAA	347
Hu.DMD.Exon46.25.016	CTTCTAGCCTGGAGAAAGAAGAATA	348
Hu.DMD.Exon46.25.017	AGCCTGGAGAAAGAAGAATAAAATT	349
Hu.DMD.Exon46.25.018	CTGGAGAAAGAAGAATAAAATTGTT	350
Hu.DMD.Exon46.20.001	GAAAGAAGAATAAAATTGTT	351
Hu.DMD.Exon46.20.002	GGAGAAAGAAGAATAAAATT	352
Hu.DMD.Exon46.20.003	AGCCTGGAGAAAGAAGAATA	353
Hu.DMD.Exon46.20.004	CTTCTAGCCTGGAGAAAGAA	354
Hu.DMD.Exon46.20.005	TTGTTCTTCTAGCCTGGAGA	355
Hu.DMD.Exon46.20.006	TTCTTTTGTTCTTCTAGCCT	356
Hu.DMD.Exon46.20.007	TGACAAGATATTCTTTTGTT	357
Hu.DMD.Exon46.20.008	ATCTCTTTGAAATTCTGACA	358
Hu.DMD.Exon46.20.009	AACAAATTCATTTAAATCTC	359
Hu.DMD.Exon46.20.010	TTCCTCCAACCATAAAACAA	360
Hu.DMD.Exon46.20.011	AGCAATGTTATCTGCTTCCT	361
Hu.DMD.Exon46.20.012	TTCAAGTGGGATACTAGCAA	362
Hu.DMD.Exon46.20.013	CTGCTCTTTTCCAGGTTCAA	363
Hu.DMD.Exon46.20.014	CTTTTCTTTTAGTTGCTGCT	364
Hu.DMD.Exon46.20.015	CTTGACTTGCTCAAGCTTTT	365
Hu.DMD.Exon46.20.016	ATTACCTTGACTTGCTCAAG	366
Hu.DMD.Exon46.20.017	ATAAAATTACCTTGACTTGC	367
Hu.DMD.Exon46.20.018	AGAAAATAAAATTACCTTGA	368
Hu.DMD.Exon46.20.019	ATTTGAGAAAATAAAATTAC	369
Hu.DMD.Exon46.20.020	GGGGGATTTGAGAAAATAAA	370
Hu.DMD.Exon47.25.001	CTGAAACAGACAAATGCAACAACGT	371
Hu.DMD.Exon47.25.002	AGTAACTGAAACAGACAAATGCAAC	372
Hu.DMD.Exon47.25.003	CCACCAGTAACTGAAACAGACAAAT	373
Hu.DMD.Exon47.25.004	CTCTTCCACCAGTAACTGAAACAGA	374
Hu.DMD.Exon47.25.005	GGCAACTCTTCCACCAGTAACTGAA	375
Hu.DMD.Exon47.25.006	GCAGGGGCAACTCTTCCACCAGTAA	376
Hu.DMD.Exon47.25.007	CTGGCGCAGGGGCAACTCTTCCACC	377
Hu.DMD.Exon47.25.008	TTTAATTGTTTGAGAATTCCCTGGC	378
Hu.DMD.Exon47.25.008.2	TTGTTTGAGAATTCCCTGGCGCAGG	379
Hu.DMD.Exon47.25.009	GCACGGGTCCTCCAGTTTCATTTAA	380
Hu.DMD.Exon47.25.009.2	TCCAGTTTCATTTAATTGTTTGAGA	381
Hu.DMD.Exon47.25.010	GCTTATGGGAGCACTTACAAGCACG	382
Hu.DMD.Exon47.25.010.2	TACAAGCACGGGTCCTCCAGTTTCA	383
Hu.DMD.Exon47.25.011	AGTTTATCTTGCTCTTCTGGGCTTA	384
Hu.DMD.Exon47.25.012	TCTGCTTGAGCTTATTTTCAAGTTT	385
Hu.DMD.Exon47.25.012.2	ATCTTGCTCTTCTGGGCTTATGGGA	386
Hu.DMD.Exon47.25.013	CTTTATCCACTGGAGATTTGTCTGC	387
Hu.DMD.Exon47.25.013.2	CTTATTTTCAAGTTTATCTTGCTCT	388
Hu.DMD.Exon47.25.014	CTAACCTTTATCCACTGGAGATTTG	389
Hu.DMD.Exon47.25.014.2	ATTTGTCTGCTTGAGCTTATTTTCA	390
Hu.DMD.Exon47.25.015	AATGTCTAACCTTTATCCACTGGAG	391
Hu.DMD.Exon47.25.016	TGGTTAATGTCTAACCTTTATCCAC	392
Hu.DMD.Exon47.25.017	AGAGATGGTTAATGTCTAACCTTTA	393
Hu.DMD.Exon47.25.018	ACGGAAGAGATGGTTAATGTCTAAC	394

TABLE 4-continued

Hu.DMD.Exon47.20.001	ACAGACAAATGCAACAACGT	395
Hu.DMD.Exon47.20.002	CTGAAACAGACAAATGCAAC	396
Hu.DMD.Exon47.20.003	AGTAACTGAAACAGACAAAT	397
Hu.DMD.Exon47.20.004	CCACCAGTAACTGAAACAGA	398
Hu.DMD.Exon47.20.005	CTCTTCCACCAGTAACTGAA	399
Hu.DMD.Exon47.20.006	GGCAACTCTTCCACCAGTAA	400
Hu.DMD.Exon47.20.007	CTGGCGCAGGGGCAACTCTT	401
Hu.DMD.Exon47.20.008	TTGTTTGAGAATTCCCTGGC	402
Hu.DMD.Exon47.20.009	TCCAGTTTCATTTAATTGTT	403
Hu.DMD.Exon47.20.010	TACAAGCACGGGTCCTCCAG	404
Hu.DMD.Exon47.20.011	GCTTATGGGAGCACTTACAA	405
Hu.DMD.Exon47.20.012	ATCTTGCTCTTCTGGGCTTA	406
Hu.DMD.Exon47.20.013	CTTATTTTCAAGTTTATCTT	407
Hu.DMD.Exon47.20.014	ATTTGTCTGCTTGAGCTTAT	408
Hu.DMD.Exon47.20.015	CTTTATCCACTGGAGATTTG	409
Hu.DMD.Exon47.20.016	CTAACCTTTATCCACTGGAG	410
Hu.DMD.Exon47.20.017	AATGTCTAACCTTTATCCAC	411
Hu.DMD.Exon47.20.018	TGGTTAATGTCTAACCTTTA	412
Hu.DMD.Exon47.20.019	AGAGATGGTTAATGTCTAAC	413
Hu.DMD.Exon47.20.020	ACGGAAGAGATGGTTAATGT	414
Hu.DMD.Exon48.25.001	CTGAAAGGAAAATACATTTTAAAAA	415
Hu.DMD.Exon48.25.002	CCTGAAAGGAAAATACATTTTAAAA	416
Hu.DMD.Exon48.25.002.2	GAAACCTGAAAGGAAAATACATTTT	417
Hu.DMD.Exon48.25.003	GGAAACCTGAAAGGAAAATACATTT	418
Hu.DMD.Exon48.25.003.2	CTCTGGAAACCTGAAAGGAAAATAC	419
Hu.DMD.Exon48.25.004	GCTCTGGAAACCTGAAAGGAAAATA	420
Hu.DMD.Exon48.25.004.2	TAAAGCTCTGGAAACCTGAAAGGAA	421
Hu.DMD.Exon48.25.005	GTAAAGCTCTGGAAACCTGAAAGGA	422
Hu.DMD.Exon48.25.005.2	TCAGGTAAAGCTCTGGAAACCTGAA	423
Hu.DMD.Exon48.25.006	CTCAGGTAAAGCTCTGGAAACCTGA	424
Hu.DMD.Exon48.25.006.2	GTTTCTCAGGTAAAGCTCTGGAAAC	425
Hu.DMD.Exon48.25.007	TGTTTCTCAGGTAAAGCTCTGGAAA	426
Hu.DMD.Exon48.25.007.2	AATTTCTCCTTGTTTCTCAGGTAAA	427
Hu.DMD.Exon48.25.008	TTTGAGCTTCAATTTCTCCTTGTTT	428
Hu.DMD.Exon48.25.008	TTTTATTTGAGCTTCAATTTCTCCT	429
Hu.DMD.Exon48.25.009	AAGCTGCCCAAGGTCTTTTATTTGA	430
Hu.DMD.Exon48.25.010	AGGTCTTCAAGCTTTTTTTCAAGCT	431
Hu.DMD.Exon48.25.010.2	TTCAAGCTTTTTTTCAAGCTGCCCA	432
Hu.DMD.Exon48.25.011	GATGATTTAACTGCTCTTCAAGGTC	433
Hu.DMD.Exon48.25.011.2	CTGCTCTTCAAGGTCTTCAAGCTTT	434
Hu.DMD.Exon48.25.012	AGGAGATAACCACAGCAGCAGATGA	435
Hu.DMD.Exon48.25.012.2	CAGCAGATGATTTAACTGCTCTTCA	436
Hu.DMD.Exon48.25.013	ATTTCCAACTGATTCCTAATAGGAG	437
Hu.DMD.Exon48.25.014	CTTGGTTTGGTTGGTTATAAATTTC	438
Hu.DMD.Exon48.25.014.2	CAACTGATTCCTAATAGGAGATAAC	439
Hu.DMD.Exon48.25.015	CTTAACGTCAAATGGTCCTTCTTGG	440
Hu.DMD.Exon48.25.015.2	TTGGTTATAAATTTCCAACTGATTC	441
Hu.DMD.Exon48.25.016	CCTACCTTAACGTCAAATGGTCCTT	442
Hu.DMD.Exon48.25.016.2	TCCTTCTTGGTTTGGTTGGTTATAA	443
Hu.DMD.Exon48.25.017	AGTTCCCTACCTTAACGTCAAATGG	444
Hu.DMD.Exon48.25.018	CAAAAAGTTCCCTACCTTAACGTCA	445
Hu.DMD.Exon48.25.019	TAAAGCAAAAAGTTCCCTACCTTAA	446
Hu.DMD.Exon48.25.020	ATATTTAAAGCAAAAAGTTCCCTAC	447
Hu.DMD.Exon48.20.001	AGGAAAATACATTTTAAAAA	448
Hu.DMD.Exon48.20.002	AAGGAAAATACATTTTAAAA	449
Hu.DMD.Exon48.20.003	CCTGAAAGGAAAATACATTT	450
Hu.DMD.Exon48.20.004	GGAAACCTGAAAGGAAAATA	451
Hu.DMD.Exon48.20.005	GCTCTGGAAACCTGAAAGGA	452
Hu.DMD.Exon48.20.006	GTAAAGCTCTGGAAACCTGA	453
Hu.DMD.Exon48.20.007	CTCAGGTAAAGCTCTGGAAA	454
Hu.DMD.Exon48.20.008	AATTTCTCCTTGTTTCTCAG	455
Hu.DMD.Exon48.20.009	TTTTATTTGAGCTTCAATTT	456
Hu.DMD.Exon48.20.010	AAGCTGCCCAAGGTCTTTTA	457
Hu.DMD.Exon48.20.011	TTCAAGCTTTTTTTCAAGCT	458
Hu.DMD.Exon48.20.012	CTGCTCTTCAAGGTCTTCAA	459
Hu.DMD.Exon48.20.013	CAGCAGATGATTTAACTGCT	460
Hu.DMD.Exon48.20.014	AGGAGATAACCACAGCAGCA	461
Hu.DMD.Exon48.20.015	CAACTGATTCCTAATAGGAG	462
Hu.DMD.Exon48.20.016	TTGGTTATAAATTTCCAACT	463
Hu.DMD.Exon48.20.017	TCCTTCTTGGTTTGGTTGGT	464
Hu.DMD.Exon48.20.018	CTTAACGTCAAATGGTCCTT	465
Hu.DMD.Exon48.20.019	CCTACCTTAACGTCAAATGG	466
Hu.DMD.Exon48.20.020	AGTTCCCTACCTTAACGTCA	467
Hu.DMD.Exon48.20.021	CAAAAAGTTCCCTACCTTAA	468
Hu.DMD.Exon48.20.022	TAAAGCAAAAAGTTCCCTAC	469
Hu.DMD.Exon48.20.023	ATATTTAAAGCAAAAAGTTC	470
Hu.DMD.Exon49.25.001	CTGGGGAAAAGAACCCATATAGTGC	471

TABLE 4-continued

Hu.DMD.Exon49.25.002	TCCTGGGGAAAAGAACCCATATAGT	472
Hu.DMD.Exon49.25.002.2	GTTTCCTGGGGAAAAGAACCCATAT	473
Hu.DMD.Exon49.25.003	CAGTTTCCTGGGGAAAAGAACCCAT	474
Hu.DMD.Exon49.25.003.2	TTTCAGTTTCCTGGGGAAAAGAACC	475
Hu.DMD.Exon49.25.004	TATTTCAGTTTCCTGGGGAAAAGAA	476
Hu.DMD.Exon49.25.004.2	TGCTATTTCAGTTTCCTGGGGAAAA	477
Hu.DMD.Exon49.25.005	ACTGCTATTTCAGTTTCCTGGGGAA	478
Hu.DMD.Exon49.25.005.2	TGAACTGCTATTTCAGTTTCCTGGG	479
Hu.DMD.Exon49.25.006	CTTGAACTGCTATTTCAGTTTCCTG	480
Hu.DMD.Exon49.25.006.2	TAGCTTGAACTGCTATTTCAGTTTC	481
Hu.DMD.Exon49.25.007	TTTAGCTTGAACTGCTATTTCAGTT	482
Hu.DMD.Exon49.25.008	TTCCACATCCGGTTGTTTAGCTTGA	483
Hu.DMD.Exon49.25.009	TGCCCTTTAGACAAAATCTCTTCCA	484
Hu.DMD.Exon49.25.009.2	TTTAGACAAAATCTCTTCCACATCC	485
Hu.DMD.Exon49.25.010	GTTTTTCCTTGTACAAATGCTGCCC	486
Hu.DMD.Exon49.25.010.2	GTACAAATGCTGCCCTTTAGACAAA	487
Hu.DMD.Exon49.25.011	CTTCACTGGCTGAGTGGCTGGTTTT	488
Hu.DMD.Exon49.25.011.2	GGCTGGTTTTTCCTTGTACAAATGC	489
Hu.DMD.Exon49.25.012	ATTACCTTCACTGGCTGAGTGGCTG	490
Hu.DMD.Exon49.25.013	GCTTCATTACCTTCACTGGCTGAGT	491
Hu.DMD.Exon49.25.014	AGGTTGCTTCATTACCTTCACTGGC	492
Hu.DMD.Exon49.25.015	GCTAGAGGTTGCTTCATTACCTTCA	493
Hu.DMD.Exon49.25.016	ATATTGCTAGAGGTTGCTTCATTAC	494
Hu.DMD.Exon49.20.001	GAAAAGAACCCATATAGTGC	495
Hu.DMD.Exon49.20.002	GGGAAAAGAACCCATATAGT	496
Hu.DMD.Exon49.20.003	TCCTGGGGAAAAGAACCCAT	497
Hu.DMD.Exon49.20.004	CAGTTTCCTGGGGAAAAGAA	498
Hu.DMD.Exon49.20.005	TATTTCAGTTTCCTGGGGAA	499
Hu.DMD.Exon49.20.006	ACTGCTATTTCAGTTTCCTG	500
Hu.DMD.Exon49.20.007	CTTGAACTGCTATTTCAGTT	501
Hu.DMD.Exon49.20.008	TTTAGCTTGAACTGCTATTT	502
Hu.DMD.Exon49.20.009	TTCCACATCCGGTTGTTTAG	503
Hu.DMD.Exon49.20.010	TTTAGACAAAATCTCTTCCA	504
Hu.DMD.Exon49.20.011	GTACAAATGCTGCCCTTTAG	505
Hu.DMD.Exon49.20.012	GGCTGGTTTTTCCTTGTACA	506
Hu.DMD.Exon49.20.013	CTTCACTGGCTGAGTGGCTG	507
Hu.DMD.Exon49.20.014	ATTACCTTCACTGGCTGAGT	508
Hu.DMD.Exon49.20.015	GCTTCATTACCTTCACTGGC	509
Hu.DMD.Exon49.20.016	AGGTTGCTTCATTACCTTCA	510
Hu.DMD.Exon49.20.017	GCTAGAGGTTGCTTCATTAC	511
Hu.DMD.Exon49.20.018	ATATTGCTAGAGGTTGCTTC	512
Hu.DMD.Exon50.25.001	CTTTAACAGAAAAGCATACACATTA	513
Hu.DMD.Exon50.25.002	TCCTCTTTAACAGAAAAGCATACAC	514
Hu.DMD.Exon50.25.002.2	TTCCTCTTTAACAGAAAAGCATACA	515
Hu.DMD.Exon50.25.003	TAACTTCCTCTTTAACAGAAAAGCA	516
Hu.DMD.Exon50.25.003.2	CTAACTTCCTCTTTAACAGAAAAGC	517
Hu.DMD.Exon50.25.004	TCTTCTAACTTCCTCTTTAACAGAA	518
Hu.DMD.Exon50.25.004.2	ATCTTCTAACTTCCTCTTTAACAGA	519
Hu.DMD.Exon50.25.005	TCAGATCTTCTAACTTCCTCTTTAA	520
Hu.DMD.Exon50.25.005.2	CTCAGATCTTCTAACTTCCTCTTTA	521
Hu.DMD.Exon50.25.006	AGAGCTCAGATCTTCTAACTTCCTC	522
Hu.DMD.Exon50.25.006.2	CAGAGCTCAGATCTTCTAACTTCCT	523
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Hu.DMD.Exon50.25.007	CACTCAGAGCTCAGATCTTCTACT	524
Hu.DMD.Exon50.25.007.2	CCTTCCACTCAGAGCTCAGATCTTC	525
Hu.DMD.Exon50.25.008	GTAAACGGTTTACCGCCTTCCACTC	526
Hu.DMD.Exon50.25.009	CTTTGCCCTCAGCTCTTGAAGTAAA	527
Hu.DMD.Exon50.25.009.2	CCCTCAGCTCTTGAAGTAAACGGTT	528
Hu.DMD.Exon50.25.010	CCAGGAGCTAGGTCAGGCTGCTTTG	529
Hu.DMD.Exon50.25.010.2	GGTCAGGCTGCTTTGCCCTCAGCTC	530
Hu.DMD.Exon50.25.011	AGGCTCCAATAGTGGTCAGTCCAGG	531
Hu.DMD.Exon50.25.011.2	TCAGTCCAGGAGCTAGGTCAGGCTG	532
Hu.DMD.Exon50.25.012	CTTACAGGCTCCAATAGTGGTCAGT	533
AVI-5038		
Hu.DMD.Exon50.25.013	GTATACTTACAGGCTCCAATAGTGG	534
Hu.DMD.Exon50.25.014	ATCCAGTATACTTACAGGCTCCAAT	535
Hu.DMD.Exon50.25.015	ATGGGATCCAGTATACTTACAGGCT	536
NG-08-0741		
Hu.DMD.Exon50.25.016	AGAGAATGGGATCCAGTATACTTAC	537
NG-08-0742		
Hu.DMD.Exon50.20.001	ACAGAAAAGCATACACATTA	538
Hu.DMD.Exon50.20.002	TTTAACAGAAAAGCATACAC	539
Hu.DMD.Exon50.20.003	TCCTCTTTAACAGAAAAGCA	540
Hu.DMD.Exon50.20.004	TAACTTCCTCTTTAACAGAA	541
Hu.DMD.Exon50.20.005	TCTTCTAACTTCCTCTTTAA	542
Hu.DMD.Exon50.20.006	TCAGATCTTCTAACTTCCTC	543
Hu.DMD.Exon50.20.007	CCTTCCACTCAGAGCTCAGA	544

TABLE 4-continued

Hu.DMD.Exon50.20.008	GTAAACGGTTTACCGCCTTC	545
Hu.DMD.Exon50.20.009	CCCTCAGCTCTTGAAGTAAA	546
Hu.DMD.Exon50.20.010	GGTCAGGCTGCTTTGCCCTC	547
Hu.DMD.Exon50.20.011	TCAGTCCAGGAGCTAGGTCA	548
Hu.DMD.Exon50.20.012	AGGCTCCAATAGTGGTCAGT	549
Hu.DMD.Exon50.20.013	CTTACAGGCTCCAATAGTGG	550
Hu.DMD.Exon50.20.014	GTATACTTACAGGCTCCAAT	551
Hu.DMD.Exon50.20.015	ATCCAGTATACTTACAGGCT	552
Hu.DMD.Exon50.20.016	ATGGGATCCAGTATACTTAC	553
Hu.DMD.Exon50.20.017	AGAGAATGGGATCCAGTATA	554
Hu.DMD.Exon51.25.001-44	CTAAAATATTTTGGGTTTTTGCAAAA	555
Hu.DMD.Exon51.25.002-45	GCTAAAATATTTTGGGTTTTTGCAAA	556
Hu.DMD.Exon51.25.002.2-46	TAGGAGCTAAAATATTTTGGGTTTTT	557
Hu.DMD.Exon51.25.003	AGTAGGAGCTAAAATATTTTGGGTT	558
Hu.DMD.Exon51.25.003.2	TGAGTAGGAGCTAAAATATTTTGGG	559
Hu.DMD.Exon51.25.004	CTGAGTAGGAGCTAAAATATTTTGGG	560
Hu.DMD.Exon51.25.004.2	CAGTCTGAGTAGGAGCTAAAATATT	561
Hu.DMD.Exon51.25.005	ACAGTCTGAGTAGGAGCTAAAATATT	562
Hu.DMD.Exon51.25.005.2	GAGTAACAGTCTGAGTAGGAGCTAAA	563
Hu.DMD.Exon51.25.006	CAGAGTAACAGTCTGAGTAGGAGCT	564
Hu.DMD.Exon51.25.006.2	CACCAGAGTAACAGTCTGAGTAGGAG	565
Hu.DMD.Exon51.25.007	GTCACCAGAGTAACAGTCTGAGTAG	566
Hu.DMD.Exon51.25.007.2	AACCACAGGTTGTGTCACCAGAGTAA	567
Hu.DMD.Exon51.25.008	GTTGTGTCACCAGAGTAACAGTCTG	568
Hu.DMD.Exon51.25.009	TGGCAGTTTCCTTAGTAACCACAGGT	569
Hu.DMD.Exon51.25.010	ATTTCTAGTTTGGAGATGGCAGTTTC	570
Hu.DMD.Exon51.25.010.2	GGAAGATGGCATTTCTAGTTTGGAG	571
Hu.DMD.Exon51.25.011	CATCAAGGAAGATGGCATTTCTAGTT	572
Hu.DMD.Exon51.25.011.2	GAGCAGGTACCTCCAACATCAAGGAA	573
Hu.DMD.Exon51.25.012	ATCTGCCAGAGCAGGTACCTCCAAC	574
Hu.DMD.Exon51.25.013	AAGTTCTGTCCAAGCCCGGTTGAAAT	575
Hu.DMD.Exon51.25.013.2	CGGTTGAAATCTGCCAGAGCAGGTAC	576
Hu.DMD.Exon51.25.014	GAGAAAGCCAGTCGGTAAGTTCTGTC	577
Hu.DMD.Exon51.25.014.2	GTCGGTAAGTTCTGTCCAAGCCCGG	578
Hu.DMD.Exon51.25.015	ATAACTTGATCAAGCAGAGAAAGCCA	579
Hu.DMD.Exon51.25.015.2	AAGCAGAGAAAGCCAGTCGGTAAGT	580
Hu.DMD.Exon51.25.016	CACCCTCTGTGATTTTATAACTTGAT	581
Hu.DMD.Exon51.25.017	CAAGGTCACCCACCATCACCCTCTGT	582
Hu.DMD.Exon51.25.017.2	CATCACCCTCTGTGATTTTATAACT	583
Hu.DMD.Exon51.25.018	CTTCTGCTTGATGATCATCTCGTTGA	584
Hu.DMD.Exon51.25.019	CCTTCTGCTTGATGATCATCTCGTTG	585
Hu.DMD.Exon51.25.019.2	ATCTCGTTGATATCCTCAAGGTCACC	586
Hu.DMD.Exon51.25.020	TCATACCTTCTGCTTGATGATCATCT	587
Hu.DMD.Exon51.25.020.2	TCATTTTTTCTCATACCTTCTGCTTG	588
Hu.DMD.Exon51.25.021	TTTTCTCATACCTTCTGCTTGATGAT	589
Hu.DMD.Exon51.25.022	TTTTATCATTTTTTCTCATACCTTCT	590
Hu.DMD.Exon51.25.023	CCAACTTTTATCATTTTTTCTCATAC	591
Hu.DMD.Exon51.20.001	ATATTTTGGGTTTTTGCAAA	592
Hu.DMD.Exon51.20.002	AAAATATTTTGGGTTTTTGC	593
Hu.DMD.Exon51.20.003	GAGCTAAAATATTTTGGGTT	594
Hu.DMD.Exon51.20.004	AGTAGGAGCTAAAATATTTT	595
Hu.DMD.Exon51.20.005	GTCTGAGTAGGAGCTAAAAT	596
Hu.DMD.Exon51.20.006	TAACAGTCTGAGTAGGAGCT	597
Hu.DMD.Exon51.20.007	CAGAGTAACAGTCTGAGTAG	598
Hu.DMD.Exon51.20.008	CACAGGTTGTGTCACCAGAG	599
Hu.DMD.Exon51.20.009	AGTTTCCTTAGTAACCACAG	600
Hu.DMD.Exon51.20.010	TAGTTTGGAGATGGCAGTTT	601
Hu.DMD.Exon51.20.011	GGAAGATGGCATTTCTAGTT	602
Hu.DMD.Exon51.20.012	TACCTCCAACATCAAGGAAG	603
Hu.DMD.Exon51.20.013	ATCTGCCAGAGCAGGTACCT	604
Hu.DMD.Exon51.20.014	CCAAGCCCGGTTGAAATCTG	605
Hu.DMD.Exon51.20.015	GTCGGTAAGTTCTGTCCAAG	606
Hu.DMD.Exon51.20.016	AAGCAGAGAAAGCCAGTCGG	607
Hu.DMD.Exon51.20.017	TTTTATAACTTGATCAAGCA	608
Hu.DMD.Exon51.20.018	CATCACCCTCTGTGATTTTA	609
Hu.DMD.Exon51.20.019	CTCAAGGTCACCCACCATCA	610
Hu.DMD.Exon51.20.020	CATCTCGTTGATATCCTCAA	611
Hu.DMD.Exon51.20.021	CTTCTGCTTGATGATCATCT	612
Hu.DMD.Exon51.20.022	CATACCTTCTGCTTGATGAT	613
Hu.DMD.Exon51.20.023	TTTCTCATACCTTCTGCTTG	614
Hu.DMD.Exon51.20.024	CATTTTTTCTCATACCTTCT	615
Hu.DMD.Exon51.20.025	TTTATCATTTTTTCTCATAC	616
Hu.DMD.Exon51.20.026	CAACTTTTATCATTTTTTCT	617
Hu.DMD.Exon52.25.001	CTGTAAGAACAAATATCCCTTAGTA	618
Hu.DMD.Exon52.25.002	TGCCTGTAAGAACAAATATCCCTTA	619
Hu.DMD.Exon52.25.002.2	GTTGCCTGTAAGAACAAATATCCCT	620
Hu.DMD.Exon52.25.003	ATTGTTGCCTGTAAGAACAAATATC	621

TABLE 4-continued

Hu.DMD.Exon52.25.003.2	GCATTGTTGCCTGTAAGAACAAATA	622
Hu.DMD.Exon52.25.004	CCTGCATTGTTGCCTGTAAGAACAA	623
Hu.DMD.Exon52.25.004.2	ATCCTGCATTGTTGCCTGTAAGAAC	624
Hu.DMD.Exon52.25.005	CAAATCCTGCATTGTTGCCTGTAAG	625
Hu.DMD.Exon52.25.005.2	TCCAAATCCTGCATTGTTGCCTGTA	626
Hu.DMD.Exon52.25.006	TGTTCCAAATCCTGCATTGTTGCCT	627
Hu.DMD.Exon52.25.006.2	TCTGTTCCAAATCCTGCATTGTTGC	628
Hu.DMD.Exon52.25.007	AACTGGGGACGCCTCTGTTCCAAAT	629
Hu.DMD.Exon52.25.007.2	GCCTCTGTTCCAAATCCTGCATTGT	630
Hu.DMD.Exon52.25.008	CAGCGGTAATGAGTTCTTCCAACTG	631
Hu.DMD.Exon52.25.008.2	CTTCCAACTGGGGACGCCTCTGTTC	632
Hu.DMD.Exon52.25.009	CTTGTTTTTCAAATTTTGGGCAGCG	633
Hu.DMD.Exon52.25.010	CTAGCCTCTTGATTGCTGGTCTTGT	634
Hu.DMD.Exon52.25.010.2	TTTTCAAATTTTGGGCAGCGGTAAT	635
Hu.DMD.Exon52.25.011	TTCGATCCGTAATGATTGTTCTAGC	636
Hu.DMD.Exon52.25.011.2	GATTGCTGGTCTTGTTTTTCAAATT	637
Hu.DMD.Exon52.25.012	CTTACTTCGATCCGTAATGATTGTT	638
Hu.DMD.Exon52.25.012.2	TTGTTCTAGCCTCTTGATTGCTGGT	639
Hu.DMD.Exon52.25.013	AAAAACTTACTTCGATCCGTAATGA	640
Hu.DMD.Exon52.25.014	TGTTAAAAAACTTACTTCGATCCGT	641
Hu.DMD.Exon52.25.015	ATGCTTGTTAAAAAACTTACTTCGA	642
Hu.DMD.Exon52.25.016	GTCCCATGCTTGTTAAAAAACTTAC	643
Hu.DMD.Exon52.20.001	AGAACAAATATCCCTTAGTA	644
Hu.DMD.Exon52.20.002	GTAAGAACAAATATCCCTTA	645
Hu.DMD.Exon52.20.003	TGCCTGTAAGAACAAATATC	646
Hu.DMD.Exon52.20.004	ATTGTTGCCTGTAAGAACAA	647
Hu.DMD.Exon52.20.005	CCTGCATTGTTGCCTGTAAG	648
Hu.DMD.Exon52.20.006	CAAATCCTGCATTGTTGCCT	649
Hu.DMD.Exon52.20.007	GCCTCTGTTCCAAATCCTGC	650
Hu.DMD.Exon52.20.008	CTTCCAACTGGGGACGCCTC	651
Hu.DMD.Exon52.20.009	CAGCGGTAATGAGTTCTTCC	652
Hu.DMD.Exon52.20.010	TTTTCAAATTTTGGGCAGCG	653
Hu.DMD.Exon52.20.011	GATTGCTGGTCTTGTTTTTC	654
Hu.DMD.Exon52.20.012	TTGTTCTAGCCTCTTGATTG	655
Hu.DMD.Exon52.20.013	TTCGATCCGTAATGATTGTT	656
Hu.DMD.Exon52.20.014	CTTACTTCGATCCGTAATGA	657
Hu.DMD.Exon52.20.015	AAAAACTTACTTCGATCCGT	658
Hu.DMD.Exon52.20.016	TGTTAAAAAACTTACTTCGA	659
Hu.DMD.Exon52.20.017	ATGCTTGTTAAAAAACTTAC	660
Hu.DMD.Exon52.20.018	GTCCCATGCTTGTTAAAAAA	661
Hu.DMD.Exon53.25.001	CTAGAATAAAAGGAAAAATAAATAT	662
Hu.DMD.Exon53.25.002	AACTAGAATAAAAGGAAAAATAAAT	663
Hu.DMD.Exon53.25.002.2	TTCAACTAGAATAAAAGGAAAAATA	664
Hu.DMD.Exon53.25.003	CTTTCAACTAGAATAAAAGGAAAAA	665
Hu.DMD.Exon53.25.003.2	ATTCTTTCAACTAGAATAAAAGGAA	666
Hu.DMD.Exon53.25.004	GAATTCTTTCAACTAGAATAAAAGG	667
Hu.DMD.Exon53.25.004.2	TCTGAATTCTTTCAACTAGAATAAA	668
Hu.DMD.Exon53.25.005	ATTCTGAATTCTTTCAACTAGAATA	669
Hu.DMD.Exon53.25.005.2	CTGATTCTGAATTCTTTCAACTAGA	670
Hu.DMD.Exon53.25.006	CACTGATTCTGAATTCTTTCAACTA	671
Hu.DMD.Exon53.25.006.2	TCCCACTGATTCTGAATTCTTTCAA	672
Hu.DMD.Exon53.25.007	CATCCCACTGATTCTGAATTCTTTC	673
Hu.DMD.Exon53.25.008	TACTTCATCCCACTGATTCTGAATT	674
Hu.DMD.Exon53.25.009	CGGTTCTGAAGGTGTTCTTGTACT	675
Hu.DMD.Exon53.25.009.2	CTGTTGCCTCCGGTTCTGAAGGTGT	676
Hu.DMD.Exon53.25.010	TTTCATTCAACTGTTGCCTCCGGTT	677
Hu.DMD.Exon53.25.010.2	TAACATTTCATTCAACTGTTGCCTC	678
Hu.DMD.Exon53.25.011	TTGTGTTGAATCCTTTAACATTTCA	679
Hu.DMD.Exon53.25.012	TCTTCCTTAGCTTCCAGCCATTGTG	680
Hu.DMD.Exon53.25.012.2	CTTAGCTTCCAGCCATTGTGTTGAA	681
Hu.DMD.Exon53.25.013	GTCCTAAGACCTGCTCAGCTTCTTC	682
Hu.DMD.Exon53.25.013.2	CTGCTCAGCTTCTTCCTTAGCTTCC	683
Hu.DMD.Exon53.25.014	CTCAAGCTTGGCTCTGGCCTGTCCT	684
Hu.DMD.Exon53.25.014.2	GGCCTGTCCTAAGACCTGCTCAGCT	685
Hu.DMD.Exon53.25.015	TAGGGACCCTCCTTCCATGACTCAA	686
Hu.DMD.Exon53.25.016	TTTGGATTGCATCTACTGTATAGGG	687
Hu.DMD.Exon53.25.016.2	ACCCTCCTTCCATGACTCAAGCTTG	688
Hu.DMD.Exon53.25.017	CTTGGTTTCTGTGATTTTCTTTTGG	689
Hu.DMD.Exon53.25.017.2	ATCTACTGTATAGGGACCCTCCTTC	690
Hu.DMD.Exon53.25.018	CTAACCTTGGTTTCTGTGATTTTCT	691
Hu.DMD.Exon53.25.018.2	TTTCTTTTGGATTGCATCTACTGTA	692
Hu.DMD.Exon53.25.019	TGATACTAACCTTGGTTTCTGTGAT	693
Hu.DMD.Exon53.25.020	ATCTTTGATACTAACCTTGGTTTCT	694
Hu.DMD.Exon53.25.021	AAGGTATCTTTGATACTAACCTTGG	695
Hu.DMD.Exon53.25.022	TTAAAAAGGTATCTTTGATACTAAC	696
Hu.DMD.Exon53.20.001	ATAAAAGGAAAAATAAATAT	697
Hu.DMD.Exon53.20.002	GAATAAAAGGAAAAATAAAT	698

TABLE 4-continued

Hu.DMD.Exon53.20.003	AACTAGAATAAAAGGAAAAA	699
Hu.DMD.Exon53.20.004	CTTTCAACTAGAATAAAAGG	700
Hu.DMD.Exon53.20.005	GAATTCTTTCAACTAGAATA	701
Hu.DMD.Exon53.20.006	ATTCTGAATTCTTTCAACTA	702
Hu.DMD.Exon53.20.007	TACTTCATCCCACTGATTCT	703
Hu.DMD.Exon53.20.008	CTGAAGGTGTTCTTGTACT	704
Hu.DMD.Exon53.20.009	CTGTTGCCTCCGGTTCTGAA	705
Hu.DMD.Exon53.20.010	TAACATTTCATTCAACTGTT	706
Hu.DMD.Exon53.20.011	TTGTGTTGAATCCTTTAACA	707
Hu.DMD.Exon53.20.012	CTTAGCTTCCAGCCATTGTG	708
Hu.DMD.Exon53.20.013	CTGCTCAGCTTCTTCCTTAG	709
Hu.DMD.Exon53.20.014	GGCCTGTCCTAAGACCTGCT	710
Hu.DMD.Exon53.20.015	CTCAAGCTTGGCTCTGGCCT	711
Hu.DMD.Exon53.20.016	ACCCTCCTTCCATGACTCAA	712
Hu.DMD.Exon53.20.017	ATCTACTGTATAGGGACCCT	713
Hu.DMD.Exon53.20.018	TTTCTTTTGGATTGCATCTA	714
Hu.DMD.Exon53.20.019	CTTGGTTTCTGTGATTTTCT	715
Hu.DMD.Exon53.20.020	CTAACCTTGGTTTCTGTGAT	716
Hu.DMD.Exon53.20.021	TGATACTAACCTTGGTTTCT	717
Hu.DMD.Exon53.20.022	ATCTTTGATACTAACCTTGG	718
Hu.DMD.Exon53.20.023	AAGGTATCTTTGATACTAAC	719
Hu.DMD.Exon53.20.024	TTAAAAAGGTATCTTTGATA	720
Hu.DMD.Exon54.25.001	CTATAGATTTTTATGAGAAAGAGA	721
Hu.DMD.Exon54.25.002	AACTGCTATAGATTTTTATGAGAAA	722
Hu.DMD.Exon54.25.003	TGGCCAACTGCTATAGATTTTTATG	723
Hu.DMD.Exon54.25.004	GTCTTTGGCCAACTGCTATAGATTT	724
Hu.DMD.Exon54.25.005	CGGAGGTCTTTGGCCAACTGCTATA	725
Hu.DMD.Exon54.25.006	ACTGGCGGAGGTCTTTGGCCAACTG	726
Hu.DMD.Exon54.25.007	TTTGTCTGCCACTGGCGGAGGTCTT	727
Hu.DMD.Exon54.25.008	AGTCATTTGCCACATCTACATTTGT	728
Hu.DMD.Exon54.25.008.2	TTTGCCACATCTACATTTGTCTGCC	729
Hu.DMD.Exon54.25.009	CCGGAGAAGTTTCAGGGCCAAGTCA	730
Hu.DMD.Exon54.25.010	GTATCATCTGCAGAATAATCCCGGA	731
Hu.DMD.Exon54.25.010.2	TAATCCCGGAGAAGTTTCAGGGCCA	732
Hu.DMD.Exon54.25.011	TTATCATGTGGACTTTTCTGGTATC	733
Hu.DMD.Exon54.25.012	AGAGGCATTGATATTCTCTGTTATC	734
Hu.DMD.Exon54.25.012.2	ATGTGGACTTTTCTGGTATCATCTG	735
Hu.DMD.Exon54.25.013	CTTTTATGAATGCTTCTCCAAGAGG	736
Hu.DMD.Exon54.25.013.2	ATATTCTCTGTTATCATGTGGACTT	737
Hu.DMD.Exon54.25.014	CATACCTTTTATGAATGCTTCTCCA	738
Hu.DMD.Exon54.25.014.2	CTCCAAGAGGCATTGATATTCTCTG	739
Hu.DMD.Exon54.25.015	TAATTCATACCTTTTATGAATGCTT	740
Hu.DMD.Exon54.25.016	TAATGTAATTCATACCTTTTATGAA	741
Hu.DMD.Exon54.25.017	AGAAATAATGTAATTCATACCTTTT	742
Hu.DMD.Exon54.25.018	GTTTTAGAAATAATGTAATTCATAC	743
Hu.DMD.Exon54.20.001	GATTTTTATGAGAAAGAGA	744
Hu.DMD.Exon54.20.002	CTATAGATTTTTATGAGAAA	745
Hu.DMD.Exon54.20.003	AACTGCTATAGATTTTTATG	746
Hu.DMD.Exon54.20.004	TGGCCAACTGCTATAGATTT	747
Hu.DMD.Exon54.20.005	GTCTTTGGCCAACTGCTATA	748
Hu.DMD.Exon54.20.006	CGGAGGTCTTTGGCCAACTG	749
Hu.DMD.Exon54.20.007	TTTGTCTGCCACTGGCGGAG	750
Hu.DMD.Exon54.20.008	TTTGCCACATCTACATTTGT	751
Hu.DMD.Exon54.20.009	TTCAGGGCCAAGTCATTTGC	752
Hu.DMD.Exon54.20.010	TAATCCCGGAGAAGTTTCAG	753
Hu.DMD.Exon54.20.011	GTATCATCTGCAGAATAATC	754
Hu.DMD.Exon54.20.012	ATGTGGACTTTTCTGGTATC	755
Hu.DMD.Exon54.20.013	ATATTCTCTGTTATCATGTG	756
Hu.DMD.Exon54.20.014	CTCCAAGAGGCATTGATATT	757
Hu.DMD.Exon54.20.015	CTTTTATGAATGCTTCTCCA	758
Hu.DMD.Exon54.20.016	CATACCTTTTATGAATGCTT	759
Hu.DMD.Exon54.20.017	TAATTCATACCTTTTATGAA	760
Hu.DMD.Exon54.20.018	TAATGTAATTCATACCTTTT	761
Hu.DMD.Exon54.20.019	AGAAATAATGTAATTCATAC	762
Hu.DMD.Exon54.20.020	GTTTTAGAAATAATGTAATT	763
Hu.DMD.Exon55.25.001	CTGCAAAGGACCAAATGTTCAGATG	764
Hu.DMD.Exon55.25.002	TCACCCTGCAAAGGACCAAATGTTC	765
Hu.DMD.Exon55.25.003	CTCACTCACCCTGCAAAGGACCAAA	766
Hu.DMD.Exon55.25.004	TCTCGCTCACTCACCCTGCAAAGGA	767
Hu.DMD.Exon55.25.005	CAGCCTCTCGCTCACTCACCCTGCA	768
Hu.DMD.Exon55.25.006	CAAAGCAGCCTCTCGCTCACTCACC	769
Hu.DMD.Exon55.25.007	TCTTCCAAAGCAGCCTCTCGCTCAC	770
Hu.DMD.Exon55.25.007.2	TCTATGAGTTTCTTCCAAAGCAGCC	771
Hu.DMD.Exon55.25.008	GTTGCAGTAATCTATGAGTTTCTTC	772
Hu.DMD.Exon55.25.008.2	GAACTGTTGCAGTAATCTATGAGTT	773
Hu.DMD.Exon55.25.009	TTCCAGGTCCAGGGGGAACTGTTGC	774
Hu.DMD.Exon55.25.010	GTAAGCCAGGCAAGAAACTTTTCCA	775

TABLE 4-continued

Hu.DMD.Exon55.25.010.2	CCAGGCAAGAAACTTTTCCAGGTCC	776
Hu.DMD.Exon55.25.011	TGGCAGTTGTTTCAGCTTCTGTAAG	777
Hu.DMD.Exon55.25.011.2	TTCAGCTTCTGTAAGCCAGGCAAGA	778
Hu.DMD.Exon55.25.012	GGTAGCATCCTGTAGGACATTGGCA	779
Hu.DMD.Exon55.25.012.2	GACATTGGCAGTTGTTTCAGCTTCT	780
Hu.DMD.Exon55.25.013	TCTAGGAGCCTTTCCTTACGGGTAG	781
Hu.DMD.Exon55.25.014	CTTTTACTCCCTTGGAGTCTTCTAG	782
Hu.DMD.Exon55.25.014.2	GAGCCTTTCCTTACGGGTAGCATCC	783
Hu.DMD.Exon55.25.015	TTGCCATTGTTTCATCAGCTCTTTT	784
Hu.DMD.Exon55.25.015.2	CTTGGAGTCTTCTAGGAGCCTTTCC	785
Hu.DMD.Exon55.25.016	CTTACTTGCCATTGTTTCATCAGCT	786
Hu.DMD.Exon55.25.016.2	CAGCTCTTTTACTCCCTTGGAGTCT	787
Hu.DMD.Exon55.25.017	CCTGACTTACTTGCCATTGTTTCAT	788
Hu.DMD.Exon55.25.018	AAATGCCTGACTTACTTGCCATTGT	789
Hu.DMD.Exon55.25.019	AGCGGAAATGCCTGACTTACTTGCC	790
Hu.DMD.Exon55.25.020	GCTAAAGCGGAAATGCCTGACTTAC	791
Hu.DMD.Exon55.20.001	AAGGACCAAATGTTCAGATG	792
Hu.DMD.Exon55.20.002	CTGCAAAGGACCAAATGTTC	793
Hu.DMD.Exon55.20.003	TCACCCTGCAAAGGACCAAA	794
Hu.DMD.Exon55.20.004	CTCACTCACCCTGCAAAGGA	795
Hu.DMD.Exon55.20.005	TCTCGCTCACTCACCCTGCA	796
Hu.DMD.Exon55.20.006	CAGCCTCTCGCTCACTCACC	797
Hu.DMD.Exon55.20.007	CAAAGCAGCCTCTCGCTCAC	798
Hu.DMD.Exon55.20.008	TCTATGAGTTTCTTCCAAAG	799
Hu.DMD.Exon55.20.009	GAACTGTTGCAGTAATCTAT	800
Hu.DMD.Exon55.20.010	TTCCAGGTCCAGGGGGAACT	801
Hu.DMD.Exon55.20.011	CCAGGCAAGAAACTTTTCCA	802
Hu.DMD.Exon55.20.012	TTCAGCTTCTGTAAGCCAGG	803
Hu.DMD.Exon55.20.013	GACATTGGCAGTTGTTTCAG	804
Hu.DMD.Exon55.20.014	GGTAGCATCCTGTAGGACAT	805
Hu.DMD.Exon55.20.015	GAGCCTTTCCTTACGGGTAG	806
Hu.DMD.Exon55.20.016	CTTGGAGTCTTCTAGGAGCC	807
Hu.DMD.Exon55.20.017	CAGCTCTTTTACTCCCTTGG	808
Hu.DMD.Exon55.20.018	TTGCCATTGTTTCATCAGCT	809
Hu.DMD.Exon55.20.019	CTTACTTGCCATTGTTTCAT	810
Hu.DMD.Exon55.20.020	CCTGACTTACTTGCCATTGT	811
Hu.DMD.Exon55.20.021	AAATGCCTGACTTACTTGCC	812
Hu.DMD.Exon55.20.022	AGCGGAAATGCCTGACTTAC	813
Hu.DMD.Exon55.20.023	GCTAAAGCGGAAATGCCTGA	814
H50A(+02 + 30)-AVI-5656	CCACTCAGAGCTCAGATCTTCTAACTTCC	815
H50D(+07 - 18)-AVI-5915	GGGATCCAGTATACTTACAGGCTCC	816
H50A(+07 + 33)	CTTCCACTCAGAGCTCAGATCTTCTAA	817
H51A(+61 + 90)-AVI-4657	ACATCAAGGAAGATGGCATTTCTAGTTTGG	818
H51A(+66 + 95)-AVI-4658	CTCCAACATCAAGGAAGATGGCATTTCTAG	819
H51A(+111 + 134)	TTCTGTCCAAGCCCGGTTGAAATC	820
H51A(+175 + 195)	CACCCACCATCACCCTCYGTG	821
H51A(+199 + 220)	ATCATCTCGTTGATATCCTCAA	822
H51A(+66 + 90)	ACATCAAGGAAGATGGCATTTCTAG	823
H51A(-01 + 25)	ACCAGAGTAACAGTCTGAGTAGGAGC	824
h51AON1	TCAAGGAAGATGGCATTTCT	825
h51AON2	CCTCTGTGATTTTATAACTTGAT	826
H51D(+08 - 17)	ATCATTTTTTCTCATACCTTCTGCT	827
H51D(+16 - 07)	CTCATACCTTCTGCTTGATGATC	828
hAON#23	TGGCATTTCTAGTTTGG	829
hAON#24	CCAGAGCAGGTACCTCCAACATC	830
h44AON1	CGCCGCCATTTCTCAACAG	831
H45A(+71 + 90)	TGTTTTTGAGGATTGCTGAA	832
h45AON1	GCTGAATTATTTCTTCCCC	833
h45AON5	GCCCAATGCCATCCTGG	834
H45A(-06 + 20)	CCAATGCCATCCTGGAGTTCCTGTAA	835
H53A(+39 + 69)	CATTCAACTGTTGCCTCCGGTTCTGAAGGTG	836
h53AON1	CTGTTGCCTCCGGTTCTG	837
H53A(-12 + 10)	ATTCTTTCAACTAGAATAAAAG	838
huEx45.30.66	GCCATCCTGGAGTTCCTGTAAGATACCAAA	839
huEx45.30.71	CCAATGCCATCCTGGAGTTCCTGTAAGATA	840
huEx45.30.79	GCCGCTGCCCAATGCCATCCTGGAGTTCCT	841
huEx45.30.83	GTTTGCCGCTGCCCAATGCCATCCTGGAGT	842
huEx45.30.88	CAACAGTTTGCCGCTGCCCAATGCCATCCT	843
huEx45.30.92	CTGACAACAGTTTGCCGCTGCCCAATGCCA	844
huEx45.30.96	TGTTCTGACAACAGTTTGCCGCTGCCCAAT	845
huEx45.30.99	CAATGTTCTGACAACAGTTTGCCGCTGCCC	846
huEx45.30.103	CATTCAATGTTCTGACAACAGTTTGCCGCT	847
huEx45.30.120	TATTTCTTCCCCAGTTGCATTCAATGTTCT	848
huEx45.30.127	GCTGAATTATTTCTTCCCCAGTTGCATTCA	849
huEx45.30.132	GGATTGCTGAATTATTTCTTCCCCAGTTGC	850
huEx45.30.137	TTTGAGGATTGCTGAATTATTTCTTCCCCA	851
huEx53.30.84	GTACTTCATCCCACTGATTCTGAATTCTTT	852

TABLE 4-continued

huEx53.30.88	TCTTGTACTTCATCCCACTGATTCTGAATT	853
huEx53.30.91	TGTTCTTGTACTTCATCCCACTGATTCTGA	854
huEx53.30.103	CGGTTCTGAAGGTGTTCTTGTACTTCATCC	855
huEx53.30.106	CTCCGGTTCTGAAGGTGTTCTTGTACTTCA	856
huEx53.30.109	TGCCTCCGGTTCTGAAGGTGTTCTTGTACT	857
huEx53.30.112	TGTTGCCTCCGGTTCTGAAGGTGTTCTTGT	858
huEx53.30.115	AACTGTTGCCTCCGGTTCTGAAGGTGTTCT	859
huEx53.30.118	TTCAACTGTTGCCTCCGGTTCTGAAGGTGT	860
h50A0N1		
h50A0N2		
	Peptide Transporters (NH_2 to COOH)*:	
rTAT	RRRQRRKKRC	861
R9F2	RRRRRRRRRFFC	862
(RRAhx)4B	RRAhxRRAhxRRAhxRRAhxB	863
(RAhxR)4AhxB; (P007)	RAhxRRAhxRRAhxRRAhxRAhxB	864
(AhxRR)4AhxB	AhxRRAhxRRAhxRRAhxRRAhxB	865
(RAhx)6B	RAhxRAhxRAhxRAhxRAhxRAhxB	866
(RAhx)8B	RAhxRAhxRAhxRAhxRAhxRAhxRAhxB	867
(RAhxR)5AhxB	RAhxRRAhxRRAhxRRAhxRRAhxRAhxB	868
(RAhxRRBR)2AhxB; (CPO6062)	RAhxRRBRRAhxRRBRAhxB	869
MSP	ASSLNIA	870
	Cell Penetrating Peptide/Homing Peptide/PMO Conjugates (NH_2 to COOH and 5' to 3')	
MSP-PMO	ASSLNIA-XB-	871
	GGCCAAACCTCGGCTTACCTGAAAT	875
CP06062-MSP-PMO	RXRRBRRXRRBR-XB-ASSLNIA-X-	872
	GGCCAAACCTCGGCTTACCTGAAAT	875
MSP-CP06062-PMO	ASSLNIA-X-RXRRBRRXRRBR-B-	873
	GGCCAAACCTCGGCTTACCTGAAAT	875
CP06062-PMO	RXRRBRRXRRBR-XB-	874
	GGCCAAACCTCGGCTTACCTGAAAT	875

*Ahx is 6-aminohexanoic acid and B is beta-alanine

SEQUENCE LISTING

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<223> OTHER INFORMATION: Synthetic (H51A(+61+90))

<400> SEQUENCE: 3

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<223> OTHER INFORMATION: Synthetic (Hu.DMD.exon51.25.001.2)

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<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
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caatgccatc ctggagttcc tg 22

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gauagguggu aucaacaucu g 21

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cacuauucca gucaaauagg ucugg 25

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auuuaccaac cuucaggauc gagua 25

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uuugaccuac auguggaaag 20

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uacauuuuug accuacaugu ggaaag 26

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auuuuugacc uacaugggaa ag 22

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<400> SEQUENCE: 24

guggucuccu uaccuaugac ugugg 25

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ggucuccuua ccuauga 17

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ugucucagua aucuucuuac cuau 24

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ucuuaccuau gacuauggau gaga 24

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<400> SEQUENCE: 28

gcaugaacuc uuguggaucc 20

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<210> SEQ ID NO 29
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<400> SEQUENCE: 29

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<400> SEQUENCE: 30

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<400> SEQUENCE: 33

aggucuagga ggcgccuccc auccuguagg u 31

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<400> SEQUENCE: 34

gcgccuccca uccuguaggu cacug 25

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<212> TYPE: RNA
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<220> FEATURE:
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cuucgaggag gucuaggagg cgccuc 26

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<223> OTHER INFORMATION: Synthetic (H3A(+30+50))

<400> SEQUENCE: 36

cucccauccu guaggucacu g 21

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<223> OTHER INFORMATION: Synthetic (H3D(+19-03))

<400> SEQUENCE: 37

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<400> SEQUENCE: 38

ucaauaugcu gcuucccaaa cugaaa 26

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cuaggaggcg ccucccaucc uguag 25

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uuaugauuuc caucuacgau gucaguacuu c 31

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<400> SEQUENCE: 41

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cuuaccugcc aguggaggau uauauuccaa a 31

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cgaugucagu acuuccaaua uucac 25

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accauucauc aggauucu 18

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accugccagu ggaggauu 18

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ccaauauuca cuaaaucaac cuguuaa 27

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acgaugucag uacuuccaau auucacuaaa u 31

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auuuccaucu acgaugucag uacuuccaau a 31

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caggagcuuc caaaugcugc a 21

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uccucagcag aaagaagcca cg 22

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uuagaaaucu cuccuugugc 20

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<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H10A(-33-14))

<400> SEQUENCE: 54

uaaauugggu guuacacaau 20

<210> SEQ ID NO 55
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H11D(+26+49))

<400> SEQUENCE: 55

cccugaggca uucccaucuu gaau 24

<210> SEQ ID NO 56
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H11D(+11-09))

<400> SEQUENCE: 56

aggacuuacu ugcuuuguuu 20

<210> SEQ ID NO 57
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H11A(+118+140))

<400> SEQUENCE: 57

cuugaauuua ggagauucau cug 23

<210> SEQ ID NO 58
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H11A(+75+97))

<400> SEQUENCE: 58

caucuucuga uaauuuuccu guu 23

<210> SEQ ID NO 59
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H12A(+52+75))

<400> SEQUENCE: 59

ucuucuguuu uuguuagcca guca 24

<210> SEQ ID NO 60
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H12A(-10+10))

<400> SEQUENCE: 60

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ucuauguaaa cugaaaauuu 20

<210> SEQ ID NO 61
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H12A(+11+30))

<400> SEQUENCE: 61

uucuggagau ccauuaaaac 20

<210> SEQ ID NO 62
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H13A(+77+100))

<400> SEQUENCE: 62

cagcaguugc gugaucucca cuag 24

<210> SEQ ID NO 63
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H13A(+55+75))

<400> SEQUENCE: 63

uucaucaacu accaccacca u 21

<210> SEQ ID NO 64
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H13D(+06-19))

<400> SEQUENCE: 64

cuaagcaaaa uaaucugacc uuaag 25

<210> SEQ ID NO 65
<211> LENGTH: 28
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H14A(+37+64))

<400> SEQUENCE: 65

cuuguaaaag aacccagcgg ucuucugu 28

<210> SEQ ID NO 66
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H14A(+14+35))

<400> SEQUENCE: 66

caucuacaga uguuugccca uc 22

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<210> SEQ ID NO 67
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H14A(+51+73))

<400> SEQUENCE: 67

gaaggauguc uuguaaaaga acc 23

<210> SEQ ID NO 68
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H14D(-02+18))

<400> SEQUENCE: 68

accuguucuu caguaagacg 20

<210> SEQ ID NO 69
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H14D(+14-10))

<400> SEQUENCE: 69

caugacacac cuguucuuca guaa 24

<210> SEQ ID NO 70
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H14A(+61+80))

<400> SEQUENCE: 70

cauuugagaa ggaugucuug 20

<210> SEQ ID NO 71
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H14A(-12+12))

<400> SEQUENCE: 71

aucucccaau accuggagaa gaga 24

<210> SEQ ID NO 72
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H15A(-12+19))

<400> SEQUENCE: 72

gccaugcacu aaaaaggcac ugcaagacau u 31

<210> SEQ ID NO 73
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H15A(+48+71))

<400> SEQUENCE: 73

ucuuuaaagc caguugugug aauc 24

<210> SEQ ID NO 74
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H15A(+08+28))

<400> SEQUENCE: 74

uuucugaaag ccaugcacua a 21

<210> SEQ ID NO 75
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H15D(+17-08))

<400> SEQUENCE: 75

guacauacgg ccaguuuuug aagac 25

<210> SEQ ID NO 76
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H16A(-12+19))

<400> SEQUENCE: 76

cuagauccgc uuuuaaaacc uguuaaaaca a 31

<210> SEQ ID NO 77
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H16A(-06+25))

<400> SEQUENCE: 77

ucuuuucuag auccgcuuuu aaaaccuguu a 31

<210> SEQ ID NO 78
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H16A(-06+19))

<400> SEQUENCE: 78

cuagauccgc uuuuaaaacc uguua 25

<210> SEQ ID NO 79
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H16A(+87+109))

<400> SEQUENCE: 79

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ccgucuucug ggucacugac uua 23

<210> SEQ ID NO 80
<211> LENGTH: 26
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H16A(-07+19))

<400> SEQUENCE: 80

cuagauccgc uuuuaaaacc uguuaa 26

<210> SEQ ID NO 81
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H16A(-07+13))

<400> SEQUENCE: 81

ccgcuuuuaa aaccuguuaa 20

<210> SEQ ID NO 82
<211> LENGTH: 26
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H16A(+12+37))

<400> SEQUENCE: 82

uggauugcuu uuucuuuucu agaucc 26

<210> SEQ ID NO 83
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H16A(+92+116))

<400> SEQUENCE: 83

caugcuuccg ucuucugggu cacug 25

<210> SEQ ID NO 84
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H16A(+45+67))

<400> SEQUENCE: 84

gaucuuguuu gagugaauac agu 23

<210> SEQ ID NO 85
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H16A(+105+126))

<400> SEQUENCE: 85

guuauccagc caugcuuccg uc 22

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<210> SEQ ID NO 86
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H16D(+05-20))

<400> SEQUENCE: 86

ugauaauugg uaucacuaac cugug 25

<210> SEQ ID NO 87
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H16D(+12-11))

<400> SEQUENCE: 87

guaucacuaa ccugugcugu ac 22

<210> SEQ ID NO 88
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H19A(+35+53))

<400> SEQUENCE: 88

cugcuggcau cuugcaguu 19

<210> SEQ ID NO 89
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H19A(+35+65))

<400> SEQUENCE: 89

gccugagcug aucugcuggc aucuugcagu u 31

<210> SEQ ID NO 90
<211> LENGTH: 28
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H20A(+44+71))

<400> SEQUENCE: 90

cuggcagaau ucgauccacc ggcuguuc 28

<210> SEQ ID NO 91
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H20A(+147+168))

<400> SEQUENCE: 91

cagcaguagu ugucaucugc uc 22

<210> SEQ ID NO 92
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H20A(+185+203))

<400> SEQUENCE: 92

ugauggggug guggguugg 19

<210> SEQ ID NO 93
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H20A(-08+17))

<400> SEQUENCE: 93

aucugcauua acacccucua gaaag 25

<210> SEQ ID NO 94
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H20A(+30+53))

<400> SEQUENCE: 94

ccggcuguuc aguuguucug aggc 24

<210> SEQ ID NO 95
<211> LENGTH: 28
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H20A(-11+17))

<400> SEQUENCE: 95

aucugcauua acacccucua gaaagaaa 28

<210> SEQ ID NO 96
<211> LENGTH: 28
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H20D(+08-20))

<400> SEQUENCE: 96

gaaggagaag agauucuuac cuuacaaa 28

<210> SEQ ID NO 97
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H20A(+44+63))

<400> SEQUENCE: 97

auucgaucca ccggcuguuc 20

<210> SEQ ID NO 98
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H20A(+149+168))

<400> SEQUENCE: 98

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cagcaguagu ugucaucugc 20

<210> SEQ ID NO 99
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H21A(-06+16))

<400> SEQUENCE: 99

gccgguugac uucauccugu gc 22

<210> SEQ ID NO 100
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H21A(+85+106))

<400> SEQUENCE: 100

cugcauccag gaacaugggu cc 22

<210> SEQ ID NO 101
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H21A(+85+108))

<400> SEQUENCE: 101

gucugcaucc aggaacaugg guc 23

<210> SEQ ID NO 102
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H21A(+08+31))

<400> SEQUENCE: 102

guugaagauc ugauagccgg uuga 24

<210> SEQ ID NO 103
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H21D(+18-07))

<400> SEQUENCE: 103

uacuuacugu cuguagcucu uucu 24

<210> SEQ ID NO 104
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H22A(+22+45))

<400> SEQUENCE: 104

cacucauggu cuccugauag cgca 24

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<210> SEQ ID NO 105
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H22A(+125+146))

<400> SEQUENCE: 105

cugcaauucc ccgagucucu gc 22

<210> SEQ ID NO 106
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H22A(+47+69))

<400> SEQUENCE: 106

acugcuggac ccauguccug aug 23

<210> SEQ ID NO 107
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H22A(+80+101))

<400> SEQUENCE: 107

cuaaguugag guauggagag u 21

<210> SEQ ID NO 108
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H22D(+13-11))

<400> SEQUENCE: 108

uauucacaga ccugcaauuc ccc 23

<210> SEQ ID NO 109
<211> LENGTH: 26
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H23A(+34+59))

<400> SEQUENCE: 109

acaguggugc ugagauagua uaggcc 26

<210> SEQ ID NO 110
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H23A(+18+39))

<400> SEQUENCE: 110

uaggccacuu uguugcucuu gc 22

<210> SEQ ID NO 111
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H23A(+72+90))

<400> SEQUENCE: 111

uucagagggc gcuuucuuc 19

<210> SEQ ID NO 112
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H24A(+48+70))

<400> SEQUENCE: 112

gggcaggcca uuccuccuuc aga 23

<210> SEQ ID NO 113
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H24A(-02+22))

<400> SEQUENCE: 113

ucuucagggu uuguauguga uucu 24

<210> SEQ ID NO 114
<211> LENGTH: 27
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H25A(+9+36))

<400> SEQUENCE: 114

cugggcugaa uugucugaau aucacug 27

<210> SEQ ID NO 115
<211> LENGTH: 26
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H25A(+131+156))

<400> SEQUENCE: 115

cuguuggcac augugauccc acugag 26

<210> SEQ ID NO 116
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H25D(+16-08))

<400> SEQUENCE: 116

gucuauaccu guuggcacau guga 24

<210> SEQ ID NO 117
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H26A(+132+156))

<400> SEQUENCE: 117

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ugcuuucugu aauucaucug gaguu 25

<210> SEQ ID NO 118
<211> LENGTH: 26
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H26A(-07+19))

<400> SEQUENCE: 118

ccuccuuucu ggcauagacc uuccac 26

<210> SEQ ID NO 119
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H26A(+68+92))

<400> SEQUENCE: 119

ugugucaucc auucgugcau cucug 25

<210> SEQ ID NO 120
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H27A(+82+106))

<400> SEQUENCE: 120

uuaaggccuc uugugcuaca ggugg 25

<210> SEQ ID NO 121
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H27A(-4+19))

<400> SEQUENCE: 121

ggggcucuuc uuuagcucuc uga 23

<210> SEQ ID NO 122
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H27D(+19-03))

<400> SEQUENCE: 122

gacuuccaaa gucuugcauu uc 22

<210> SEQ ID NO 123
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H28A(-05+19))

<400> SEQUENCE: 123

gccaacaugc ccaaacuucc uaag 24

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<210> SEQ ID NO 124
<211> LENGTH: 26
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H28A(+99+124))

<400> SEQUENCE: 124

cagagauuuc cucagcuccg ccagga 26

<210> SEQ ID NO 125
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H28D(+16-05))

<400> SEQUENCE: 125

cuuacaucua gcaccucaga g 21

<210> SEQ ID NO 126
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H29A(+57+81))

<400> SEQUENCE: 126

uccgccaucu guuagggucu gugcc 25

<210> SEQ ID NO 127
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H29A(+18+42))

<400> SEQUENCE: 127

auuuggguua uccucugaau gucgc 25

<210> SEQ ID NO 128
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H29D(+17-05))

<400> SEQUENCE: 128

cauaccucuu cauguaguuc cc 22

<210> SEQ ID NO 129
<211> LENGTH: 26
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H30A(+122+147))

<400> SEQUENCE: 129

cauuugagcu gcguccaccu ugucug 26

<210> SEQ ID NO 130
<211> LENGTH: 26
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H30A(+25+50))

<400> SEQUENCE: 130

uccugggcag acuggaugcu cuguuc 26

<210> SEQ ID NO 131
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H30D(+19-04))

<400> SEQUENCE: 131

uugccugggc uuccugaggc auu 23

<210> SEQ ID NO 132
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H31D(+06-18))

<400> SEQUENCE: 132

uucugaaaua acauauaccu gugc 24

<210> SEQ ID NO 133
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H31D(+03-22))

<400> SEQUENCE: 133

uaguuucuga aauaacauau accug 25

<210> SEQ ID NO 134
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H31A(+05+25))

<400> SEQUENCE: 134

gacuugucaa aucagauugg a 21

<210> SEQ ID NO 135
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H31D(+04-20))

<400> SEQUENCE: 135

guuucugaaa uaacauauac cugu 24

<210> SEQ ID NO 136
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H32D(+04-16))

<400> SEQUENCE: 136

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caccagaaau acauaccaca 20

<210> SEQ ID NO 137
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H32A(+151+170))

<400> SEQUENCE: 137

caaugauuua gcugugacug 20

<210> SEQ ID NO 138
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H32A(+10+32))

<400> SEQUENCE: 138

cgaaacuuca uggagacauc uug 23

<210> SEQ ID NO 139
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H32A(+49+73))

<400> SEQUENCE: 139

cuuguagacg cugcucaaaa uuggc 25

<210> SEQ ID NO 140
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H33D(+09-11))

<400> SEQUENCE: 140

caugcacaca ccuuugcucc 20

<210> SEQ ID NO 141
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H33A(+53+76))

<400> SEQUENCE: 141

ucuguacaau cugacgucca gucu 24

<210> SEQ ID NO 142
<211> LENGTH: 27
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H33A(+30+56))

<400> SEQUENCE: 142

gucuuuauca ccauuuccac uucagac 27

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<210> SEQ ID NO 143
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H33A(+64+88))

<400> SEQUENCE: 143

ccgucugcuu uuucuguaca aucug 25

<210> SEQ ID NO 144
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H34A(+83+104))

<400> SEQUENCE: 144

uccauaucug uagcugccag cc 22

<210> SEQ ID NO 145
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H34A(+143+165))

<400> SEQUENCE: 145

ccaggcaacu ucagaaucca aau 23

<210> SEQ ID NO 146
<211> LENGTH: 30
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H34A(-20+10))

<400> SEQUENCE: 146

uuucuguuac cugaaaagaa uuauaaugaa 30

<210> SEQ ID NO 147
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H34A(+46+70))

<400> SEQUENCE: 147

cauucauuuc cuuucgcauc uuacg 25

<210> SEQ ID NO 148
<211> LENGTH: 26
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H34A(+95+120))

<400> SEQUENCE: 148

ugaucucuuu gucaauucca uaucug 26

<210> SEQ ID NO 149
<211> LENGTH: 30
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H34D(+10-20))

<400> SEQUENCE: 149

uucagugaua uagguuuuac cuuuccccag 30

<210> SEQ ID NO 150
<211> LENGTH: 26
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H34A(+72+96))

<400> SEQUENCE: 150

cuguagcugc cagccauucu gucaag 26

<210> SEQ ID NO 151
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H35A(+141+161))

<400> SEQUENCE: 151

ucuucugcuc gggaggugac a 21

<210> SEQ ID NO 152
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H35A(+116+135))

<400> SEQUENCE: 152

ccaguuacua uucagaagac 20

<210> SEQ ID NO 153
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H35A(+24+43))

<400> SEQUENCE: 153

ucuucaggug caccuucugu 20

<210> SEQ ID NO 154
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H36A(+26+50))

<400> SEQUENCE: 154

ugugaugugg uccacauucu gguca 25

<210> SEQ ID NO 155
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H36A(-02+18))

<400> SEQUENCE: 155

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ccauguguuu cugguauucc 20

<210> SEQ ID NO 156
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H37A(+26+50))

<400> SEQUENCE: 156

cguguagagu ccaccuuugg gcgua 25

<210> SEQ ID NO 157
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H37A(+82+105))

<400> SEQUENCE: 157

uacuaauuuc cugcaguggu cacc 24

<210> SEQ ID NO 158
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H37A(+134+157))

<400> SEQUENCE: 158

uucuguguga aauggcugca aauc 24

<210> SEQ ID NO 159
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H38A(-01+19))

<400> SEQUENCE: 159

ccuucaaagg aauggaggcc 20

<210> SEQ ID NO 160
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H38A(+59+83))

<400> SEQUENCE: 160

ugcugaauuu cagccuccag ugguu 25

<210> SEQ ID NO 161
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H38A(+88+112))

<400> SEQUENCE: 161

ugaagucuuc cucuuucaga uucac 25

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<210> SEQ ID NO 162
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H39A(+62+85))

<400> SEQUENCE: 162

cuggcuuucu cucaucugug auuc 24

<210> SEQ ID NO 163
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H39A(+39+58))

<400> SEQUENCE: 163

guuguaaguu gucuccucuu 20

<210> SEQ ID NO 164
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H39A(+102+121))

<400> SEQUENCE: 164

uugucuguaa cagcugcugu 20

<210> SEQ ID NO 165
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H39D(+10-10))

<400> SEQUENCE: 165

gcucuaauac cuugagagca 20

<210> SEQ ID NO 166
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H40A(-05+17))

<400> SEQUENCE: 166

cuuugagacc ucaaauccug uu 22

<210> SEQ ID NO 167
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H40A(+129+153))

<400> SEQUENCE: 167

cuuuauuuuc cuuucaucuc ugggc 25

<210> SEQ ID NO 168
<211> LENGTH: 27
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H42A(-04+23))

<400> SEQUENCE: 168

aucguuucuu cacggacagu gugcugg 27

<210> SEQ ID NO 169
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H42A(+86+109))

<400> SEQUENCE: 169

gggcuuguga gacaugagug auuu 24

<210> SEQ ID NO 170
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H42D(+19-02))

<400> SEQUENCE: 170

accuucagag gacuccucuu gc 22

<210> SEQ ID NO 171
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H43D(+10-15))

<400> SEQUENCE: 171

uauguguuac cuacccuugu cgguc 25

<210> SEQ ID NO 172
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H43A(+101+120))

<400> SEQUENCE: 172

ggagagagcu uccuguagcu 20

<210> SEQ ID NO 173
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H43A(+78+100))

<400> SEQUENCE: 173

ucacccuuuc cacaggcguu gca 23

<210> SEQ ID NO 174
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(+85+104))

<400> SEQUENCE: 174

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uuugugucuu ucugagaaac 20

<210> SEQ ID NO 175
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44D(+10-10))

<400> SEQUENCE: 175

aaagacuuac cuuaagauac 20

<210> SEQ ID NO 176
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(-06+14))

<400> SEQUENCE: 176

aucugucaaa ucgccugcag 20

<210> SEQ ID NO 177
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H46D(+16-04))

<400> SEQUENCE: 177

uuaccuugac uugcucaagc 20

<210> SEQ ID NO 178
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H46A(+90+109))

<400> SEQUENCE: 178

uccagguuca agugggauac 20

<210> SEQ ID NO 179
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H47A(+76+100))

<400> SEQUENCE: 179

gcucuucugg gcuuauggga gcacu 25

<210> SEQ ID NO 180
<211> LENGTH: 27
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H47D(+25-02))

<400> SEQUENCE: 180

accuuuaucc acuggagauu ugucugc 27

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<210> SEQ ID NO 181
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H47A(-9+12))

<400> SEQUENCE: 181

uuccaccagu aacugaaaca g 21

<210> SEQ ID NO 182
<211> LENGTH: 29
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H50A(+02+30))

<400> SEQUENCE: 182

ccacucagag cucagaucuu cuaacuucc 29

<210> SEQ ID NO 183
<211> LENGTH: 27
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H50A(+07+33))

<400> SEQUENCE: 183

cuuccacuca gagcucagau cuucuaa 27

<210> SEQ ID NO 184
<211> LENGTH: 26
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H51A(-01+25))

<400> SEQUENCE: 184

accagaguaa cagucugagu aggagc 26

<210> SEQ ID NO 185
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H51D(+16-07))

<400> SEQUENCE: 185

cucauaccuu cugcuugaug auc 23

<210> SEQ ID NO 186
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H51A(+111 +134))

<400> SEQUENCE: 186

uucuguccaa gcccgguuga aauc 24

<210> SEQ ID NO 187
<211> LENGTH: 30
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H51A(+66+95))

<400> SEQUENCE: 187

cuccaacauc aaggaagaug gcauuucuag 30

<210> SEQ ID NO 188
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H51D(+08-17))

<400> SEQUENCE: 188

aucauuuuuu cucauaccuu cugcu 25

<210> SEQ ID NO 189
<211> LENGTH: 36
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H51A/D(+08-17)& (-15+))

<400> SEQUENCE: 189

aucauuuuuu cucauaccuu cugcuaggag cuaaaa 36

<210> SEQ ID NO 190
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H51A(+175+195))

<400> SEQUENCE: 190

cacccaccau cacccucugu g 21

<210> SEQ ID NO 191
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H51A(+199+220))

<400> SEQUENCE: 191

aucaucucgu ugauauccuc aa 22

<210> SEQ ID NO 192
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H52A(-07+14))

<400> SEQUENCE: 192

uccugcauug uugccuguaa g 21

<210> SEQ ID NO 193
<211> LENGTH: 30
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H52A(+12+41))

<400> SEQUENCE: 193

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uccaacuggg gacgccucug uuccaaaucc 30

<210> SEQ ID NO 194
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H52A(+17+37))

<400> SEQUENCE: 194

acuggggacg ccucuguucc a 21

<210> SEQ ID NO 195
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H52A(+93+112))

<400> SEQUENCE: 195

ccguaaugau uguucuagcc 20

<210> SEQ ID NO 196
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H52D(+05-15))

<400> SEQUENCE: 196

uguuaaaaaa cuuacuucga 20

<210> SEQ ID NO 197
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+45+69))

<400> SEQUENCE: 197

cauucaacug uugccuccgg uucug 25

<210> SEQ ID NO 198
<211> LENGTH: 24
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+39+62))

<400> SEQUENCE: 198

cuguugccuc cgguucugaa ggug 24

<210> SEQ ID NO 199
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+39+69))

<400> SEQUENCE: 199

cauucaacug uugccuccgg uucugaaggu g 31

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<210> SEQ ID NO 200
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53D(+14-07))

<400> SEQUENCE: 200

uacuaaccuu gguuucugug a 21

<210> SEQ ID NO 201
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+23+47))

<400> SEQUENCE: 201

cugaaggugu ucuuguacuu caucc 25

<210> SEQ ID NO 202
<211> LENGTH: 27
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+150+176))

<400> SEQUENCE: 202

uguauaggga cccuccuucc augacuc 27

<210> SEQ ID NO 203
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53D(+20-05))

<400> SEQUENCE: 203

cuaaccuugg uuucugugau uuucu 25

<210> SEQ ID NO 204
<211> LENGTH: 27
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53D(+09-18))

<400> SEQUENCE: 204

gguaucuuug auacuaaccu ugguuuc 27

<210> SEQ ID NO 205
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(-12+10))

<400> SEQUENCE: 205

auucuuucaa cuagaauaaa ag 22

<210> SEQ ID NO 206
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(-07+18))

<400> SEQUENCE: 206

gauucugaau ucuuucaacu agaau 25

<210> SEQ ID NO 207
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+07+26))

<400> SEQUENCE: 207

aucccacuga uucugaauuc 20

<210> SEQ ID NO 208
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+124+145))

<400> SEQUENCE: 208

uuggcucugg ccuguccuaa ga 22

<210> SEQ ID NO 209
<211> LENGTH: 30
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H46A(+86+115))

<400> SEQUENCE: 209

cucuuuucca gguucaagug ggauacuagc 30

<210> SEQ ID NO 210
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H46A(+107+137))

<400> SEQUENCE: 210

caagcuuuuc uuuuaguugc ugcucuuuuc c 31

<210> SEQ ID NO 211
<211> LENGTH: 30
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H46A(-10+20))

<400> SEQUENCE: 211

uauucuuuug uucuucuagc cuggagaaag 30

<210> SEQ ID NO 212
<211> LENGTH: 28
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H46A(+50+77))

<400> SEQUENCE: 212

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cugcuuccuc caaccauaaa acaaauuc 28

<210> SEQ ID NO 213
<211> LENGTH: 26
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H45A(-06+20))

<400> SEQUENCE: 213

ccaaugccau ccuggaguuc cuguaa 26

<210> SEQ ID NO 214
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H45A(+91 +110))

<400> SEQUENCE: 214

uccuguagaa uacuggcauc 20

<210> SEQ ID NO 215
<211> LENGTH: 27
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H45A(+125+151))

<400> SEQUENCE: 215

ugcagaccuc cugccaccgc agauuca 27

<210> SEQ ID NO 216
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H45D(+16 -04))

<400> SEQUENCE: 216

cuaccucuuu uuucugucug 20

<210> SEQ ID NO 217
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H45A(+71+90))

<400> SEQUENCE: 217

uguuuuugag gauugcugaa 20

<210> SEQ ID NO 218
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+33+60))

<400> SEQUENCE: 218

gttgcctccg gttctgaagg tgttcttg 28

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<210> SEQ ID NO 219
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+23+47))

<400> SEQUENCE: 219

ctgaaggtgt tcttgtactt catcc 25

<210> SEQ ID NO 220
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+33+62))

<400> SEQUENCE: 220

ctgttgcctc cggttctgaa ggtgttcttg 30

<210> SEQ ID NO 221
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+33+65))

<400> SEQUENCE: 221

caactgttgc ctccggttct gaaggtgttc ttg 33

<210> SEQ ID NO 222
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+31+55))

<400> SEQUENCE: 222

ctccggttct gaaggtgttc ttgta 25

<210> SEQ ID NO 223
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+46+73))

<400> SEQUENCE: 223

atttcattca actgttgcct ccggttct 28

<210> SEQ ID NO 224
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+22+46))

<400> SEQUENCE: 224

tgaaggtgtt cttgtacttc atccc 25

<210> SEQ ID NO 225
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+46+69))

<400> SEQUENCE: 225

cattcaactg ttgcctccgg ttct 24

<210> SEQ ID NO 226
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+40+61))

<400> SEQUENCE: 226

tgttgcctcc ggttctgaag gt 22

<210> SEQ ID NO 227
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+30+60))

<400> SEQUENCE: 227

gttgcctccg gttctgaagg tgttc 25

<210> SEQ ID NO 228
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+30+57))

<400> SEQUENCE: 228

gcctccggtt ctgaaggtgt tcttgtac 28

<210> SEQ ID NO 229
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+30+56))

<400> SEQUENCE: 229

cctccggttc tgaaggtgtt cttgtac 27

<210> SEQ ID NO 230
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+30+55))

<400> SEQUENCE: 230

ctccggttct gaaggtgttc ttgtac 26

<210> SEQ ID NO 231
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+33+57))

<400> SEQUENCE: 231

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gcctccggtt ctgaaggtgt tcttg 25

<210> SEQ ID NO 232
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(-07+17))

<400> SEQUENCE: 232

cagatctgtc aaatcgcctg cagg 24

<210> SEQ ID NO 233
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(-07+20))

<400> SEQUENCE: 233

caacagatct gtcaaatcgc ctgcagg 27

<210> SEQ ID NO 234
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(-07+22))

<400> SEQUENCE: 234

ctcaacagat ctgtcaaatc gcctgcagg 29

<210> SEQ ID NO 235
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(+77+101))

<400> SEQUENCE: 235

gtgtctttct gagaaactgt tcagc 25

<210> SEQ ID NO 236
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(+64+91))

<400> SEQUENCE: 236

gagaaactgt tcagcttctg ttagccac 28

<210> SEQ ID NO 237
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(+62+89))

<400> SEQUENCE: 237

gaaactgttc agcttctgtt agccactg 28

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<210> SEQ ID NO 238
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(+62+85))

<400> SEQUENCE: 238

ctgttcagct tctgttagcc actg 24

<210> SEQ ID NO 239
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(-06+14))

<400> SEQUENCE: 239

atctgtcaaa tcgcctgcag 20

<210> SEQ ID NO 240
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(+85+104))

<400> SEQUENCE: 240

tttgtgtctt tctgagaaac 20

<210> SEQ ID NO 241
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(+61+84))

<400> SEQUENCE: 241

tgttcagctt ctgttagcca ctga 24

<210> SEQ ID NO 242
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(-10+15))

<400> SEQUENCE: 242

gatctgtcaa atcgcctgca ggtaa 25

<210> SEQ ID NO 243
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(+64+88))

<400> SEQUENCE: 243

aaactgttca gcttctgtta gccac 25

<210> SEQ ID NO 244
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(+79+103))

<400> SEQUENCE: 244

ttgtgtcttt ctgagaaact gttca 25

<210> SEQ ID NO 245
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(-06+20))

<400> SEQUENCE: 245

caacagatct gtcaaatcgc ctgcag 26

<210> SEQ ID NO 246
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(-09+17))

<400> SEQUENCE: 246

cagatctgtc aaatcgcctg caggta 26

<210> SEQ ID NO 247
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(+59+85))

<400> SEQUENCE: 247

ctgttcagct tctgttagcc actgatt 27

<210> SEQ ID NO 248
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(+59+89))

<400> SEQUENCE: 248

gaaactgttc agcttctgtt agccactgat t 31

<210> SEQ ID NO 249
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H44A(+65+90))

<400> SEQUENCE: 249

agaaactgtt cagcttctgt tagcca 26

<210> SEQ ID NO 250
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon44.25.001)

<400> SEQUENCE: 250

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ctgcaggtaa aagcatatgg atcaa 25

<210> SEQ ID NO 251
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon44.25.002)

<400> SEQUENCE: 251

atcgcctgca ggtaaaagca tatgg 25

<210> SEQ ID NO 252
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon44.25.003)

<400> SEQUENCE: 252

gtcaaatcgc ctgcaggtaa aagca 25

<210> SEQ ID NO 253
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon44.25.005)

<400> SEQUENCE: 253

caacagatct gtcaaatcgc ctgca 25

<210> SEQ ID NO 254
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon44.25.006)

<400> SEQUENCE: 254

tttctcaaca gatctgtcaa atcgc 25

<210> SEQ ID NO 255
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon44.25.007)

<400> SEQUENCE: 255

ccatttctca acagatctgt caaat 25

<210> SEQ ID NO 256
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon44.25.008)

<400> SEQUENCE: 256

ataatgaaaa cgccgccatt tctca 25

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<210> SEQ ID NO 257
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon44.25.009)

<400> SEQUENCE: 257

aaatatcttt atatcataat gaaaa 25

<210> SEQ ID NO 258
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon44.25.010)

<400> SEQUENCE: 258

tgttagccac tgattaaata tcttt 25

<210> SEQ ID NO 259
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon44.25.013)

<400> SEQUENCE: 259

ccaattctca ggaatttgtg tcttt 25

<210> SEQ ID NO 260
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon44.25.014)

<400> SEQUENCE: 260

gtatttagca tgttcccaat tctca 25

<210> SEQ ID NO 261
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon44.25.015)

<400> SEQUENCE: 261

cttaagatac catttgtatt tagca 25

<210> SEQ ID NO 262
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon44.25.016)

<400> SEQUENCE: 262

cttaccttaa gataccattt gtatt 25

<210> SEQ ID NO 263
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon44.25.017)

<400> SEQUENCE: 263

aaagacttac cttaagatac cattt 25

<210> SEQ ID NO 264
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon44.25.018)

<400> SEQUENCE: 264

aaatcaaaga cttaccttaa gatac 25

<210> SEQ ID NO 265
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon44.25.019)

<400> SEQUENCE: 265

aaaacaaatc aaagacttac cttaa 25

<210> SEQ ID NO 266
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon44.25.020)

<400> SEQUENCE: 266

tcgaaaaaac aaatcaaaga cttac 25

<210> SEQ ID NO 267
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.001)

<400> SEQUENCE: 267

ctgtaagata ccaaaaaggc aaaac 25

<210> SEQ ID NO 268
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.002)

<400> SEQUENCE: 268

cctgtaagat accaaaaagg caaaa 25

<210> SEQ ID NO 269
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.002.2)

<400> SEQUENCE: 269

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agttcctgta agataccaaa aaggc 25

<210> SEQ ID NO 270
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.003)

<400> SEQUENCE: 270

gagttcctgt aagataccaa aaagg 25

<210> SEQ ID NO 271
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.003.2)

<400> SEQUENCE: 271

cctggagttc ctgtaagata ccaaa 25

<210> SEQ ID NO 272
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.004)

<400> SEQUENCE: 272

tcctggagtt cctgtaagat accaa 25

<210> SEQ ID NO 273
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.004.2)

<400> SEQUENCE: 273

gccatcctgg agttcctgta agata 25

<210> SEQ ID NO 274
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.005)

<400> SEQUENCE: 274

tgccatcctg gagttcctgt aagat 25

<210> SEQ ID NO 275
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.005.2)

<400> SEQUENCE: 275

ccaatgccat cctggagttc ctgta 25

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<210> SEQ ID NO 276
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.006)

<400> SEQUENCE: 276

cccaatgcca tcctggagtt cctgt 25

<210> SEQ ID NO 277
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.006.2)

<400> SEQUENCE: 277

gctgcccaat gccatcctgg agttc 25

<210> SEQ ID NO 278
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.007)

<400> SEQUENCE: 278

cgctgcccaa tgccatcctg gagtt 25

<210> SEQ ID NO 279
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.008)

<400> SEQUENCE: 279

aacagtttgc cgctgcccaa tgcca 25

<210> SEQ ID NO 280
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.008.2)

<400> SEQUENCE: 280

ctgacaacag tttgccgctg cccaa 25

<210> SEQ ID NO 281
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.009)

<400> SEQUENCE: 281

gttgcattca atgttctgac aacag 25

<210> SEQ ID NO 282
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.010)

<400> SEQUENCE: 282

gctgaattat ttcttcccca gttgc 25

<210> SEQ ID NO 283
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.010.2)

<400> SEQUENCE: 283

attatttctt ccccagttgc attca 25

<210> SEQ ID NO 284
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.011)

<400> SEQUENCE: 284

ggcatctgtt tttgaggatt gctga 25

<210> SEQ ID NO 285
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.011.2)

<400> SEQUENCE: 285

tttgaggatt gctgaattat ttctt 25

<210> SEQ ID NO 286
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.012)

<400> SEQUENCE: 286

aatttttcct gtagaatact ggcat 25

<210> SEQ ID NO 287
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.012.2)

<400> SEQUENCE: 287

atactggcat ctgtttttga ggatt 25

<210> SEQ ID NO 288
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.013)

<400> SEQUENCE: 288

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accgcagatt caggcttccc aattt 25

<210> SEQ ID NO 289
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.014)

<400> SEQUENCE: 289

ctgtttgcag acctcctgcc accgc 25

<210> SEQ ID NO 290
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.014.2)

<400> SEQUENCE: 290

agattcaggc ttcccaattt ttcct 25

<210> SEQ ID NO 291
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.015)

<400> SEQUENCE: 291

ctctttttc tgtctgacag ctgtt 25

<210> SEQ ID NO 292
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.015.2)

<400> SEQUENCE: 292

acctcctgcc accgcagatt caggc 25

<210> SEQ ID NO 293
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.016)

<400> SEQUENCE: 293

cctacctctt ttttctgtct gacag 25

<210> SEQ ID NO 294
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.016.2)

<400> SEQUENCE: 294

gacagctgtt tgcagacctc ctgcc 25

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<210> SEQ ID NO 295
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.017)

<400> SEQUENCE: 295

gtcgccctac ctctttttc tgtct 25

<210> SEQ ID NO 296
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.018)

<400> SEQUENCE: 296

gatctgtcgc cctacctctt ttttc 25

<210> SEQ ID NO 297
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.019)

<400> SEQUENCE: 297

tattagatct gtcgccctac ctctt 25

<210> SEQ ID NO 298
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.25.020)

<400> SEQUENCE: 298

attcctatta gatctgtcgc cctac 25

<210> SEQ ID NO 299
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.001)

<400> SEQUENCE: 299

agataccaaa aaggcaaaac 20

<210> SEQ ID NO 300
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.002)

<400> SEQUENCE: 300

aagataccaa aaaggcaaaa 20

<210> SEQ ID NO 301
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.003)

<400> SEQUENCE: 301

cctgtaagat accaaaaagg 20

<210> SEQ ID NO 302
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.004)

<400> SEQUENCE: 302

gagttcctgt aagataccaa 20

<210> SEQ ID NO 303
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.005)

<400> SEQUENCE: 303

tcctggagtt cctgtaagat 20

<210> SEQ ID NO 304
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.006)

<400> SEQUENCE: 304

tgccatcctg gagttcctgt 20

<210> SEQ ID NO 305
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.007)

<400> SEQUENCE: 305

cccaatgcca tcctggagtt 20

<210> SEQ ID NO 306
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.008)

<400> SEQUENCE: 306

cgctgcccaa tgccatcctg 20

<210> SEQ ID NO 307
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.009)

<400> SEQUENCE: 307

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ctgacaacag tttgccgctg 20

<210> SEQ ID NO 308
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.010)

<400> SEQUENCE: 308

gttgcattca atgttctgac 20

<210> SEQ ID NO 309
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.011)

<400> SEQUENCE: 309

attatttctt ccccagttgc 20

<210> SEQ ID NO 310
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.012)

<400> SEQUENCE: 310

tttgaggatt gctgaattat 20

<210> SEQ ID NO 311
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.013)

<400> SEQUENCE: 311

atactggcat ctgtttttga 20

<210> SEQ ID NO 312
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.014)

<400> SEQUENCE: 312

aatttttcct gtagaatact 20

<210> SEQ ID NO 313
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.015)

<400> SEQUENCE: 313

agattcaggc ttcccaattt 20

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<210> SEQ ID NO 314
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.016)

<400> SEQUENCE: 314

acctcctgcc accgcagatt 20

<210> SEQ ID NO 315
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.017)

<400> SEQUENCE: 315

gacagctgtt tgcagacctc 20

<210> SEQ ID NO 316
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.018)

<400> SEQUENCE: 316

ctctttttc tgtctgacag 20

<210> SEQ ID NO 317
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.019)

<400> SEQUENCE: 317

cctacctctt ttttctgtct 20

<210> SEQ ID NO 318
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.020)

<400> SEQUENCE: 318

gtcgccctac ctctttttc 20

<210> SEQ ID NO 319
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.021)

<400> SEQUENCE: 319

gatctgtcgc cctacctctt 20

<210> SEQ ID NO 320
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.022)

<400> SEQUENCE: 320

tattagatct gtcgccctac 20

<210> SEQ ID NO 321
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon45.20.023)

<400> SEQUENCE: 321

attcctatta gatctgtcgc 20

<210> SEQ ID NO 322
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.001)

<400> SEQUENCE: 322

gggggatttg agaaaataaa attac 25

<210> SEQ ID NO 323
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.002)

<400> SEQUENCE: 323

atttgagaaa ataaaattac cttga 25

<210> SEQ ID NO 324
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.002.2)

<400> SEQUENCE: 324

ctagcctgga gaaagaagaa taaaa 25

<210> SEQ ID NO 325
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.003)

<400> SEQUENCE: 325

agaaaataaa attaccttga cttgc 25

<210> SEQ ID NO 326
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.003.2)

<400> SEQUENCE: 326

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ttcttctagc ctggagaaag aagaa 25

<210> SEQ ID NO 327
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.004)

<400> SEQUENCE: 327

ataaaattac cttgacttgc tcaag 25

<210> SEQ ID NO 328
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.004.2)

<400> SEQUENCE: 328

ttttgttctt ctagcctgga gaaag 25

<210> SEQ ID NO 329
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.005)

<400> SEQUENCE: 329

attaccttga cttgctcaag ctttt 25

<210> SEQ ID NO 330
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.005.2)

<400> SEQUENCE: 330

tattcttttg ttcttctagc ctgga 25

<210> SEQ ID NO 331
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.006)

<400> SEQUENCE: 331

cttgacttgc tcaagctttt ctttt 25

<210> SEQ ID NO 332
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.006.2)

<400> SEQUENCE: 332

caagatattc ttttgttctt ctagc 25

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<210> SEQ ID NO 333
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.007)

<400> SEQUENCE: 333

cttttagttg ctgctctttt ccagg 25

<210> SEQ ID NO 334
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.008)

<400> SEQUENCE: 334

ccaggttcaa gtgggatact agcaa 25

<210> SEQ ID NO 335
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.008.2)

<400> SEQUENCE: 335

atctctttga aattctgaca agata 25

<210> SEQ ID NO 336
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.009)

<400> SEQUENCE: 336

agcaatgtta tctgcttcct ccaac 25

<210> SEQ ID NO 337
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.009.2)

<400> SEQUENCE: 337

aacaaattca tttaaatctc tttga 25

<210> SEQ ID NO 338
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.010)

<400> SEQUENCE: 338

ccaaccataa aacaaattca tttaa 25

<210> SEQ ID NO 339
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.010.2)

<400> SEQUENCE: 339

ttcctccaac cataaaacaa attca 25

<210> SEQ ID NO 340
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.011)

<400> SEQUENCE: 340

tttaaatctc tttgaaattc tgaca 25

<210> SEQ ID NO 341
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.012)

<400> SEQUENCE: 341

tgacaagata ttcttttgtt cttct 25

<210> SEQ ID NO 342
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.012.2)

<400> SEQUENCE: 342

ttcaagtggg atactagcaa tgtta 25

<210> SEQ ID NO 343
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.013)

<400> SEQUENCE: 343

agatattctt ttgttcttct agcct 25

<210> SEQ ID NO 344
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.013.2)

<400> SEQUENCE: 344

ctgctctttt ccaggttcaa gtggg 25

<210> SEQ ID NO 345
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.014)

<400> SEQUENCE: 345

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ttcttttgtt cttctagcct ggaga 25

<210> SEQ ID NO 346
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.014.2)

<400> SEQUENCE: 346

cttttctttt agttgctgct ctttt 25

<210> SEQ ID NO 347
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.015)

<400> SEQUENCE: 347

ttgttcttct agcctggaga aagaa 25

<210> SEQ ID NO 348
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.016)

<400> SEQUENCE: 348

cttctagcct ggagaaagaa gaata 25

<210> SEQ ID NO 349
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.017)

<400> SEQUENCE: 349

agcctggaga aagaagaata aaatt 25

<210> SEQ ID NO 350
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.25.018)

<400> SEQUENCE: 350

ctggagaaag aagaataaaa ttgtt 25

<210> SEQ ID NO 351
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.001)

<400> SEQUENCE: 351

gaaagaagaa taaaattgtt 20

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<210> SEQ ID NO 352
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.002)

<400> SEQUENCE: 352

ggagaaagaa gaataaaatt 20

<210> SEQ ID NO 353
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.003)

<400> SEQUENCE: 353

agcctggaga aagaagaata 20

<210> SEQ ID NO 354
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.004)

<400> SEQUENCE: 354

cttctagcct ggagaaagaa 20

<210> SEQ ID NO 355
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.005)

<400> SEQUENCE: 355

ttgttcttct agcctggaga 20

<210> SEQ ID NO 356
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.006)

<400> SEQUENCE: 356

ttcttttgtt cttctagcct 20

<210> SEQ ID NO 357
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.007)

<400> SEQUENCE: 357

tgacaagata ttcttttgtt 20

<210> SEQ ID NO 358
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.008)

<400> SEQUENCE: 358

atctctttga aattctgaca 20

<210> SEQ ID NO 359
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.009)

<400> SEQUENCE: 359

aacaaattca tttaaatctc 20

<210> SEQ ID NO 360
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.010)

<400> SEQUENCE: 360

ttcctccaac cataaaacaa 20

<210> SEQ ID NO 361
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.011)

<400> SEQUENCE: 361

agcaatgtta tctgcttcct 20

<210> SEQ ID NO 362
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.012)

<400> SEQUENCE: 362

ttcaagtggg atactagcaa 20

<210> SEQ ID NO 363
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.013)

<400> SEQUENCE: 363

ctgctctttt ccaggttcaa 20

<210> SEQ ID NO 364
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.014)

<400> SEQUENCE: 364

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cttttctttt agttgctgct 20

<210> SEQ ID NO 365
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.015)

<400> SEQUENCE: 365

cttgacttgc tcaagctttt 20

<210> SEQ ID NO 366
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.016)

<400> SEQUENCE: 366

attaccttga cttgctcaag 20

<210> SEQ ID NO 367
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.017)

<400> SEQUENCE: 367

ataaaattac cttgacttgc 20

<210> SEQ ID NO 368
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.018)

<400> SEQUENCE: 368

agaaaataaa attaccttga 20

<210> SEQ ID NO 369
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.019)

<400> SEQUENCE: 369

atttgagaaa ataaaattac 20

<210> SEQ ID NO 370
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon46.20.020)

<400> SEQUENCE: 370

gggggatttg agaaaataaa 20

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<210> SEQ ID NO 371
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.001)

<400> SEQUENCE: 371

ctgaaacaga caaatgcaac aacgt 25

<210> SEQ ID NO 372
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.002)

<400> SEQUENCE: 372

agtaactgaa acagacaaat gcaac 25

<210> SEQ ID NO 373
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.003)

<400> SEQUENCE: 373

ccaccagtaa ctgaaacaga caaat 25

<210> SEQ ID NO 374
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.004)

<400> SEQUENCE: 374

ctcttccacc agtaactgaa acaga 25

<210> SEQ ID NO 375
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.005)

<400> SEQUENCE: 375

ggcaactctt ccaccagtaa ctgaa 25

<210> SEQ ID NO 376
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.006)

<400> SEQUENCE: 376

gcaggggcaa ctcttccacc agtaa 25

<210> SEQ ID NO 377
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.007)

<400> SEQUENCE: 377

ctggcgcagg ggcaactctt ccacc 25

<210> SEQ ID NO 378
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.008)

<400> SEQUENCE: 378

tttaattgtt tgagaattcc ctggc 25

<210> SEQ ID NO 379
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.008.2)

<400> SEQUENCE: 379

ttgtttgaga attccctggc gcagg 25

<210> SEQ ID NO 380
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.009)

<400> SEQUENCE: 380

gcacgggtcc tccagtttca tttaa 25

<210> SEQ ID NO 381
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.009.2)

<400> SEQUENCE: 381

tccagtttca tttaattgtt tgaga 25

<210> SEQ ID NO 382
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.010)

<400> SEQUENCE: 382

gcttatggga gcacttacaa gcacg 25

<210> SEQ ID NO 383
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.010.2)

<400> SEQUENCE: 383

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tacaagcacg ggtcctccag tttca 25

<210> SEQ ID NO 384
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.011)

<400> SEQUENCE: 384

agtttatctt gctcttctgg gctta 25

<210> SEQ ID NO 385
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.012)

<400> SEQUENCE: 385

tctgcttgag cttattttca agttt 25

<210> SEQ ID NO 386
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.012.2)

<400> SEQUENCE: 386

atcttgctct tctgggctta tggga 25

<210> SEQ ID NO 387
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.013)

<400> SEQUENCE: 387

ctttatccac tggagatttg tctgc 25

<210> SEQ ID NO 388
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.013.2)

<400> SEQUENCE: 388

cttattttca agtttatctt gctct 25

<210> SEQ ID NO 389
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.014)

<400> SEQUENCE: 389

ctaacctta tccactggag atttg 25

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<210> SEQ ID NO 390
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.014.2)

<400> SEQUENCE: 390

atttgtctgc ttgagcttat tttca 25

<210> SEQ ID NO 391
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.015)

<400> SEQUENCE: 391

aatgtctaac ctttatccac tggag 25

<210> SEQ ID NO 392
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.016)

<400> SEQUENCE: 392

tggttaatgt ctaaccttta tccac 25

<210> SEQ ID NO 393
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.017)

<400> SEQUENCE: 393

agagatggtt aatgtctaac cttta 25

<210> SEQ ID NO 394
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.25.018)

<400> SEQUENCE: 394

acggaagaga tggttaatgt ctaac 25

<210> SEQ ID NO 395
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.001)

<400> SEQUENCE: 395

acagacaaat gcaacaacgt 20

<210> SEQ ID NO 396
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.002)

<400> SEQUENCE: 396

ctgaaacaga caaatgcaac 20

<210> SEQ ID NO 397
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.003)

<400> SEQUENCE: 397

agtaactgaa acagacaaat 20

<210> SEQ ID NO 398
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.004)

<400> SEQUENCE: 398

ccaccagtaa ctgaaacaga 20

<210> SEQ ID NO 399
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.005)

<400> SEQUENCE: 399

ctcttccacc agtaactgaa 20

<210> SEQ ID NO 400
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.006)

<400> SEQUENCE: 400

ggcaactctt ccaccagtaa 20

<210> SEQ ID NO 401
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.007)

<400> SEQUENCE: 401

ctggcgcagg ggcaactctt 20

<210> SEQ ID NO 402
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.008)

<400> SEQUENCE: 402

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ttgtttgaga attccctggc 20

<210> SEQ ID NO 403
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.009)

<400> SEQUENCE: 403

tccagtttca tttaattgtt 20

<210> SEQ ID NO 404
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.010)

<400> SEQUENCE: 404

tacaagcacg ggtcctccag 20

<210> SEQ ID NO 405
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.011)

<400> SEQUENCE: 405

gcttatggga gcacttacaa 20

<210> SEQ ID NO 406
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.012)

<400> SEQUENCE: 406

atcttgctct tctgggctta 20

<210> SEQ ID NO 407
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.013)

<400> SEQUENCE: 407

cttattttca agtttatctt 20

<210> SEQ ID NO 408
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.014)

<400> SEQUENCE: 408

atttgtctgc ttgagcttat 20

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<210> SEQ ID NO 409
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.015)

<400> SEQUENCE: 409

ctttatccac tggagatttg 20

<210> SEQ ID NO 410
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.016)

<400> SEQUENCE: 410

ctaaccttta tccactggag 20

<210> SEQ ID NO 411
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.017)

<400> SEQUENCE: 411

aatgtctaac ctttatccac 20

<210> SEQ ID NO 412
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.018)

<400> SEQUENCE: 412

tggttaatgt ctaaccttta 20

<210> SEQ ID NO 413
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.019)

<400> SEQUENCE: 413

agagatggtt aatgtctaac 20

<210> SEQ ID NO 414
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon47.20.020)

<400> SEQUENCE: 414

acggaagaga tggttaatgt 20

<210> SEQ ID NO 415
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.001)

<400> SEQUENCE: 415

ctgaaaggaa aatacatttt aaaaa 25

<210> SEQ ID NO 416
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.002)

<400> SEQUENCE: 416

cctgaaagga aaatacattt taaaa 25

<210> SEQ ID NO 417
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.002.2)

<400> SEQUENCE: 417

gaaacctgaa aggaaaatac atttt 25

<210> SEQ ID NO 418
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.003)

<400> SEQUENCE: 418

ggaaacctga aaggaaaata cattt 25

<210> SEQ ID NO 419
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.003.2)

<400> SEQUENCE: 419

ctctggaaac ctgaaaggaa aatac 25

<210> SEQ ID NO 420
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.004)

<400> SEQUENCE: 420

gctctggaaa cctgaaagga aaata 25

<210> SEQ ID NO 421
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.004.2)

<400> SEQUENCE: 421

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taaagctctg gaaacctgaa aggaa 25

<210> SEQ ID NO 422
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.005)

<400> SEQUENCE: 422

gtaaagctct ggaaacctga aagga 25

<210> SEQ ID NO 423
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.005.2)

<400> SEQUENCE: 423

tcaggtaaag ctctggaaac ctgaa 25

<210> SEQ ID NO 424
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.006)

<400> SEQUENCE: 424

ctcaggtaaa gctctggaaa cctga 25

<210> SEQ ID NO 425
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.006.2)

<400> SEQUENCE: 425

gtttctcagg taaagctctg gaaac 25

<210> SEQ ID NO 426
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.007)

<400> SEQUENCE: 426

tgtttctcag gtaaagctct ggaaa 25

<210> SEQ ID NO 427
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.007.2)

<400> SEQUENCE: 427

aatttctcct tgtttctcag gtaaa 25

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<210> SEQ ID NO 428
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.008)

<400> SEQUENCE: 428

tttgagcttc aatttctcct tgttt 25

<210> SEQ ID NO 429
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.008)

<400> SEQUENCE: 429

ttttatttga gcttcaattt ctcct 25

<210> SEQ ID NO 430
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.009)

<400> SEQUENCE: 430

aagctgccca aggtctttta tttga 25

<210> SEQ ID NO 431
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.010)

<400> SEQUENCE: 431

aggtcttcaa gctttttttc aagct 25

<210> SEQ ID NO 432
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.010.2)

<400> SEQUENCE: 432

ttcaagcttt ttttcaagct gccca 25

<210> SEQ ID NO 433
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.011)

<400> SEQUENCE: 433

gatgatttaa ctgctcttca aggtc 25

<210> SEQ ID NO 434
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.011.2)

<400> SEQUENCE: 434

ctgctcttca aggtcttcaa gcttt 25

<210> SEQ ID NO 435
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.012)

<400> SEQUENCE: 435

aggagataac cacagcagca gatga 25

<210> SEQ ID NO 436
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.012.2)

<400> SEQUENCE: 436

cagcagatga tttaactgct cttca 25

<210> SEQ ID NO 437
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.013)

<400> SEQUENCE: 437

atttccaact gattcctaat aggag 25

<210> SEQ ID NO 438
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.014)

<400> SEQUENCE: 438

cttggtttgg ttggttataa atttc 25

<210> SEQ ID NO 439
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.014.2)

<400> SEQUENCE: 439

caactgattc ctaataggag ataac 25

<210> SEQ ID NO 440
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.015)

<400> SEQUENCE: 440

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cttaacgtca aatggtcctt cttgg 25

<210> SEQ ID NO 441
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.015.2)

<400> SEQUENCE: 441

ttggttataa atttccaact gattc 25

<210> SEQ ID NO 442
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.016)

<400> SEQUENCE: 442

cctaccttaa cgtcaaatgg tcctt 25

<210> SEQ ID NO 443
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.016.2)

<400> SEQUENCE: 443

tccttcttgg tttggttggt tataa 25

<210> SEQ ID NO 444
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.017)

<400> SEQUENCE: 444

agttccctac cttaacgtca aatgg 25

<210> SEQ ID NO 445
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.018)

<400> SEQUENCE: 445

caaaaagttc cctaccttaa cgtca 25

<210> SEQ ID NO 446
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.019)

<400> SEQUENCE: 446

taaagcaaaa agttccctac cttaa 25

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<210> SEQ ID NO 447
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.25.020)

<400> SEQUENCE: 447

atatttaaag caaaaagttc cctac 25

<210> SEQ ID NO 448
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.001)

<400> SEQUENCE: 448

aggaaaatac attttaaaaa 20

<210> SEQ ID NO 449
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.002)

<400> SEQUENCE: 449

aaggaaaata cattttaaaa 20

<210> SEQ ID NO 450
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.003)

<400> SEQUENCE: 450

cctgaaagga aaatacattt 20

<210> SEQ ID NO 451
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.004)

<400> SEQUENCE: 451

ggaaacctga aaggaaaata 20

<210> SEQ ID NO 452
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.005)

<400> SEQUENCE: 452

gctctggaaa cctgaaagga 20

<210> SEQ ID NO 453
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.006)

<400> SEQUENCE: 453

gtaaagctct ggaaacctga 20

<210> SEQ ID NO 454
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.007)

<400> SEQUENCE: 454

ctcaggtaaa gctctggaaa 20

<210> SEQ ID NO 455
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.008)

<400> SEQUENCE: 455

aatttctcct tgtttctcag 20

<210> SEQ ID NO 456
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.009)

<400> SEQUENCE: 456

ttttatttga gcttcaattt 20

<210> SEQ ID NO 457
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.010)

<400> SEQUENCE: 457

aagctgccca aggtctttta 20

<210> SEQ ID NO 458
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.011)

<400> SEQUENCE: 458

ttcaagcttt ttttcaagct 20

<210> SEQ ID NO 459
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.012)

<400> SEQUENCE: 459

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ctgctcttca aggtcttcaa 20

<210> SEQ ID NO 460
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.013)

<400> SEQUENCE: 460

cagcagatga tttaactgct 20

<210> SEQ ID NO 461
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.014)

<400> SEQUENCE: 461

aggagataac cacagcagca 20

<210> SEQ ID NO 462
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.015)

<400> SEQUENCE: 462

caactgattc ctaataggag 20

<210> SEQ ID NO 463
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.016)

<400> SEQUENCE: 463

ttggttataa atttccaact 20

<210> SEQ ID NO 464
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.017)

<400> SEQUENCE: 464

tccttcttgg tttggttggt 20

<210> SEQ ID NO 465
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.018)

<400> SEQUENCE: 465

cttaacgtca aatggtcctt 20

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<210> SEQ ID NO 466
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.019)

<400> SEQUENCE: 466

cctaccttaa cgtcaaatgg 20

<210> SEQ ID NO 467
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.020)

<400> SEQUENCE: 467

agttccctac cttaacgtca 20

<210> SEQ ID NO 468
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.021)

<400> SEQUENCE: 468

caaaaagttc cctaccttaa 20

<210> SEQ ID NO 469
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.022)

<400> SEQUENCE: 469

taaagcaaaa agttccctac 20

<210> SEQ ID NO 470
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon48.20.023)

<400> SEQUENCE: 470

atatttaaag caaaaagttc 20

<210> SEQ ID NO 471
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.001)

<400> SEQUENCE: 471

ctggggaaaa gaacccatat agtgc 25

<210> SEQ ID NO 472
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.002)

<400> SEQUENCE: 472

tcctggggaa aagaacccat atagt 25

<210> SEQ ID NO 473
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.002.2)

<400> SEQUENCE: 473

gtttcctggg gaaaagaacc catat 25

<210> SEQ ID NO 474
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.003)

<400> SEQUENCE: 474

cagtttcctg gggaaaagaa cccat 25

<210> SEQ ID NO 475
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.003.2)

<400> SEQUENCE: 475

tttcagtttc ctggggaaaa gaacc 25

<210> SEQ ID NO 476
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.004)

<400> SEQUENCE: 476

tatttcagtt tcctggggaa aagaa 25

<210> SEQ ID NO 477
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.004.2)

<400> SEQUENCE: 477

tgctatttca gtttcctggg gaaaa 25

<210> SEQ ID NO 478
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.005)

<400> SEQUENCE: 478

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actgctattt cagtttcctg gggaa 25

<210> SEQ ID NO 479
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.005.2)

<400> SEQUENCE: 479

tgaactgcta tttcagtttc ctggg 25

<210> SEQ ID NO 480
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.006)

<400> SEQUENCE: 480

cttgaactgc tatttcagtt tcctg 25

<210> SEQ ID NO 481
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.006.2)

<400> SEQUENCE: 481

tagcttgaac tgctatttca gtttc 25

<210> SEQ ID NO 482
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.007)

<400> SEQUENCE: 482

tttagcttga actgctattt cagtt 25

<210> SEQ ID NO 483
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.008)

<400> SEQUENCE: 483

ttccacatcc ggttgtttag cttga 25

<210> SEQ ID NO 484
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.009)

<400> SEQUENCE: 484

tgcccttag acaaaatctc ttcca 25

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<210> SEQ ID NO 485
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.009.2)

<400> SEQUENCE: 485

tttagacaaa atctcttcca catcc 25

<210> SEQ ID NO 486
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.010)

<400> SEQUENCE: 486

gtttttcctt gtacaaatgc tgccc 25

<210> SEQ ID NO 487
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.010.2)

<400> SEQUENCE: 487

gtacaaatgc tgcccttag acaaa 25

<210> SEQ ID NO 488
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.011)

<400> SEQUENCE: 488

cttcactggc tgagtggctg gtttt 25

<210> SEQ ID NO 489
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.011.2)

<400> SEQUENCE: 489

ggctggtttt tccttgtaca aatgc 25

<210> SEQ ID NO 490
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.012)

<400> SEQUENCE: 490

attaccttca ctggctgagt ggctg 25

<210> SEQ ID NO 491
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.013)

<400> SEQUENCE: 491

gcttcattac cttcactggc tgagt 25

<210> SEQ ID NO 492
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.014)

<400> SEQUENCE: 492

aggttgcttc attaccttca ctggc 25

<210> SEQ ID NO 493
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.015)

<400> SEQUENCE: 493

gctagaggtt gcttcattac cttca 25

<210> SEQ ID NO 494
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.25.016)

<400> SEQUENCE: 494

atattgctag aggttgcttc attac 25

<210> SEQ ID NO 495
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.001)

<400> SEQUENCE: 495

gaaaagaacc catatagtgc 20

<210> SEQ ID NO 496
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.002)

<400> SEQUENCE: 496

gggaaaagaa cccatatagt 20

<210> SEQ ID NO 497
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.003)

<400> SEQUENCE: 497

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tcctggggaa aagaacccat 20

<210> SEQ ID NO 498
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.004)

<400> SEQUENCE: 498

cagtttcctg gggaaaagaa 20

<210> SEQ ID NO 499
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.005)

<400> SEQUENCE: 499

tatttcagtt tcctggggaa 20

<210> SEQ ID NO 500
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.006)

<400> SEQUENCE: 500

actgctattt cagtttcctg 20

<210> SEQ ID NO 501
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.007)

<400> SEQUENCE: 501

cttgaactgc tatttcagtt 20

<210> SEQ ID NO 502
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.008)

<400> SEQUENCE: 502

tttagcttga actgctattt 20

<210> SEQ ID NO 503
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.009)

<400> SEQUENCE: 503

ttccacatcc ggttgtttag 20

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<210> SEQ ID NO 504
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.010)

<400> SEQUENCE: 504

tttagacaaa atctcttcca 20

<210> SEQ ID NO 505
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.011)

<400> SEQUENCE: 505

gtacaaatgc tgccctttag 20

<210> SEQ ID NO 506
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.012)

<400> SEQUENCE: 506

ggctggtttt tccttgtaca 20

<210> SEQ ID NO 507
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.013)

<400> SEQUENCE: 507

cttcactggc tgagtggctg 20

<210> SEQ ID NO 508
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.014)

<400> SEQUENCE: 508

attaccttca ctggctgagt 20

<210> SEQ ID NO 509
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.015)

<400> SEQUENCE: 509

gcttcattac cttcactggc 20

<210> SEQ ID NO 510
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.016)

<400> SEQUENCE: 510

aggttgcttc attaccttca 20

<210> SEQ ID NO 511
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.017)

<400> SEQUENCE: 511

gctagaggtt gcttcattac 20

<210> SEQ ID NO 512
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon49.20.018)

<400> SEQUENCE: 512

atattgctag aggttgcttc 20

<210> SEQ ID NO 513
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.001)

<400> SEQUENCE: 513

ctttaacaga aaagcataca catta 25

<210> SEQ ID NO 514
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.002)

<400> SEQUENCE: 514

tcctctttaa cagaaaagca tacac 25

<210> SEQ ID NO 515
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.002.2)

<400> SEQUENCE: 515

ttcctctttа acagaaaagc ataca 25

<210> SEQ ID NO 516
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.003)

<400> SEQUENCE: 516

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taacttcctc tttaacagaa aagca 25

<210> SEQ ID NO 517
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.003.2)

<400> SEQUENCE: 517

ctaacttcct ctttaacaga aaagc 25

<210> SEQ ID NO 518
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.004)

<400> SEQUENCE: 518

tcttctaact tcctctttaa cagaa 25

<210> SEQ ID NO 519
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.004.2)

<400> SEQUENCE: 519

atcttctaac ttcctcttta acaga 25

<210> SEQ ID NO 520
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.005)

<400> SEQUENCE: 520

tcagatcttc taacttcctc tttaa 25

<210> SEQ ID NO 521
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.005.2)

<400> SEQUENCE: 521

ctcagatctt ctaacttcct cttta 25

<210> SEQ ID NO 522
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.006)

<400> SEQUENCE: 522

agagctcaga tcttctaact tcctc 25

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<210> SEQ ID NO 523
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.006.2 NG-08-0731)

<400> SEQUENCE: 523

cagagctcag atcttctaac ttcct 25

<210> SEQ ID NO 524
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.007)

<400> SEQUENCE: 524

cactcagagc tcagatcttc tact 24

<210> SEQ ID NO 525
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.007.2)

<400> SEQUENCE: 525

ccttccactc agagctcaga tcttc 25

<210> SEQ ID NO 526
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.008)

<400> SEQUENCE: 526

gtaaacggtt taccgccttc cactc 25

<210> SEQ ID NO 527
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.009)

<400> SEQUENCE: 527

ctttgccctc agctcttgaa gtaaa 25

<210> SEQ ID NO 528
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.009.2)

<400> SEQUENCE: 528

ccctcagctc ttgaagtaaa cggtt 25

<210> SEQ ID NO 529
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.010)

<400> SEQUENCE: 529

ccaggagcta ggtcaggctg ctttg 25

<210> SEQ ID NO 530
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.010.2)

<400> SEQUENCE: 530

ggtcaggctg ctttgccctc agctc 25

<210> SEQ ID NO 531
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.011)

<400> SEQUENCE: 531

aggctccaat agtggtcagt ccagg 25

<210> SEQ ID NO 532
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.011.2)

<400> SEQUENCE: 532

tcagtccagg agctaggtca ggctg 25

<210> SEQ ID NO 533
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.012 AVI-5038)

<400> SEQUENCE: 533

cttacaggct ccaatagtgg tcagt 25

<210> SEQ ID NO 534
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.013)

<400> SEQUENCE: 534

gtatacttac aggctccaat agtgg 25

<210> SEQ ID NO 535
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.014)

<400> SEQUENCE: 535

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atccagtata cttacaggct ccaat 25

<210> SEQ ID NO 536
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.015 NG-08-0741)

<400> SEQUENCE: 536

atgggatcca gtatacttac aggct 25

<210> SEQ ID NO 537
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.25.016 NG-08-0742)

<400> SEQUENCE: 537

agagaatggg atccagtata cttac 25

<210> SEQ ID NO 538
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.20.001)

<400> SEQUENCE: 538

acagaaaagc atacacatta 20

<210> SEQ ID NO 539
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.20.002)

<400> SEQUENCE: 539

tttaacagaa aagcatacac 20

<210> SEQ ID NO 540
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.20.003)

<400> SEQUENCE: 540

tcctctttaa cagaaaagca 20

<210> SEQ ID NO 541
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.20.004)

<400> SEQUENCE: 541

taacttcctc tttaacagaa 20

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<210> SEQ ID NO 542
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.20.005)

<400> SEQUENCE: 542

tcttctaact tcctctttaa 20

<210> SEQ ID NO 543
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.20.006)

<400> SEQUENCE: 543

tcagatcttc taacttcctc 20

<210> SEQ ID NO 544
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.20.007)

<400> SEQUENCE: 544

ccttccactc agagctcaga 20

<210> SEQ ID NO 545
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.20.008)

<400> SEQUENCE: 545

gtaaacggtt taccgccttc 20

<210> SEQ ID NO 546
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.20.009)

<400> SEQUENCE: 546

ccctcagctc ttgaagtaaa 20

<210> SEQ ID NO 547
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.20.010)

<400> SEQUENCE: 547

ggtcaggctg ctttgccctc 20

<210> SEQ ID NO 548
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.20.011)

<400> SEQUENCE: 548

tcagtccagg agctaggtca 20

<210> SEQ ID NO 549
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.20.012)

<400> SEQUENCE: 549

aggctccaat agtggtcagt 20

<210> SEQ ID NO 550
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.20.013)

<400> SEQUENCE: 550

cttacaggct ccaatagtgg 20

<210> SEQ ID NO 551
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.20.014)

<400> SEQUENCE: 551

gtatacttac aggctccaat 20

<210> SEQ ID NO 552
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.20.015)

<400> SEQUENCE: 552

atccagtata cttacaggct 20

<210> SEQ ID NO 553
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.20.016)

<400> SEQUENCE: 553

atgggatcca gtatacttac 20

<210> SEQ ID NO 554
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon50.20.017)

<400> SEQUENCE: 554

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agagaatggg atccagtata 20

<210> SEQ ID NO 555
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.001-44)

<400> SEQUENCE: 555

ctaaaatatt ttgggttttt gcaaaa 26

<210> SEQ ID NO 556
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.002-45)

<400> SEQUENCE: 556

gctaaaatat tttgggtttt tgcaaa 26

<210> SEQ ID NO 557
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.002.2-46)

<400> SEQUENCE: 557

taggagctaa aatattttgg gttttt 26

<210> SEQ ID NO 558
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.003)

<400> SEQUENCE: 558

agtaggagct aaaatatttt gggtt 25

<210> SEQ ID NO 559
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.003.2)

<400> SEQUENCE: 559

tgagtaggag ctaaaatatt ttggg 25

<210> SEQ ID NO 560
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.004)

<400> SEQUENCE: 560

ctgagtagga gctaaaatat tttggg 26

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<210> SEQ ID NO 561
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.004.2)

<400> SEQUENCE: 561

cagtctgagt aggagctaaa atatt 25

<210> SEQ ID NO 562
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.005)

<400> SEQUENCE: 562

acagtctgag taggagctaa aatatt 26

<210> SEQ ID NO 563
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.005.2)

<400> SEQUENCE: 563

gagtaacagt ctgagtagga gctaaa 26

<210> SEQ ID NO 564
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.006)

<400> SEQUENCE: 564

cagagtaaca gtctgagtag gagct 25

<210> SEQ ID NO 565
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.006.2)

<400> SEQUENCE: 565

caccagagta acagtctgag taggag 26

<210> SEQ ID NO 566
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.007)

<400> SEQUENCE: 566

gtcaccagag taacagtctg agtag 25

<210> SEQ ID NO 567
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.007.2)

<400> SEQUENCE: 567

aaccacaggt tgtgtcacca gagtaa 26

<210> SEQ ID NO 568
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.008)

<400> SEQUENCE: 568

gttgtgtcac cagagtaaca gtctg 25

<210> SEQ ID NO 569
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.009)

<400> SEQUENCE: 569

tggcagtttc cttagtaacc acaggt 26

<210> SEQ ID NO 570
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.010)

<400> SEQUENCE: 570

atttctagtt tggagatggc agtttc 26

<210> SEQ ID NO 571
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.010.2)

<400> SEQUENCE: 571

ggaagatggc atttctagtt tggag 25

<210> SEQ ID NO 572
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.011)

<400> SEQUENCE: 572

catcaaggaa gatggcattt ctagtt 26

<210> SEQ ID NO 573
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.011.2)

<400> SEQUENCE: 573

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gagcaggtac ctccaacatc aaggaa 26

<210> SEQ ID NO 574
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.012)

<400> SEQUENCE: 574

atctgccaga gcaggtacct ccaac 25

<210> SEQ ID NO 575
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.013)

<400> SEQUENCE: 575

aagttctgtc caagcccggt tgaaat 26

<210> SEQ ID NO 576
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.013.2)

<400> SEQUENCE: 576

cggttgaaat ctgccagagc aggtac 26

<210> SEQ ID NO 577
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.014)

<400> SEQUENCE: 577

gagaaagcca gtcggtaagt tctgtc 26

<210> SEQ ID NO 578
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.014.2)

<400> SEQUENCE: 578

gtcggtaagt tctgtccaag cccgg 25

<210> SEQ ID NO 579
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.015)

<400> SEQUENCE: 579

ataacttgat caagcagaga aagcca 26

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<210> SEQ ID NO 580
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.015.2)

<400> SEQUENCE: 580

aagcagagaa agccagtcgg taagt 25

<210> SEQ ID NO 581
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.016)

<400> SEQUENCE: 581

caccctctgt gattttataa cttgat 26

<210> SEQ ID NO 582
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.017)

<400> SEQUENCE: 582

caaggtcacc caccatcacc ctctgt 26

<210> SEQ ID NO 583
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.017.2)

<400> SEQUENCE: 583

catcaccctc tgtgatttta taact 25

<210> SEQ ID NO 584
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.018)

<400> SEQUENCE: 584

cttctgcttg atgatcatct cgttga 26

<210> SEQ ID NO 585
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.019)

<400> SEQUENCE: 585

ccttctgctt gatgatcatc tcgttg 26

<210> SEQ ID NO 586
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.019.2)

<400> SEQUENCE: 586

atctcgttga tatcctcaag gtcacc 26

<210> SEQ ID NO 587
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.020)

<400> SEQUENCE: 587

tcataccttc tgcttgatga tcatct 26

<210> SEQ ID NO 588
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.020.2)

<400> SEQUENCE: 588

tcatttttc tcataccttc tgcttg 26

<210> SEQ ID NO 589
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.021)

<400> SEQUENCE: 589

ttttctcata ccttctgctt gatgat 26

<210> SEQ ID NO 590
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.022)

<400> SEQUENCE: 590

ttttatcatt ttttctcata ccttct 26

<210> SEQ ID NO 591
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.25.023)

<400> SEQUENCE: 591

ccaacttta tcatttttc tcatac 26

<210> SEQ ID NO 592
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.001)

<400> SEQUENCE: 592

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atattttggg tttttgcaaa 20

<210> SEQ ID NO 593
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.002)

<400> SEQUENCE: 593

aaaatatttt gggtttttgc 20

<210> SEQ ID NO 594
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.003)

<400> SEQUENCE: 594

gagctaaaat attttgggtt 20

<210> SEQ ID NO 595
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.004)

<400> SEQUENCE: 595

agtaggagct aaaatatttt 20

<210> SEQ ID NO 596
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.005)

<400> SEQUENCE: 596

gtctgagtag gagctaaaat 20

<210> SEQ ID NO 597
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.006)

<400> SEQUENCE: 597

taacagtctg agtaggagct 20

<210> SEQ ID NO 598
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.007)

<400> SEQUENCE: 598

cagagtaaca gtctgagtag 20

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<210> SEQ ID NO 599
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.008)

<400> SEQUENCE: 599

cacaggttgt gtcaccagag 20

<210> SEQ ID NO 600
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.009)

<400> SEQUENCE: 600

agtttcctta gtaaccacag 20

<210> SEQ ID NO 601
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.010)

<400> SEQUENCE: 601

tagtttggag atggcagttt 20

<210> SEQ ID NO 602
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.011)

<400> SEQUENCE: 602

ggaagatggc atttctagtt 20

<210> SEQ ID NO 603
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.012)

<400> SEQUENCE: 603

tacctccaac atcaaggaag 20

<210> SEQ ID NO 604
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.013)

<400> SEQUENCE: 604

atctgccaga gcaggtacct 20

<210> SEQ ID NO 605
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.014)

<400> SEQUENCE: 605

ccaagcccgg ttgaaatctg 20

<210> SEQ ID NO 606
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.015)

<400> SEQUENCE: 606

gtcggtaagt tctgtccaag 20

<210> SEQ ID NO 607
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.016)

<400> SEQUENCE: 607

aagcagagaa agccagtcgg 20

<210> SEQ ID NO 608
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.017)

<400> SEQUENCE: 608

ttttataact tgatcaagca 20

<210> SEQ ID NO 609
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.018)

<400> SEQUENCE: 609

catcaccctc tgtgatttta 20

<210> SEQ ID NO 610
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.019)

<400> SEQUENCE: 610

ctcaaggtca cccaccatca 20

<210> SEQ ID NO 611
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.020)

<400> SEQUENCE: 611

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catctcgttg atatcctcaa 20

<210> SEQ ID NO 612
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.021)

<400> SEQUENCE: 612

cttctgcttg atgatcatct 20

<210> SEQ ID NO 613
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.022)

<400> SEQUENCE: 613

cataccttct gcttgatgat 20

<210> SEQ ID NO 614
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.023)

<400> SEQUENCE: 614

tttctcatac cttctgcttg 20

<210> SEQ ID NO 615
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.024)

<400> SEQUENCE: 615

catttttct cataccttct 20

<210> SEQ ID NO 616
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.025)

<400> SEQUENCE: 616

tttatcattt tttctcatac 20

<210> SEQ ID NO 617
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon51.20.026)

<400> SEQUENCE: 617

caacttttat catttttct 20

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<210> SEQ ID NO 618
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.001)

<400> SEQUENCE: 618

ctgtaagaac aaatatccct tagta 25

<210> SEQ ID NO 619
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.002)

<400> SEQUENCE: 619

tgcctgtaag aacaaatatc cctta 25

<210> SEQ ID NO 620
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.002.2)

<400> SEQUENCE: 620

gttgcctgta agaacaaata tccct 25

<210> SEQ ID NO 621
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.003)

<400> SEQUENCE: 621

attgttgcct gtaagaacaa atatc 25

<210> SEQ ID NO 622
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.003.2)

<400> SEQUENCE: 622

gcattgttgc ctgtaagaac aaata 25

<210> SEQ ID NO 623
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.004)

<400> SEQUENCE: 623

cctgcattgt tgcctgtaag aacaa 25

<210> SEQ ID NO 624
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.004.2)

<400> SEQUENCE: 624

atcctgcatt gttgcctgta agaac 25

<210> SEQ ID NO 625
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.005)

<400> SEQUENCE: 625

caaatcctgc attgttgcct gtaag 25

<210> SEQ ID NO 626
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.005.2)

<400> SEQUENCE: 626

tccaaatcct gcattgttgc ctgta 25

<210> SEQ ID NO 627
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.006)

<400> SEQUENCE: 627

tgttccaaat cctgcattgt tgcct 25

<210> SEQ ID NO 628
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.006.2)

<400> SEQUENCE: 628

tctgttccaa atcctgcatt gttgc 25

<210> SEQ ID NO 629
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.007)

<400> SEQUENCE: 629

aactggggac gcctctgttc caaat 25

<210> SEQ ID NO 630
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.007.2)

<400> SEQUENCE: 630

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gcctctgttc caaatcctgc attgt 25

<210> SEQ ID NO 631
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.008)

<400> SEQUENCE: 631

cagcggtaat gagttcttcc aactg 25

<210> SEQ ID NO 632
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.008.2)

<400> SEQUENCE: 632

cttccaactg gggacgcctc tgttc 25

<210> SEQ ID NO 633
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.009)

<400> SEQUENCE: 633

cttgtttttc aaattttggg cagcg 25

<210> SEQ ID NO 634
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.010)

<400> SEQUENCE: 634

ctagcctctt gattgctggt cttgt 25

<210> SEQ ID NO 635
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.010.2)

<400> SEQUENCE: 635

ttttcaaatt ttgggcagcg gtaat 25

<210> SEQ ID NO 636
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.011)

<400> SEQUENCE: 636

ttcgatccgt aatgattgtt ctagc 25

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<210> SEQ ID NO 637
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.011.2)

<400> SEQUENCE: 637

gattgctggt cttgtttttc aaatt 25

<210> SEQ ID NO 638
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 638

cttacttcga tccgtaatga ttgtt 25

<210> SEQ ID NO 639
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.012.2)

<400> SEQUENCE: 639

ttgttctagc ctcttgattg ctggt 25

<210> SEQ ID NO 640
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.013)

<400> SEQUENCE: 640

aaaaacttac ttcgatccgt aatga 25

<210> SEQ ID NO 641
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.014)

<400> SEQUENCE: 641

tgttaaaaaa cttacttcga tccgt 25

<210> SEQ ID NO 642
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.015)

<400> SEQUENCE: 642

atgcttgtta aaaaacttac ttcga 25

<210> SEQ ID NO 643
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.25.016)

<400> SEQUENCE: 643

gtcccatgct tgttaaaaaa cttac 25

<210> SEQ ID NO 644
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.001)

<400> SEQUENCE: 644

agaacaaata tcccttagta 20

<210> SEQ ID NO 645
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.002)

<400> SEQUENCE: 645

gtaagaacaa atatcccttа 20

<210> SEQ ID NO 646
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.003)

<400> SEQUENCE: 646

tgcctgtaag aacaaatatc 20

<210> SEQ ID NO 647
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.004)

<400> SEQUENCE: 647

attgttgcct gtaagaacaa 20

<210> SEQ ID NO 648
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.005)

<400> SEQUENCE: 648

cctgcattgt tgcctgtaag 20

<210> SEQ ID NO 649
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.006)

<400> SEQUENCE: 649

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caaatcctgc attgttgcct 20

<210> SEQ ID NO 650
<211> LENGTH: 20
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.007)

<400> SEQUENCE: 650

gcctctgttc caaatcctgc 20

<210> SEQ ID NO 651
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.008)

<400> SEQUENCE: 651

cttccaactg gggacgcctc 20

<210> SEQ ID NO 652
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.009)

<400> SEQUENCE: 652

cagcggtaat gagttcttcc 20

<210> SEQ ID NO 653
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.010)

<400> SEQUENCE: 653

ttttcaaatt ttgggcagcg 20

<210> SEQ ID NO 654
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.011)

<400> SEQUENCE: 654

gattgctggt cttgtttttc 20

<210> SEQ ID NO 655
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.012)

<400> SEQUENCE: 655

ttgttctagc ctcttgattg 20

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<210> SEQ ID NO 656
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.013)

<400> SEQUENCE: 656

ttcgatccgt aatgattgtt 20

<210> SEQ ID NO 657
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.014)

<400> SEQUENCE: 657

cttacttcga tccgtaatga 20

<210> SEQ ID NO 658
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.015)

<400> SEQUENCE: 658

aaaaacttac ttcgatccgt 20

<210> SEQ ID NO 659
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.016)

<400> SEQUENCE: 659

tgttaaaaaa cttacttcga 20

<210> SEQ ID NO 660
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.017)

<400> SEQUENCE: 660

atgcttgtta aaaaacttac 20

<210> SEQ ID NO 661
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon52.20.018)

<400> SEQUENCE: 661

gtcccatgct tgttaaaaaa 20

<210> SEQ ID NO 662
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.001)

<400> SEQUENCE: 662

ctagaataaa aggaaaaata aatat 25

<210> SEQ ID NO 663
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.002)

<400> SEQUENCE: 663

aactagaata aaaggaaaaa taaat 25

<210> SEQ ID NO 664
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.002.2)

<400> SEQUENCE: 664

ttcaactaga ataaaaggaa aaata 25

<210> SEQ ID NO 665
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.003)

<400> SEQUENCE: 665

ctttcaacta gaataaaagg aaaaa 25

<210> SEQ ID NO 666
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.003.2)

<400> SEQUENCE: 666

attctttcaa ctagaataaa aggaa 25

<210> SEQ ID NO 667
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.004)

<400> SEQUENCE: 667

gaattctttc aactagaata aaagg 25

<210> SEQ ID NO 668
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.004.2)

<400> SEQUENCE: 668

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tctgaattct ttcaactaga ataaa 25

<210> SEQ ID NO 669
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.005)

<400> SEQUENCE: 669

attctgaatt ctttcaacta gaata 25

<210> SEQ ID NO 670
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.005.2)

<400> SEQUENCE: 670

ctgattctga attctttcaa ctaga 25

<210> SEQ ID NO 671
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.006)

<400> SEQUENCE: 671

cactgattct gaattctttc aacta 25

<210> SEQ ID NO 672
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.006.2)

<400> SEQUENCE: 672

tcccactgat tctgaattct ttcaa 25

<210> SEQ ID NO 673
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.007)

<400> SEQUENCE: 673

catcccactg attctgaatt ctttc 25

<210> SEQ ID NO 674
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.008)

<400> SEQUENCE: 674

tacttcatcc cactgattct gaatt 25

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<210> SEQ ID NO 675
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.009)

<400> SEQUENCE: 675

cggttctgaa ggtgttcttg tact 24

<210> SEQ ID NO 676
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.009.2)

<400> SEQUENCE: 676

ctgttgcctc cggttctgaa ggtgt 25

<210> SEQ ID NO 677
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.010)

<400> SEQUENCE: 677

tttcattcaa ctgttgcctc cggtt 25

<210> SEQ ID NO 678
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.010.2)

<400> SEQUENCE: 678

taacatttca ttcaactgtt gcctc 25

<210> SEQ ID NO 679
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.011)

<400> SEQUENCE: 679

ttgtgttgaa tcctttaaca tttca 25

<210> SEQ ID NO 680
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.012)

<400> SEQUENCE: 680

tcttccttag cttccagcca ttgtg 25

<210> SEQ ID NO 681
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.012.2)

<400> SEQUENCE: 681

cttagcttcc agccattgtg ttgaa 25

<210> SEQ ID NO 682
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.013)

<400> SEQUENCE: 682

gtcctaagac ctgctcagct tcttc 25

<210> SEQ ID NO 683
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.013.2)

<400> SEQUENCE: 683

ctgctcagct tcttccttag cttcc 25

<210> SEQ ID NO 684
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.014)

<400> SEQUENCE: 684

ctcaagcttg gctctggcct gtcct 25

<210> SEQ ID NO 685
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.014.2)

<400> SEQUENCE: 685

ggcctgtcct aagacctgct cagct 25

<210> SEQ ID NO 686
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.015)

<400> SEQUENCE: 686

tagggaccct ccttccatga ctcaa 25

<210> SEQ ID NO 687
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.016)

<400> SEQUENCE: 687

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tttggattgc atctactgta taggg 25

<210> SEQ ID NO 688
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.016.2)

<400> SEQUENCE: 688

accctccttc catgactcaa gcttg 25

<210> SEQ ID NO 689
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.017)

<400> SEQUENCE: 689

cttggtttct gtgattttct tttgg 25

<210> SEQ ID NO 690
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.017.2)

<400> SEQUENCE: 690

atctactgta tagggaccct ccttc 25

<210> SEQ ID NO 691
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.018)

<400> SEQUENCE: 691

ctaaccttgg tttctgtgat tttct 25

<210> SEQ ID NO 692
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.018.2)

<400> SEQUENCE: 692

tttcttttgg attgcatcta ctgta 25

<210> SEQ ID NO 693
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.019)

<400> SEQUENCE: 693

tgatactaac cttggtttct gtgat 25

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<210> SEQ ID NO 694
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.020)

<400> SEQUENCE: 694

atctttgata ctaaccttgg tttct 25

<210> SEQ ID NO 695
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.021)

<400> SEQUENCE: 695

aaggtatctt tgatactaac cttgg 25

<210> SEQ ID NO 696
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.25.022)

<400> SEQUENCE: 696

ttaaaaaggt atctttgata ctaac 25

<210> SEQ ID NO 697
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.001)

<400> SEQUENCE: 697

ataaaaggaa aaataaatat 20

<210> SEQ ID NO 698
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.002)

<400> SEQUENCE: 698

gaataaaagg aaaaataaat 20

<210> SEQ ID NO 699
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.003)

<400> SEQUENCE: 699

aactagaata aaaggaaaaa 20

<210> SEQ ID NO 700
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.004)

<400> SEQUENCE: 700

ctttcaacta gaataaaagg 20

<210> SEQ ID NO 701
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.005)

<400> SEQUENCE: 701

gaattctttc aactagaata 20

<210> SEQ ID NO 702
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.006)

<400> SEQUENCE: 702

attctgaatt ctttcaacta 20

<210> SEQ ID NO 703
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.007)

<400> SEQUENCE: 703

tacttcatcc cactgattct 20

<210> SEQ ID NO 704
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.008)

<400> SEQUENCE: 704

ctgaaggtgt tcttgtact 19

<210> SEQ ID NO 705
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.009)

<400> SEQUENCE: 705

ctgttgcctc cggttctgaa 20

<210> SEQ ID NO 706
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.010)

<400> SEQUENCE: 706

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taacatttca ttcaactgtt 20

<210> SEQ ID NO 707
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.011)

<400> SEQUENCE: 707

ttgtgttgaa tcctttaaca 20

<210> SEQ ID NO 708
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.012)

<400> SEQUENCE: 708

cttagcttcc agccattgtg 20

<210> SEQ ID NO 709
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.013)

<400> SEQUENCE: 709

ctgctcagct tcttccttag 20

<210> SEQ ID NO 710
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.014)

<400> SEQUENCE: 710

ggcctgtcct aagacctgct 20

<210> SEQ ID NO 711
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.015)

<400> SEQUENCE: 711

ctcaagcttg gctctggcct 20

<210> SEQ ID NO 712
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.016)

<400> SEQUENCE: 712

accctccttc catgactcaa 20

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<210> SEQ ID NO 713
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.017)

<400> SEQUENCE: 713

atctactgta tagggaccct 20

<210> SEQ ID NO 714
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.018)

<400> SEQUENCE: 714

tttcttttgg attgcatcta 20

<210> SEQ ID NO 715
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.019)

<400> SEQUENCE: 715

cttggtttct gtgattttct 20

<210> SEQ ID NO 716
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.020)

<400> SEQUENCE: 716

ctaaccttgg tttctgtgat 20

<210> SEQ ID NO 717
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.021)

<400> SEQUENCE: 717

tgatactaac cttggtttct 20

<210> SEQ ID NO 718
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.022)

<400> SEQUENCE: 718

atctttgata ctaaccttgg 20

<210> SEQ ID NO 719
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.023)

<400> SEQUENCE: 719

aaggtatctt tgatactaac 20

<210> SEQ ID NO 720
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon53.20.024)

<400> SEQUENCE: 720

ttaaaaaggt atctttgata 20

<210> SEQ ID NO 721
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.001)

<400> SEQUENCE: 721

ctatagattt ttatgagaaa gaga 24

<210> SEQ ID NO 722
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.002)

<400> SEQUENCE: 722

aactgctata gatttttatg agaaa 25

<210> SEQ ID NO 723
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.003)

<400> SEQUENCE: 723

tggccaactg ctatagattt ttatg 25

<210> SEQ ID NO 724
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.004)

<400> SEQUENCE: 724

gtctttggcc aactgctata gattt 25

<210> SEQ ID NO 725
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.005)

<400> SEQUENCE: 725

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cggaggtctt tggccaactg ctata 25

<210> SEQ ID NO 726
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.006)

<400> SEQUENCE: 726

actggcggag gtctttggcc aactg 25

<210> SEQ ID NO 727
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.007)

<400> SEQUENCE: 727

tttgtctgcc actggcggag gtctt 25

<210> SEQ ID NO 728
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.008)

<400> SEQUENCE: 728

agtcatttgc cacatctaca tttgt 25

<210> SEQ ID NO 729
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.008.2)

<400> SEQUENCE: 729

tttgccacat ctacatttgt ctgcc 25

<210> SEQ ID NO 730
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.009)

<400> SEQUENCE: 730

ccggagaagt ttcagggcca agtca 25

<210> SEQ ID NO 731
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.010)

<400> SEQUENCE: 731

gtatcatctg cagaataatc ccgga 25

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<210> SEQ ID NO 732
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.010.2)

<400> SEQUENCE: 732

taatcccgga gaagtttcag ggcca 25

<210> SEQ ID NO 733
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.011)

<400> SEQUENCE: 733

ttatcatgtg gacttttctg gtatc 25

<210> SEQ ID NO 734
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.012)

<400> SEQUENCE: 734

agaggcattg atattctctg ttatc 25

<210> SEQ ID NO 735
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.012.2)

<400> SEQUENCE: 735

atgtggactt ttctggtatc atctg 25

<210> SEQ ID NO 736
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.013)

<400> SEQUENCE: 736

cttttatgaa tgcttctcca agagg 25

<210> SEQ ID NO 737
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.013.2)

<400> SEQUENCE: 737

atattctctg ttatcatgtg gactt 25

<210> SEQ ID NO 738
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.014)

<400> SEQUENCE: 738

cataccttttt atgaatgctt ctcca 25

<210> SEQ ID NO 739
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.014.2)

<400> SEQUENCE: 739

ctccaagagg cattgatatt ctctg 25

<210> SEQ ID NO 740
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.015)

<400> SEQUENCE: 740

taattcatac cttttatgaa tgctt 25

<210> SEQ ID NO 741
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.016)

<400> SEQUENCE: 741

taatgtaatt cataccttttt atgaa 25

<210> SEQ ID NO 742
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.017)

<400> SEQUENCE: 742

agaaataatg taattcatac ctttt 25

<210> SEQ ID NO 743
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.25.018)

<400> SEQUENCE: 743

gttttagaaa taatgtaatt catac 25

<210> SEQ ID NO 744
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.001)

<400> SEQUENCE: 744

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gatttttatg agaaagaga 19

<210> SEQ ID NO 745
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.002)

<400> SEQUENCE: 745

ctatagattt ttatgagaaa 20

<210> SEQ ID NO 746
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.003)

<400> SEQUENCE: 746

aactgctata gatttttatg 20

<210> SEQ ID NO 747
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.004)

<400> SEQUENCE: 747

tggccaactg ctatagattt 20

<210> SEQ ID NO 748
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.005)

<400> SEQUENCE: 748

gtctttggcc aactgctata 20

<210> SEQ ID NO 749
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.006)

<400> SEQUENCE: 749

cggaggtctt tggccaactg 20

<210> SEQ ID NO 750
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.007)

<400> SEQUENCE: 750

tttgtctgcc actggcggag 20

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<210> SEQ ID NO 751
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.008)

<400> SEQUENCE: 751

tttgccacat ctacatttgt 20

<210> SEQ ID NO 752
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.009)

<400> SEQUENCE: 752

ttcagggcca agtcatttgc 20

<210> SEQ ID NO 753
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.010)

<400> SEQUENCE: 753

taatcccgga gaagtttcag 20

<210> SEQ ID NO 754
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.011)

<400> SEQUENCE: 754

gtatcatctg cagaataatc 20

<210> SEQ ID NO 755
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.012)

<400> SEQUENCE: 755

atgtggactt ttctggtatc 20

<210> SEQ ID NO 756
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.013)

<400> SEQUENCE: 756

atattctctg ttatcatgtg 20

<210> SEQ ID NO 757
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.014)

<400> SEQUENCE: 757

ctccaagagg cattgatatt 20

<210> SEQ ID NO 758
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.015)

<400> SEQUENCE: 758

cttttatgaa tgcttctcca 20

<210> SEQ ID NO 759
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.016)

<400> SEQUENCE: 759

catacctttt atgaatgctt 20

<210> SEQ ID NO 760
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.017)

<400> SEQUENCE: 760

taattcatac cttttatgaa 20

<210> SEQ ID NO 761
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.018)

<400> SEQUENCE: 761

taatgtaatt catacctttt 20

<210> SEQ ID NO 762
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.019)

<400> SEQUENCE: 762

agaaataatg taattcatac 20

<210> SEQ ID NO 763
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon54.20.020)

<400> SEQUENCE: 763

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gttttagaaa taatgtaatt 20

<210> SEQ ID NO 764
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.001)

<400> SEQUENCE: 764

ctgcaaagga ccaaatgttc agatg 25

<210> SEQ ID NO 765
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.002)

<400> SEQUENCE: 765

tcaccctgca aaggaccaaa tgttc 25

<210> SEQ ID NO 766
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.003)

<400> SEQUENCE: 766

ctcactcacc ctgcaaagga ccaaa 25

<210> SEQ ID NO 767
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.004)

<400> SEQUENCE: 767

tctcgctcac tcaccctgca aagga 25

<210> SEQ ID NO 768
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.005)

<400> SEQUENCE: 768

cagcctctcg ctcactcacc ctgca 25

<210> SEQ ID NO 769
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.006)

<400> SEQUENCE: 769

caaagcagcc tctcgctcac tcacc 25

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<210> SEQ ID NO 770
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.007)

<400> SEQUENCE: 770

tcttccaaag cagcctctcg ctcac 25

<210> SEQ ID NO 771
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.007.2)

<400> SEQUENCE: 771

tctatgagtt tcttccaaag cagcc 25

<210> SEQ ID NO 772
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.008)

<400> SEQUENCE: 772

gttgcagtaa tctatgagtt tcttc 25

<210> SEQ ID NO 773
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.008.2)

<400> SEQUENCE: 773

gaactgttgc agtaatctat gagtt 25

<210> SEQ ID NO 774
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.009)

<400> SEQUENCE: 774

ttccaggtcc agggggaact gttgc 25

<210> SEQ ID NO 775
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.010)

<400> SEQUENCE: 775

gtaagccagg caagaaactt ttcca 25

<210> SEQ ID NO 776
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.010.2)

<400> SEQUENCE: 776

ccaggcaaga aacttttcca ggtcc 25

<210> SEQ ID NO 777
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.011)

<400> SEQUENCE: 777

tggcagttgt ttcagcttct gtaag 25

<210> SEQ ID NO 778
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.011.2)

<400> SEQUENCE: 778

ttcagcttct gtaagccagg caaga 25

<210> SEQ ID NO 779
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.012)

<400> SEQUENCE: 779

ggtagcatcc tgtaggacat tggca 25

<210> SEQ ID NO 780
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.012.2)

<400> SEQUENCE: 780

gacattggca gttgtttcag cttct 25

<210> SEQ ID NO 781
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.013)

<400> SEQUENCE: 781

tctaggagcc tttccttacg ggtag 25

<210> SEQ ID NO 782
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.014)

<400> SEQUENCE: 782

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cttttactcc cttggagtct tctag 25

<210> SEQ ID NO 783
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.014.2)

<400> SEQUENCE: 783

gagcctttcc ttacgggtag catcc 25

<210> SEQ ID NO 784
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.015)

<400> SEQUENCE: 784

ttgccattgt ttcatcagct ctttt 25

<210> SEQ ID NO 785
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.015.2)

<400> SEQUENCE: 785

cttggagtct tctaggagcc tttcc 25

<210> SEQ ID NO 786
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.016)

<400> SEQUENCE: 786

cttacttgcc attgtttcat cagct 25

<210> SEQ ID NO 787
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.016.2)

<400> SEQUENCE: 787

cagctctttt actcccttgg agtct 25

<210> SEQ ID NO 788
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.017)

<400> SEQUENCE: 788

cctgacttac ttgccattgt ttcat 25

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<210> SEQ ID NO 789
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.018)

<400> SEQUENCE: 789

aaatgcctga cttacttgcc attgt 25

<210> SEQ ID NO 790
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.019)

<400> SEQUENCE: 790

agcggaaatg cctgacttac ttgcc 25

<210> SEQ ID NO 791
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.25.020)

<400> SEQUENCE: 791

gctaaagcgg aaatgcctga cttac 25

<210> SEQ ID NO 792
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.001)

<400> SEQUENCE: 792

aaggaccaaa tgttcagatg 20

<210> SEQ ID NO 793
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.002)

<400> SEQUENCE: 793

ctgcaaagga ccaaatgttc 20

<210> SEQ ID NO 794
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.003)

<400> SEQUENCE: 794

tcaccctgca aaggaccaaa 20

<210> SEQ ID NO 795
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.004)

<400> SEQUENCE: 795

ctcactcacc ctgcaaagga 20

<210> SEQ ID NO 796
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.005)

<400> SEQUENCE: 796

tctcgctcac tcaccctgca 20

<210> SEQ ID NO 797
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.006)

<400> SEQUENCE: 797

cagcctctcg ctcactcacc 20

<210> SEQ ID NO 798
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.007)

<400> SEQUENCE: 798

caaagcagcc tctcgctcac 20

<210> SEQ ID NO 799
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.008)

<400> SEQUENCE: 799

tctatgagtt tcttccaaag 20

<210> SEQ ID NO 800
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.009)

<400> SEQUENCE: 800

gaactgttgc agtaatctat 20

<210> SEQ ID NO 801
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.010)

<400> SEQUENCE: 801

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ttccaggtcc agggggaact 20

<210> SEQ ID NO 802
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.011)

<400> SEQUENCE: 802

ccaggcaaga aacttttcca 20

<210> SEQ ID NO 803
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.012)

<400> SEQUENCE: 803

ttcagcttct gtaagccagg 20

<210> SEQ ID NO 804
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.013)

<400> SEQUENCE: 804

gacattggca gttgtttcag 20

<210> SEQ ID NO 805
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.014)

<400> SEQUENCE: 805

ggtagcatcc tgtaggacat 20

<210> SEQ ID NO 806
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.015)

<400> SEQUENCE: 806

gagcctttcc ttacgggtag 20

<210> SEQ ID NO 807
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.016)

<400> SEQUENCE: 807

cttggagtct tctaggagcc 20

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<210> SEQ ID NO 808
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.017)

<400> SEQUENCE: 808

cagctctttt actcccttgg 20

<210> SEQ ID NO 809
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.018)

<400> SEQUENCE: 809

ttgccattgt ttcatcagct 20

<210> SEQ ID NO 810
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.019)

<400> SEQUENCE: 810

cttacttgcc attgtttcat 20

<210> SEQ ID NO 811
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.020)

<400> SEQUENCE: 811

cctgacttac ttgccattgt 20

<210> SEQ ID NO 812
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.021)

<400> SEQUENCE: 812

aaatgcctga cttacttgcc 20

<210> SEQ ID NO 813
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.022)

<400> SEQUENCE: 813

agcggaaatg cctgacttac 20

<210> SEQ ID NO 814
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Hu.DMD.Exon55.20.023)

<400> SEQUENCE: 814

gctaaagcgg aaatgcctga 20

<210> SEQ ID NO 815
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H50A(+02+30)-AVI-5656)

<400> SEQUENCE: 815

ccactcagag ctcagatctt ctaacttcc 29

<210> SEQ ID NO 816
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H50D(+07-18)-AVI-5915)

<400> SEQUENCE: 816

gggatccagt atacttacag gctcc 25

<210> SEQ ID NO 817
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H50A(+07+33))

<400> SEQUENCE: 817

cttccactca gagctcagat cttctaa 27

<210> SEQ ID NO 818
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H51A(+61+90)-AVI-4657)

<400> SEQUENCE: 818

acatcaagga agatggcatt tctagtttgg 30

<210> SEQ ID NO 819
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H51A(+66+95)-AVI-4658)

<400> SEQUENCE: 819

ctccaacatc aaggaagatg gcatttctag 30

<210> SEQ ID NO 820
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H51A(+111+134))

<400> SEQUENCE: 820

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ttctgtccaa gcccggttga aatc 24

<210> SEQ ID NO 821
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H51A(+175+195))

<400> SEQUENCE: 821

cacccaccat caccctcygt g 21

<210> SEQ ID NO 822
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H51A(+199+220))

<400> SEQUENCE: 822

atcatctcgt tgatatcctc aa 22

<210> SEQ ID NO 823
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H51A(+66+90))

<400> SEQUENCE: 823

acatcaagga agatggcatt tctag 25

<210> SEQ ID NO 824
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H51A(-01+25))

<400> SEQUENCE: 824

accagagtaa cagtctgagt aggagc 26

<210> SEQ ID NO 825
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (h51AON1)

<400> SEQUENCE: 825

tcaaggaaga tggcatttct 20

<210> SEQ ID NO 826
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (h51AON2)

<400> SEQUENCE: 826

cctctgtgat tttataactt gat 23

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<210> SEQ ID NO 827
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H51D(+08-17))

<400> SEQUENCE: 827

atcatttttt ctcatacctt ctgct 25

<210> SEQ ID NO 828
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H51D(+16-07))

<400> SEQUENCE: 828

ctcatacctt ctgcttgatg atc 23

<210> SEQ ID NO 829
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (hAON#23)

<400> SEQUENCE: 829

tggcatttct agtttgg 17

<210> SEQ ID NO 830
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (hAON#24)

<400> SEQUENCE: 830

ccagagcagg tacctccaac atc 23

<210> SEQ ID NO 831
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (h44AON1)

<400> SEQUENCE: 831

cgccgccatt tctcaacag 19

<210> SEQ ID NO 832
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H45A(+71+90))

<400> SEQUENCE: 832

tgtttttgag gattgctgaa 20

<210> SEQ ID NO 833
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (h45AON1)

<400> SEQUENCE: 833

gctgaattat ttcttcccc 19

<210> SEQ ID NO 834
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (h45AON5)

<400> SEQUENCE: 834

gcccaatgcc atcctgg 17

<210> SEQ ID NO 835
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H45A(-06+20))

<400> SEQUENCE: 835

ccaatgccat cctggagttc ctgtaa 26

<210> SEQ ID NO 836
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(+39+69))

<400> SEQUENCE: 836

cattcaactg ttgcctccgg ttctgaaggt g 31

<210> SEQ ID NO 837
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (h53AON1)

<400> SEQUENCE: 837

ctgttgcctc cggttctg 18

<210> SEQ ID NO 838
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (H53A(-12+10))

<400> SEQUENCE: 838

attctttcaa ctagaataaa ag 22

<210> SEQ ID NO 839
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx45.30.66)

<400> SEQUENCE: 839

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gccatcctgg agttcctgta agataccaaa 30

<210> SEQ ID NO 840
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx45.30.71)

<400> SEQUENCE: 840

ccaatgccat cctggagttc ctgtaagata 30

<210> SEQ ID NO 841
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx45.30.79)

<400> SEQUENCE: 841

gccgctgccc aatgccatcc tggagttcct 30

<210> SEQ ID NO 842
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx45.30.83)

<400> SEQUENCE: 842

gtttgccgct gcccaatgcc atcctggagt 30

<210> SEQ ID NO 843
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx45.30.88)

<400> SEQUENCE: 843

caacagtttg ccgctgccca atgccatcct 30

<210> SEQ ID NO 844
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx45.30.92)

<400> SEQUENCE: 844

ctgacaacag tttgccgctg cccaatgcca 30

<210> SEQ ID NO 845
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx45.30.96)

<400> SEQUENCE: 845

tgttctgaca acagtttgcc gctgcccaat 30

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<210> SEQ ID NO 846
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx45.30.99)

<400> SEQUENCE: 846

caatgttctg acaacagttt gccgctgccc 30

<210> SEQ ID NO 847
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx45.30.103)

<400> SEQUENCE: 847

cattcaatgt tctgacaaca gtttgccgct 30

<210> SEQ ID NO 848
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx45.30.120)

<400> SEQUENCE: 848

tatttcttcc ccagttgcat tcaatgttct 30

<210> SEQ ID NO 849
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx45.30.127)

<400> SEQUENCE: 849

gctgaattat ttcttcccca gttgcattca 30

<210> SEQ ID NO 850
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx45.30.132)

<400> SEQUENCE: 850

ggattgctga attatttctt ccccagttgc 30

<210> SEQ ID NO 851
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx45.30.137)

<400> SEQUENCE: 851

tttgaggatt gctgaattat ttcttcccca 30

<210> SEQ ID NO 852
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx53.30.84)

<400> SEQUENCE: 852

gtacttcatc ccactgattc tgaattcttt 30

<210> SEQ ID NO 853
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx53.30.88)

<400> SEQUENCE: 853

tcttgtactt catcccactg attctgaatt 30

<210> SEQ ID NO 854
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx53.30.91)

<400> SEQUENCE: 854

tgttcttgta cttcatccca ctgattctga 30

<210> SEQ ID NO 855
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx53.30.103)

<400> SEQUENCE: 855

cggttctgaa ggtgttcttg tacttcatcc 30

<210> SEQ ID NO 856
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx53.30.106)

<400> SEQUENCE: 856

ctccggttct gaaggtgttc ttgtacttca 30

<210> SEQ ID NO 857
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx53.30.109)

<400> SEQUENCE: 857

tgcctccggt tctgaaggtg ttcttgtact 30

<210> SEQ ID NO 858
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx53.30.112)

<400> SEQUENCE: 858

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tgttgcctcc ggttctgaag gtgttcttgt 30

<210> SEQ ID NO 859
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx53.30.115)

<400> SEQUENCE: 859

aactgttgcc tccggttctg aaggtgttct 30

<210> SEQ ID NO 860
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (huEx53.30.118)

<400> SEQUENCE: 860

ttcaactgtt gcctccggtt ctgaaggtgt 30

<210> SEQ ID NO 861
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (rTAT)

<400> SEQUENCE: 861

Arg Arg Arg Gln Arg Arg Lys Lys Arg Cys
1 5 10

<210> SEQ ID NO 862
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (R9F2)

<400> SEQUENCE: 862

Arg Arg Arg Arg Arg Arg Arg Arg Arg Phe Phe Cys
1 5 10

<210> SEQ ID NO 863
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic ((RRAhx)4B)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(9)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)

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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: Xaa is beta-alanine

<400> SEQUENCE: 863

Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Xaa
1 5 10

<210> SEQ ID NO 864
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic ((RAhxR)4AhxB; (P007))
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: Xaa is beta-alanine

<400> SEQUENCE: 864

Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Xaa Xaa
1 5 10

<210> SEQ ID NO 865
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic ((AhxRR)4AhxB)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: Xaa is beta-alanine

<400> SEQUENCE: 865

Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Xaa
1 5 10

<210> SEQ ID NO 866
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic ((RAhx)6B)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: Xaa is beta-alanine

<400> SEQUENCE: 866

Arg Xaa Arg Xaa Arg Xaa Arg Xaa Arg Xaa Arg Xaa Xaa
1 5 10

<210> SEQ ID NO 867
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic ((RAhx)8B)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)

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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(15)
<223> OTHER INFORMATION: Xaa is beta-alanine

<400> SEQUENCE: 867

Arg Xaa Arg Xaa Arg Xaa Arg Xaa Arg Xaa Arg Xaa Arg Xaa Xaa
1 5 10 15

<210> SEQ ID NO 868
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic ((RAhxR)5AhxB)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(16)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (17)..(17)
<223> OTHER INFORMATION: Xaa is beta-alanine

<400> SEQUENCE: 868

Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Xaa
1 5 10 15

Xaa

<210> SEQ ID NO 869
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic ((RAhxRRBR)2AhxB; (CPO6062))
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Xaa is beta-alanine

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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: Xaa is beta-alanine
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid (Ahx)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: Xaa is beta-alanine

<400> SEQUENCE: 869

Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Xaa Xaa
1 5 10

<210> SEQ ID NO 870
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (MSP)

<400> SEQUENCE: 870

Ala Ser Ser Leu Asn Ile Ala
1 5

<210> SEQ ID NO 871
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (MSP-PMO)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(9)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 871

Ala Ser Ser Leu Asn Ile Ala Xaa Xaa
1 5

<210> SEQ ID NO 872
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (CP06062-MSP-PMO)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Xaa is beta-alanine
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: Xaa is beta-alanine
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: Xaa is beta-alanine
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (22)..(22)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 872

Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Xaa Xaa Ala Ser
1 5 10 15

Ser Leu Asn Ile Ala Xaa
20

<210> SEQ ID NO 873
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (MSP-CP06062-PMO)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: Xaa is beta-alanine
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(16)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: Xaa is beta-alanine
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: Xaa is beta-alanine

<400> SEQUENCE: 873

Ala Ser Ser Leu Asn Ile Ala Xaa Arg Xaa Arg Arg Xaa Arg Arg Xaa
1 5 10 15

Arg Arg Xaa Arg Xaa
20

<210> SEQ ID NO 874
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (CP06062-PMO)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Xaa is beta-alanine
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: Xaa is beta-alanine
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: Xaa is beta-alanine

<400> SEQUENCE: 874

Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Xaa Xaa
1 5 10

<210> SEQ ID NO 875
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (PMO)

<400> SEQUENCE: 875

ggccaaacct cggcttacct gaaat 25

<210> SEQ ID NO 876
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (rTAT)

<400> SEQUENCE: 876

Arg Arg Arg Gln Arg Arg Lys Lys Arg
1 5

<210> SEQ ID NO 877
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (Tat)

<400> SEQUENCE: 877

Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5

<210> SEQ ID NO 878
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (R9F2)

<400> SEQUENCE: 878

Arg Arg Arg Arg Arg Arg Arg Arg Arg Phe Phe
1 5 10

<210> SEQ ID NO 879
<211> LENGTH: 11
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (R5F2R4)

<400> SEQUENCE: 879

Arg Arg Arg Arg Arg Phe Phe Arg Arg Arg Arg
1 5 10

<210> SEQ ID NO 880
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (R4)

<400> SEQUENCE: 880

Arg Arg Arg Arg
1

<210> SEQ ID NO 881
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (R5)

<400> SEQUENCE: 881

Arg Arg Arg Arg Arg
1 5

<210> SEQ ID NO 882
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (R6)

<400> SEQUENCE: 882

Arg Arg Arg Arg Arg Arg
1 5

<210> SEQ ID NO 883
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (R7)

<400> SEQUENCE: 883

Arg Arg Arg Arg Arg Arg Arg
1 5

<210> SEQ ID NO 884
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (R8)

<400> SEQUENCE: 884

Arg Arg Arg Arg Arg Arg Arg Arg
1 5

<210> SEQ ID NO 885

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<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic (R9)

<400> SEQUENCE: 885

Arg Arg Arg Arg Arg Arg Arg Arg Arg
1 5

<210> SEQ ID NO 886
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic ((RX)8)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(16)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 886

Arg Xaa Arg Xaa Arg Xaa Arg Xaa Arg Xaa Arg Xaa Arg Xaa Arg Xaa
1 5 10 15

<210> SEQ ID NO 887
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic ((RAhxR)4; (P007))
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid

<400> SEQUENCE: 887

Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg
1 5 10

<210> SEQ ID NO 888
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic ((RAhxR)5; (CP04057))
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid

<400> SEQUENCE: 888

Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg
1 5 10 15

<210> SEQ ID NO 889
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic ((RAhxRRBR)2; (CP06062))
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: Xaa is beta-alanine
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: Xaa is 6-aminohexanoic acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: Xaa is beta-alanine

<400> SEQUENCE: 889

Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg Arg Xaa Arg
1 5 10

<210> SEQ ID NO 890
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic ((RAR)4F2)

<400> SEQUENCE: 890

Arg Ala Arg Arg Ala Arg Arg Ala Arg Arg Ala Arg Phe Phe
1 5 10

<210> SEQ ID NO 891
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic ((RGR)4F2))

<400> SEQUENCE: 891

Arg Gly Arg Arg Gly Arg Arg Gly Arg Arg Gly Arg Phe Phe
1 5 10

1. A method of treating Duchenne muscular dystrophy or Becker muscular dystrophy in a human subject comprising administering about 30 mg/kg to about 50 mg/kg of a composition comprising an antisense oligonucleotide of 20 to 50 nucleotides in length comprising at least 10 consecutive nucleotides complementary to a target region in an exon of the human dystrophin gene, wherein the antisense oligonucleotide specifically hybridizes to the target region inducing exon skipping, thereby treating Duchenne muscular dystrophy or Becker muscular dystrophy in the subject.

2. The method of claim **1**, wherein treatment increases the number of dystrophin-positive fibers to at least 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 95% of normal in the subject.

3. The method of claim **2**, wherein the number of dystrophin-positive fibers is increased to between 20-60% of normal in the human subject.

4. The method of claim **2**, wherein the number of dystrophin-positive fibers is increased to between 30-50% of normal in the human subject.

5. The method of claim **1**, wherein about 30 mg/kg of the composition is administered to the human subject.

6. The method of claim **1**, wherein about 50 mg/kg of the composition is administered to the human subject.

7. The method of claim **1**, wherein treatment improves or maintains a stable walking distance in a 6 minute walk test from a 20% deficit in the subject relative to a healthy peer.

8. The method of claim **1**, wherein the antisense oligonucleotide is substantially uncharged.

9. The method of claim **1**, wherein the antisense oligonucleotide comprises morpholino subunits linked by phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit.

10. The method of claim **1**, wherein the antisense oligonucleotide comprises morpholino subunits linked by substantially uncharged phosphorus-containing intersubunit linkages joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit.

11. The method of claim **1**, wherein the antisense oligonucleotide comprises morpholino subunits and phosphorodiamidate intersubunit linkages.

12. The method of claim **1**, wherein the antisense oligonucleotide is chemically linked to one or more moieties or conjugates that enhance the activity, cellular distribution, or cellular uptake of the antisense oligonucleotide.

13. The method of claim **12**, wherein the antisense oligonucleotide is conjugated to an arginine-rich peptide.

14. The method of claim **1**, wherein the antisense oligonucleotide is 30 to 50 nucleotides in length.

15. The method of claim **1**, wherein the antisense oligonucleotide is 20 to 30 nucleotides in length.

16. The method of claim **1**, wherein the exon in the human dystrophin gene is selected from the group consisting of exon 51, exon 50, exon 53, exon 45, exon 46, exon 44, exon 52, exon 55 and exon 8.

17. The method of claim **1**, wherein the antisense oligonucleotide is selected from the group consisting of SEQ ID NOS: 1-9.

18. The method of claim **1**, wherein the antisense oligonucleotide is SEQ ID NO: 1.

19. The method of claim **1**, wherein the antisense oligonucleotide is any one or a combination of the nucleotide sequences set forth in Tables 3 and 4, wherein uracil bases in the antisense oligonucleotide are optionally thymine bases.

20. The method of claim **1**, wherein the composition further comprises phosphate-buffered saline.

21. The method of claim **1**, wherein the composition is administered by systemic administration.

22. The method of claim **1**, wherein the composition is administered once weekly by infusion.

23. The method of claim **1**, further comprising administering a steroid to the human subject.

* * * * *