

COMPOSITIONS AND METHODS OF TREATING FACIOSCAPULOHUMERAL MUSCULAR DYSTROPHY

CROSS-REFERENCE

[0001] This application claims the benefit of U.S. Provisional Application No. 62/992,071 filed March 19, 2020, and U.S. Provisional Application No. 63/066,655 filed August 17, 2020, each of which is incorporated herein by reference in its entirety.

BACKGROUND OF THE DISCLOSURE

[0002] Gene suppression by RNA-induced gene silencing provides several levels of control: transcription inactivation, small interfering RNA (siRNA)-induced mRNA degradation, and siRNA-induced transcriptional attenuation. In some instances, RNA interference (RNAi) provides long lasting effect over multiple cell divisions. As such, RNAi represents a viable method useful for drug target validation, gene function analysis, pathway analysis, and disease therapeutics.

INCORPORATION BY REFERENCE

[0003] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

SUMMARY OF THE DISCLOSURE

[0004] Disclosed herein, in certain embodiments, are polynucleic acid molecules and pharmaceutical compositions for modulating a gene associated with muscle atrophy, especially Facioscapulohumeral muscular dystrophy (FSHD). In some embodiments, also described herein are methods of treating muscle atrophy, especially FSHD, with a polynucleic acid molecule or a polynucleic acid molecule conjugate disclosed herein.

[0005] Disclosed herein, in certain embodiments, is a polynucleic acid molecule conjugate comprising an antibody or antigen binding fragment thereof conjugated to a polynucleic acid molecule that hybridizes to a target sequence of *DUX4*, and the polynucleic acid molecule conjugate mediates RNA interference against the *DUX4*. In certain embodiments, the antibody or antigen binding fragment thereof comprises a non-human antibody or binding fragment thereof, a human antibody or antigen binding fragment thereof, a humanized antibody or antigen binding fragment thereof, chimeric antibody or antigen binding fragment thereof, monoclonal antibody or antigen binding fragment thereof, monovalent Fab', divalent Fab2, single-chain variable fragment (scFv), diabody, minibody, nanobody, single-domain antibody

(sdAb), or camelid antibody or antigen binding fragment thereof. In certain embodiments, the antibody or antigen binding fragment thereof is an anti-transferrin receptor antibody or antigen binding fragment thereof.

[0006] In certain embodiments, the polynucleic acid molecule comprises a sense strand and/or an antisense strand, and wherein the sense strand and/or the antisense strand each independently comprises at least one 2' modified nucleotide, at least one modified internucleotide linkage, or at least one inverted abasic moiety. In certain embodiments, the polynucleotide hybridizes to at least 8 contiguous bases of the target sequence of *DUX4*. In certain embodiments, the polynucleotide is from about 8 to about 50 nucleotides in length or from about 10 to about 30 nucleotides in length. In certain embodiments, the polynucleic acid molecule comprises a sense strand and/or an antisense strand, and the sense strand comprises at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical to a sequence selected from SEQ ID NOs: 1-70 or SEQ ID NOs: 141-210. Alternatively and/or additionally, the polynucleic acid molecule comprises a sense strand and/or an antisense strand, and the antisense strand comprises at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical to a sequence selected from SEQ ID NOs: 71-140 or SEQ ID NOs: 211-280.

[0007] In certain embodiments, the polynucleotide comprises at least one 2' modified nucleotide, and further the 2' modified nucleotide comprises 2'-O-methyl, 2'-O-methoxyethyl (2'-O-MOE), 2'-O-aminopropyl, 2'-deoxy, 2'-deoxy-2'-fluoro, 2'-O-aminopropyl (2'-O-AP), 2'-O-dimethylaminoethyl (2'-O-DMAOE), 2'-O-dimethylaminopropyl (2'-O-DMAP), 2'-O-dimethylaminoethoxyethyl (2'-O-DMAEOE), or 2'-O-N-methylacetamido (2'-O-NMA) modified nucleotide, or comprises locked nucleic acid (LNA) or ethylene nucleic acid (ENA), or comprises a combination thereof. In certain embodiments, the at least one modified internucleotide linkage comprises a phosphorothioate linkage or a phosphorodithioate linkage. In certain embodiments, the polynucleic acid molecule comprises 3 or more 2' modified nucleotides selected from 2'-O-methyl and 2'-deoxy-2'-fluoro. In certain embodiments, the polynucleic acid molecule comprises a 5'-terminal vinylphosphonate modified nucleotide, such as those described in U.S. Publication No. 2019/0192681.

[0008] In certain embodiments, the 2' modified nucleotide is 2'-O-methyl modified nucleotide, and 2'-O-methyl modified nucleotide is at the 5'-end of the sense strand and/or the antisense strand. In some embodiments, the 2'-O-methyl modified nucleotide is a purine nucleotide, or the 2'-O-methyl modified nucleotide is a pyridine nucleotide. In certain embodiments, the sense and/or antisense strands comprise at least two, three, four consecutive the 2'-O-methyl modified nucleotides at the 5'-end.

[0009] In certain embodiments, the polynucleic acid molecule conjugate comprises a linker connecting the target cell binding moiety to the polynucleic acid moiety. In such embodiments, the linker is C1-C6 alkyl linker, or the linker is a homobifunctional linker or heterobifunctional linker, and comprises a maleimide group, a dipeptide moiety, a benzoic acid group, or its derivative thereof. Alternatively and/or additionally, the linker is a cleavable or non-cleavable linker. In certain embodiments, a ratio between the polynucleic acid moiety and the target cell binding moiety is about 1:1, 2:1, 3:1, or 4:1.

[0010] In certain embodiments, the polynucleic acid moiety mediates RNA interference against the human *DUX4* and modulates symptoms of muscle dystrophy in a subject. In some embodiments, the RNA interference comprises reducing expression of the mRNA transcript of *DUX4* gene at least 50%, at least 60%, or at least 70% or more compared to a quantity of the mRNA transcript of *DUX4* gene in an untreated cell. Alternatively and/or additionally, the RNA interference comprises affecting expression of a marker gene selected from a group comprising or consisting of *MBD3L2*, *TRIM43*, *PRAMEF1*, *ZSCAN4*, *KHDC1L*, and *LEUTX* in a cell. In some embodiments, the affecting expression of the marker gene is reducing expression of the marker gene at least 20%, at least 30%, at least 40%, at least 50%, at least 60% or more. In some embodiments, the muscle dystrophy is Facioscapulohumeral muscular dystrophy (FSHD).

[0011] In certain embodiments, polynucleic acid molecule conjugate comprises a molecule of Formula (I): A-X-B, where A is the antibody or antigen binding fragment thereof, B is the polynucleic acid molecule that hybridizes to a target sequence of *DUX4*, X is a bond or a non-polymeric linker, which is conjugated to a cysteine residue of A.

[0012] Disclosed herein, in certain embodiments, is a pharmaceutical composition comprising a polynucleic acid molecule conjugate as described herein, and a pharmaceutically acceptable excipient. In some embodiments, the pharmaceutical composition is formulated as a nanoparticle formulation. In some embodiments, the pharmaceutical composition is formulated for parenteral, oral, intranasal, buccal, rectal, transdermal, or intravenous, subcutaneous, or intrathecal administration.

[0013] The symptoms of FSHD include affects on skeletal muscles. The skeletal muscles affected by FSHD include muscles around the eyes and mouth, muscle of the shoulders, muscle of the upper arms, muscle of the lower legs, abdominal muscles and hip muscles. In some instances, the symptoms of FSHD also affects vision and hearing. In some instances, the symptoms of FSHD also affect the function of the heart or lungs. In some instances, the symptoms of FSHD include muscle weakness, muscle atrophy, muscle dystrophy, pain inflammation, contractures, scoliosis, lordosis, hypoventilation, abnormalities of the retina,

exposure to keratitis, mild hearing loss, and EMG abnormality. The term muscle atrophy as used herein refers to a wide range of muscle related effects of FSHD.

[0014] Disclosed herein, in certain embodiments, is a method for treating muscular dystrophy in a subject in need thereof by providing a polynucleic acid conjugate as described herein, and administering the polynucleic acid conjugate to the subject in need thereof to treat the muscular dystrophy. The polynucleic acid conjugate reduces a quantity of the mRNA transcript of human *DUX4*. In some embodiments, the polynucleic acid moiety mediates RNA interference against the human *DUX4* modulates muscle atrophy in a subject. In certain embodiments, the RNA interference comprises affecting expression of a marker gene selected from a group comprising or consisting of MBD3L2, TRIM43, PRAMEF1, ZSCAN4, KHDC1L, and LEUTX in a cell affected by a muscle dystrophy. Preferably, the muscular dystrophy is Facioscapulohumeral muscular dystrophy (FSHD).

[0015] Disclosed herein, in certain embodiments, is a use of the polynucleic acid molecule conjugate or a pharmaceutical composition as described herein for treating in a subject diagnosed with or suspected to have Facioscapulohumeral muscular dystrophy (FSHD). Also disclosed herein, in certain embodiments, is a use of the polynucleic acid molecule conjugate or the pharmaceutical composition as described herein for manufacturing a medicament for treating in a subject diagnosed with or suspected to have Facioscapulohumeral muscular dystrophy (FSHD).

[0016] Disclosed herein, in certain embodiments, is a kit comprising the polynucleic acid molecule conjugate or the pharmaceutical composition as described herein.

BRIEF DESCRIPTION OF THE DRAWINGS

[0017] Various aspects of the disclosure are set forth with particularity in the appended claims. A better understanding of the features and advantages of the present disclosure will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the disclosure are utilized, and the accompanying drawings below. The patent application file contains at least one drawing executed in color. Copies of this patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

[0018] FIG. 1 illustrates a diagram of FSHD pathology.

[0019] FIG. 2 shows a flowchart diagram of in silico selection of DUX4 siRNA.

[0020] FIG. 3 illustrates the location and numbers of selected DUX4 siRNA in the DUX4 mRNA transcript.

- [0021] FIG. 4 shows immunofluorescent detection of DUX4 expression in myonuclei.
- [0022] FIG. 5 shows bar graphs of siRNA-mediated reduction of DUX4-target biomarker gene expressions.
- [0023] FIGs. 6A-B show graphs of the siRNA-mediated reduction of DUX4-target biomarker gene expressions in cultured FSHD primary myotubes and a FSHD composite of the siRNA-mediated reduction of DUX4-target biomarker gene expressions in cultured FSHD primary myotubes
- [0024] FIG. 7 shows a bar graph of ACTA1 gene expression in myotubes with treatment of DUX4 siRNA at a concentration of 10 nM.
- [0025] FIG. 8 shows FSHD composite expression in myotubes with treatment of DUX4 siRNA at a concentration of 10 nM.
- [0026] FIG. 9 shows FSHD composite expression in myotubes with treatment of DUX4 siRNA at a concentration of 0.5 nM.
- [0027] FIG. 10 shows a flowchart diagram of the selection of DUX4 top 28 siRNAs based on data from initial screening.
- [0028] FIGs. 11A-B show FSHD composite expression in two FSHD primary myotubes upon treatment with DUX4 siRNAs at a concentration of 10 nM and 0.5 nM.
- [0029] FIG. 12 shows a KD correlation analysis identifying DUX4 siRNA effective in one or more FSHD primary myotubes.
- [0030] FIG. 13 shows ACTA1 gene expression in patient-derived myotubes with treatment of DUX4 siRNA at a concentration of 10 nM.
- [0031] FIG. 14 shows FSHD composite expression in patient-derived myotubes with treatment of DUX4 siRNA at a concentration of 10 nM.
- [0032] FIG. 15 shows FSHD composite expression in 6 patient-derived myotubes with treatment of DUX4 siRNA.
- [0033] FIGs. 16A-C show graphs of FSHD composite expression in 3 patient-derived myotubes with treatment of 14 selected DUX4 siRNAs.
- [0034] FIGs. 17 A-C show graphs of FSHD composite expression in 3 FSHD patient-derived myotubes with treatment of 8 selected DUX4 siRNAs.
- [0035] FIGs. 18 A-B show graphs of FSHD composite expression in cultured FSHD primary myotubes with treatment of 8 antibody DUX4-siRNA conjugates (DUX4-AOCs) without vinylphosphonate or 8 antibody DUX4-siRNA conjugates with vinylphosphonate.
- [0036] FIG. 19 shows graphs of the AOC-mediated *in vivo* reduction of nuclear localized Inc-RNA Malat1 levels in skeletal muscles in mice.

[0037] FIG. 20 shows a graph of the sustained SSB-AOC-mediated *in vivo* reduction of SSB mRNA levels in murine skeletal muscles with a single dose of 3mg/kg siRNA during an 8-week period.

DETAILED DESCRIPTION OF THE DISCLOSURE

[0038] Muscle atrophy is the loss of muscle mass or the progressive weakening and degeneration of muscles, such as skeletal or voluntary muscles that controls movement, cardiac muscles, and smooth muscles. Various pathophysiological conditions including disuse, starvation, cancer, diabetes, and renal failure, or treatment with glucocorticoids result in muscle atrophy and loss of strength. The phenotypical effects of muscle atrophy are induced by various molecular events, including inhibition of muscle protein synthesis, enhanced turnover of muscle proteins, abnormal regulation of satellite cells differentiation, and abnormal conversion of muscle fibers types.

[0039] FSHD is a rare, progressive and disabling disease for which there are no approved treatments. FSHD is one of the most common forms of muscular dystrophy and affects both sexes equally, with onset typically in teens and young adults. FSHD is characterized by progressive skeletal muscle loss that initially causes weakness in muscles in the face, shoulders, arms and trunk and progresses to weakness in muscles in lower extremities and the pelvic girdle. Skeletal muscle weakness results in significant physical limitations, including progressive loss of facial muscles that can cause an inability to smile or communicate, difficulty using arms for activities of daily living and difficulty getting out of bed, with many patients ultimately becoming dependent upon the use of a wheelchair for daily mobility activities. The majority of patients with FSHD also report experiencing chronic pain, anxiety and depression.

[0040] FSHD is caused by aberrant expression of a gene, DUX4, in skeletal muscle resulting in the inappropriate presence of DUX4 protein. DUX4 itself is a transcription factor that induces the expression of other genes and it is these inappropriately expressed downstream genes that result in the muscle pathology. Normally DUX4-driven gene expression is limited to germline and early stem cell development. In patients with FSHD, the DUX4 protein in skeletal muscle regulates other gene products, some of which are toxic to the muscle. Evidence of aberrant DUX4-driven gene expression is the major molecular signature that distinguishes muscle tissue affected by FSHD from healthy muscle. The result of aberrant DUX4 expression in FSHD is death of muscle and its replacement by fat, resulting in skeletal muscle weakness and progressive disability. Data suggest that reducing expression of the DUX4 gene and its downstream transcriptional program could provide a disease-modifying therapeutic approach for the treatment of FSHD at its root cause.

[0041] There are two ways the DUX4 gene can be unsilenced, or de-repressed. In FSHD1, which comprises approximately 95% of FSHD patients, there are mutations that lead to the shortening of an array of DNA in a region near the end of the long arm of chromosome 4, known as D4Z4, which has repeats in the subtelomeric region of the chromosome. The D4Z4 region is abnormally shortened and contains between 1-10 repeats instead of the normal 11 to 100 repeats. This contraction causes hypomethylation of the D4Z4 region and de-repression of DUX4. Patients with FSHD2 do not have a meaningful D4Z4 repeat contraction, but have mutations in a regulatory gene, known as the SMCHD1 gene, that normally contributes to the repression of the DUX4 gene via DNA methylation. When that repression is lost due to the mutations of the SMCHD1 gene leading to the hypomethylation of the D4Z4 region, DUX4 is inappropriately expressed, inducing the disease state. FIG. 1 shows an illustrative diagram of FSHD pathology.

[0042] Nucleic acid (*e.g.*, RNAi) therapy is a targeted therapy with high selectivity and specificity. However, in some instances, nucleic acid therapy is also hindered by poor intracellular uptake, limited blood stability and non-specific immune stimulation. To address these issues, various modifications of the nucleic acid composition are explored, such as for example, novel linkers for better stabilizing and/or lower toxicity, optimization of binding moiety for increased target specificity and/or target delivery, and nucleic acid polymer modifications for increased stability and/or reduced off-target effect.

[0043] In some embodiments, the arrangement or order of the different components that make-up the nucleic acid composition further effects intracellular uptake, stability, toxicity, efficacy, and/or non-specific immune stimulation. For example, if the nucleic acid component includes a binding moiety, a polymer, and a polynucleic acid molecule (or polynucleotide), the order or arrangement of the binding moiety, the polymer, and/or the polynucleic acid molecule (or polynucleotide) (*e.g.*, binding moiety-polynucleic acid molecule-polymer, binding moiety-polymer-polynucleic acid molecule, or polymer-binding moiety-polynucleic acid molecule) further effects intracellular uptake, stability, toxicity, efficacy, and/or non-specific immune stimulation.

[0044] In some embodiments, described herein include polynucleic acid molecules and polynucleic acid molecule conjugates for the treatment of Facioscapulohumeral Muscular Dystrophy (FSHD) especially muscle dystrophy and/or muscle atrophy associated therewith. In some instances, the polynucleic acid molecule conjugates described herein enhance intracellular uptake, stability, and/or efficacy. In some cases, the polynucleic acid molecule conjugates comprise an antibody or antigen binding fragment thereof conjugated to a polynucleic acid

molecule. In some cases, the polynucleic acid molecules that hybridize to target sequences of DUX4, preferably human DUX4.

[0045] Additional embodiments described herein include methods of treating FSHD, comprising administering to a subject a polynucleic acid molecule or a polynucleic acid molecule conjugate described herein.

Polynucleic Acid Molecules

[0046] In certain embodiments, a polynucleic acid molecule hybridizes to a target sequence of Double homeobox 4 (DUX4) gene. In some instances, a polynucleic acid molecule described herein hybridizes to a target sequence of human DUX4 gene (*DUX4*) and reduces DUX4 mRNA in muscle cells.

[0047] In some embodiments, the polynucleic acid molecule comprises a sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 1-70. In some embodiments, the polynucleic acid molecule comprises a sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 141-210. In some embodiments, the polynucleic acid molecule comprises a sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 71-140. In some embodiments, the polynucleic acid molecule comprises a sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 211-280.

[0048] In some embodiments, the polynucleic acid molecule comprises a first polynucleotide and a second polynucleotide. In some instances, the first polynucleotide comprises a sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 1-70. In some cases, the second polynucleotide comprises a sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 71-140. In some cases, the polynucleic acid molecule comprises a first polynucleotide and a second polynucleotide. In some instances, the first polynucleotide comprises a sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 141-210. In some cases, the second polynucleotide comprises a sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOSs: 211-280.

[0049] In some embodiments, the polynucleic acid molecule comprises a sense strand (*e.g.*, a passenger strand) and an antisense strand (*e.g.*, a guide strand). In some instances, the sense strand (*e.g.*, the passenger strand) comprises a sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 1-70. In some instances, the antisense strand (*e.g.*, the guide strand) comprises a sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 71-140. In some embodiments, the polynucleic acid molecule comprises a sense strand (*e.g.*, a passenger strand) and an antisense strand (*e.g.*, a guide strand). In some instances, the sense strand (*e.g.*, the passenger strand) comprises a sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 141-210. In some instances, the antisense strand (*e.g.*, the guide strand) comprises a sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 211-280.

[0050] In some instances, the sense strand comprises a sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 1, 2, 3, 6, 14, 36, 52, 56, 61, 62, 63, 65, 66. In some instances, the antisense strand comprises a sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from 71, 72, 73, 76, 84, 106, 122, 127, 131, 132, 133, 135, 136. In some instances, the siRNA comprises sense strand and antisense strand as presented in Table 11.

[0051] In some instances, the sense strand comprises a sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 141, 142, 143, 146, 176, 192, 196, 201, 202, 203, 205, 206. In some instances, the antisense strand comprises a sequence having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 211, 212, 213, 216, 246, 262, 266, 271, 272, 273, 275, 276. In some instances, the siRNA comprises sense strand and antisense strand as presented in Table 12.

[0052] In some embodiments, the polynucleic acid molecule described herein comprises RNA or DNA. In some cases, the polynucleic acid molecule comprises RNA. In some instances, RNA comprises short interfering RNA (siRNA), short hairpin RNA (shRNA), microRNA (miRNA), double-stranded RNA (dsRNA), transfer RNA (tRNA), ribosomal RNA (rRNA), or heterogeneous nuclear RNA (hnRNA). In some instances, RNA comprises shRNA. In some

instances, RNA comprises miRNA. In some instances, RNA comprises dsRNA. In some instances, RNA comprises tRNA. In some instances, RNA comprises rRNA. In some instances, RNA comprises hnRNA. In some instances, the oligonucleotide is a phosphorodiamidate morpholino oligomers (PMO), which are short single-stranded oligonucleotide analogs that are built upon a backbone of morpholine rings connected by phosphorodiamidate linkages. In some instances, the RNA comprises siRNA. In some instances, the polynucleic acid molecule comprises siRNA.

[0053] In some embodiments, the polynucleic acid molecule is from about 8 to about 50 nucleotides in length. In some embodiments, the polynucleic acid molecule is from about 10 to about 50 nucleotides in length. In some instances, the polynucleic acid molecule is from about 10 to about 30, from about 15 to about 30, from about 18 to about 25, from about 18 to about 24, from about 19 to about 23, or from about 20 to about 22 nucleotides in length.

[0054] In some embodiments, the polynucleic acid molecule is about 50 nucleotides in length. In some instances, the polynucleic acid molecule is about 45 nucleotides in length. In some instances, the polynucleic acid molecule is about 40 nucleotides in length. In some instances, the polynucleic acid molecule is about 35 nucleotides in length. In some instances, the polynucleic acid molecule is about 30 nucleotides in length. In some instances, the polynucleic acid molecule is about 25 nucleotides in length. In some instances, the polynucleic acid molecule is about 20 nucleotides in length. In some instances, the polynucleic acid molecule is about 19 nucleotides in length. In some instances, the polynucleic acid molecule is about 18 nucleotides in length. In some instances, the polynucleic acid molecule is about 17 nucleotides in length. In some instances, the polynucleic acid molecule is about 16 nucleotides in length. In some instances, the polynucleic acid molecule is about 15 nucleotides in length. In some instances, the polynucleic acid molecule is about 14 nucleotides in length. In some instances, the polynucleic acid molecule is about 13 nucleotides in length. In some instances, the polynucleic acid molecule is about 12 nucleotides in length. In some instances, the polynucleic acid molecule is about 11 nucleotides in length. In some instances, the polynucleic acid molecule is about 10 nucleotides in length. In some instances, the polynucleic acid molecule is about 8 nucleotides in length. In some instances, the polynucleic acid molecule is between about 8 and about 50 nucleotides in length. In some instances, the polynucleic acid molecule is between about 10 and about 50 nucleotides in length. In some instances, the polynucleic acid molecule is between about 10 and about 45 nucleotides in length. In some instances, the polynucleic acid molecule is between about 10 and about 40 nucleotides in length. In some instances, the polynucleic acid molecule is between about 10 and about 35 nucleotides in length. In some instances, the polynucleic acid molecule is between about 10 and about 30 nucleotides

in length. In some instances, the polynucleic acid molecule is between about 10 and about 25 nucleotides in length. In some instances, the polynucleic acid molecule is between about 10 and about 20 nucleotides in length. In some instances, the polynucleic acid molecule is between about 15 and about 25 nucleotides in length. In some instances, the polynucleic acid molecule is between about 15 and about 30 nucleotides in length. In some instances, the polynucleic acid molecule is between about 12 and about 30 nucleotides in length.

[0055] In some embodiments, the polynucleic acid molecule comprises a first polynucleotide. In some instances, the polynucleic acid molecule comprises a second polynucleotide. In some instances, the polynucleic acid molecule comprises a first polynucleotide and a second polynucleotide. In some instances, the first polynucleotide is a sense strand or passenger strand. In some instances, the second polynucleotide is an antisense strand or guide strand.

[0056] In some embodiments, the polynucleic acid molecule is a first polynucleotide. In some embodiments, the first polynucleotide is from about 8 to about 50 nucleotides in length. In some embodiments, the first polynucleotide is from about 10 to about 50 nucleotides in length. In some instances, the first polynucleotide is from about 10 to about 30, from about 15 to about 30, from about 18 to about 25, from about 18 to about 24, from about 19 to about 23, or from about 20 to about 22 nucleotides in length.

[0057] In some instances, the first polynucleotide is about 50 nucleotides in length. In some instances, the first polynucleotide is about 45 nucleotides in length. In some instances, the first polynucleotide is about 40 nucleotides in length. In some instances, the first polynucleotide is about 35 nucleotides in length. In some instances, the first polynucleotide is about 30 nucleotides in length. In some instances, the first polynucleotide is about 25 nucleotides in length. In some instances, the first polynucleotide is about 20 nucleotides in length. In some instances, the first polynucleotide is about 19 nucleotides in length. In some instances, the first polynucleotide is about 18 nucleotides in length. In some instances, the first polynucleotide is about 17 nucleotides in length. In some instances, the first polynucleotide is about 16 nucleotides in length. In some instances, the first polynucleotide is about 15 nucleotides in length. In some instances, the first polynucleotide is about 14 nucleotides in length. In some instances, the first polynucleotide is about 13 nucleotides in length. In some instances, the first polynucleotide is about 12 nucleotides in length. In some instances, the first polynucleotide is about 11 nucleotides in length. In some instances, the first polynucleotide is about 10 nucleotides in length. In some instances, the first polynucleotide is about 8 nucleotides in length. In some instances, the first polynucleotide is between about 8 and about 50 nucleotides in length. In some instances, the first polynucleotide is between about 10 and about 50 nucleotides in length. In some instances, the first polynucleotide is between about 10 and about 45

nucleotides in length. In some instances, the first polynucleotide is between about 10 and about 40 nucleotides in length. In some instances, the first polynucleotide is between about 10 and about 35 nucleotides in length. In some instances, the first polynucleotide is between about 10 and about 30 nucleotides in length. In some instances, the first polynucleotide is between about 10 and about 25 nucleotides in length. In some instances, the first polynucleotide is between about 10 and about 20 nucleotides in length. In some instances, the first polynucleotide is between about 15 and about 25 nucleotides in length. In some instances, the first polynucleotide is between about 15 and about 30 nucleotides in length. In some instances, the first polynucleotide is between about 12 and about 30 nucleotides in length.

[0058] In some embodiments, the polynucleic acid molecule is a second polynucleotide. In some embodiments, the second polynucleotide is from about 8 to about 50 nucleotides in length. In some embodiments, the second polynucleotide is from about 10 to about 50 nucleotides in length. In some instances, the second polynucleotide is from about 10 to about 30, from about 15 to about 30, from about 18 to about 25, from about 18 to about 24, from about 19 to about 23, or from about 20 to about 22 nucleotides in length.

[0059] In some instances, the second polynucleotide is about 50 nucleotides in length. In some instances, the second polynucleotide is about 45 nucleotides in length. In some instances, the second polynucleotide is about 40 nucleotides in length. In some instances, the second polynucleotide is about 35 nucleotides in length. In some instances, the second polynucleotide is about 30 nucleotides in length. In some instances, the second polynucleotide is about 25 nucleotides in length. In some instances, the second polynucleotide is about 20 nucleotides in length. In some instances, the second polynucleotide is about 19 nucleotides in length. In some instances, the second polynucleotide is about 18 nucleotides in length. In some instances, the second polynucleotide is about 17 nucleotides in length. In some instances, the second polynucleotide is about 16 nucleotides in length. In some instances, the second polynucleotide is about 15 nucleotides in length. In some instances, the second polynucleotide is about 14 nucleotides in length. In some instances, the second polynucleotide is about 13 nucleotides in length. In some instances, the second polynucleotide is about 12 nucleotides in length. In some instances, the second polynucleotide is about 11 nucleotides in length. In some instances, the second polynucleotide is about 10 nucleotides in length. In some instances, the second polynucleotide is about 8 nucleotides in length. In some instances, the second polynucleotide is between about 8 and about 50 nucleotides in length. In some instances, the second polynucleotide is between about 10 and about 50 nucleotides in length. In some instances, the second polynucleotide is between about 10 and about 45 nucleotides in length. In some instances, the second polynucleotide is between about 10 and about 40 nucleotides in length. In

some instances, the second polynucleotide is between about 10 and about 35 nucleotides in length. In some instances, the second polynucleotide is between about 10 and about 30 nucleotides in length. In some instances, the second polynucleotide is between about 10 and about 25 nucleotides in length. In some instances, the second polynucleotide is between about 10 and about 20 nucleotides in length. In some instances, the second polynucleotide is between about 15 and about 25 nucleotides in length. In some instances, the second polynucleotide is between about 15 and about 30 nucleotides in length. In some instances, the second polynucleotide is between about 12 and about 30 nucleotides in length.

[0060] In some embodiments, the polynucleic acid molecule comprises a first polynucleotide and a second polynucleotide. In some instances, the polynucleic acid molecule further comprises a blunt terminus, an overhang, or a combination thereof. In some instances, the blunt terminus is a 5' blunt terminus, a 3' blunt terminus, or both. In some cases, the overhang is a 5' overhang, 3' overhang, or both. In some cases, the overhang comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 non-base pairing nucleotides. In some cases, the overhang comprises 1, 2, 3, 4, 5, or 6 non-base pairing nucleotides. In some cases, the overhang comprises 1, 2, 3, or 4 non-base pairing nucleotides. In some cases, the overhang comprises 1 non-base pairing nucleotide. In some cases, the overhang comprises 2 non-base pairing nucleotides. In some cases, the overhang comprises 3 non-base pairing nucleotides. In some cases, the overhang comprises 4 non-base pairing nucleotides. In some embodiments, the polynucleic acid molecule comprises a sense strand and an antisense strand, and the antisense strand includes two non-base pairing nucleotides as an overhang at the 3'-end while the sense strand has no overhang. Optionally, in such embodiments, the non-base pairing nucleotides have a sequence of TT, dTdT, or UU. In some embodiments, the polynucleic acid molecule comprises a sense strand and an antisense strand, and the sense strand has one or more nucleotides at the 5'-end that are complementary to the antisense sequence.

[0061] In some embodiments, the sequence of the polynucleic acid molecule is at least 40%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99%, or 99.5% complementary to a target sequence of DUX4. In some embodiments, the target sequence of *DUX4* is a nucleic acid sequence of about 10-50 base pair length, about 15-50 base pair length, 15-40 base pair length, 15-30 base pair length, or 15-25 base pair length sequences in *DUX4*, in which the first nucleotide of the target sequence starts at any nucleotide in *DUX4* mRNA transcript in the coding region, or in the 5' or 3'-untranslated region (UTR). For example, the first nucleotide of the target sequence can be selected so that it starts at the nucleic acid location (nal, number starting from the 5'-end of the full length of *DUX* mRNA, *e.g.*, the 5'-end first nucleotide is nal.1) 1, nal 2, nal 3, nal 4, nal 5, nal 6, nal 7, nal 8, nal 9, nal 10, nal 11, nal 12, nal 13, nal 14,

nal 15, nal 15, nal 16, nal 17, or any other nucleic acid location in the coding or noncoding regions (5' or 3'-untranslated region) of DUX mRNA. In some embodiments, the first nucleotide of the target sequence can be selected so that it starts at a location within, or between, nal 10- nal 15, nal 10- nal 20, nal 50- nal 60, nal 55- nal 65, nal 75- nal 85, nal 95- nal 105, nal 135- nal 145, nal 155- nal 165, nal 225- nal 235, nal 265- nal 275, nal 275- nal 285, nal 285- nal 295, nal 325- nal 335, nal 335- nal 345, nal 385- nal 395, nal 515- nal 525, nal 665- nal 675, nal 675- nal 685, nal 695- nal 705, nal 705- nal 715, nal 875- nal 885, nal 885- nal 895, nal 895- nal 905, nal 1035- nal 1045, nal 1045- nal 1055, nal 1125- nal 1135, nal 1135- nal 1145, nal 1145- nal 1155, nal 1155- nal 1165, nal 1125- nal 1135, nal 1155- nal 1165, nal 1225- nal 1235, nal 1235- nal 1245, nal 1275- nal 1285, nal 1285- nal 1295, nal 1305- nal 1315, nal 1125- nal 1135, nal 1155- nal 1165, nal 1225- nal 1235, nal 1235- nal 1245, nal 1275- nal 1285, nal 1285- nal 1295, nal 1305- nal 1315, nal 1315- nal 1325, nal 1335- nal 1345, nal 1345- nal 1355, nal 1525- nal 1535, nal 1535- nal 1545, nal 1605- nal 1615, nal 1615- c.1625, nal 1625- nal 1635.

[0062] In some embodiments, the sequence of the polynucleic acid molecule is at least 50% complementary to a target sequence described herein. In some embodiments, the sequence of the polynucleic acid molecule is at least 60% complementary to a target sequence described herein. In some embodiments, the sequence of the polynucleic acid molecule is at least 70% complementary to a target sequence described herein. In some embodiments, the sequence of the polynucleic acid molecule is at least 80% complementary to a target sequence described herein. In some embodiments, the sequence of the polynucleic acid molecule is at least 90% complementary to a target sequence described herein. In some embodiments, the sequence of the polynucleic acid molecule is at least 95% complementary to a target sequence described herein. In some embodiments, the sequence of the polynucleic acid molecule is at least 99% complementary to a target sequence described herein. In some instances, the sequence of the polynucleic acid molecule is 100% complementary to a target sequence described herein.

[0063] In some embodiments, the sequence of the polynucleic acid molecule has 5 or less mismatches to a target sequence described herein. In some embodiments, the sequence of the polynucleic acid molecule has 4 or less mismatches to a target sequence described herein. In some instances, the sequence of the polynucleic acid molecule has 3 or less mismatches to a target sequence described herein. In some cases, the sequence of the polynucleic acid molecule has 2 or less mismatches to a target sequence described herein. In some cases, the sequence of the polynucleic acid molecule has 1 or less mismatches to a target sequence described herein.

[0064] In some embodiments, a group of polynucleic acid molecules among all the polynucleic acid molecules potentially binds to the target sequence of *DUX4* are selected to generate a polynucleic acid molecule library. In certain embodiments, such selection process is conducted

in silico via one or more steps of eliminating less desirable polynucleic acid molecules from candidates. For example, in some embodiments, the selection process comprises an elimination step of one or more polynucleic acid molecule that has single nucleotide polymorphism (SNP) and/or MEF < -5. Alternatively and/or additionally, in some embodiments, the selection process comprises an elimination step of one or more polynucleic acid molecule with 0 and 1 mismatch (MM) in the human transcriptome (such that only hits allowed are DUX, DUX5, and DBET). Alternatively and/or additionally, in some embodiments, the selection process comprises an elimination step of one or more polynucleic acid molecule with 0 MM in the human intragenic regions (such that only hits allowed are DUX1, DUX5 and DBET pseudogenes). Alternatively and/or additionally, in some embodiments, the selection process comprises an elimination step of one or more polynucleic acid molecule with a MM to DUX4 human sequence used in FLExDUX4 FSHD mouse model. Alternatively and/or additionally, in some embodiments, the selection process comprises an elimination step of one or more polynucleic acid molecule predicted viability < 60. Alternatively and/or additionally, such selection process comprises carrying forward one or more polynucleic acid molecule predicted viability ≥ 60 . Alternatively and/or additionally, in some embodiments, the selection process comprises an elimination step of one or more polynucleic acid molecule with a match to a seed region of known miRNAs 1-1000. Alternatively and/or additionally, in some embodiments, the selection process comprises an elimination step of one or more polynucleic acid molecule with %GC content 75 and above. Alternatively and/or additionally, in some embodiments, the selection process comprises a selection step of 8 or less predicted off-target hits with 2 MM. In some embodiments, for the region 295-1132 (nal 295-1132), 12 or less predicted off-target hits with 2 MM is allowed.

[0065] In some embodiments, selection process is conducted in silico via one or more consecutive steps of eliminating less desirable polynucleic acid molecules from candidates. For example, in some embodiments, selection process begins with collecting candidate polynucleic acid molecules to generate a library. From the library, the first eliminating step comprises eliminating one or more polynucleic acid molecule that has single nucleotide polymorphism (SNP) and/or MEF < -5. Then, the second eliminating step comprises eliminating one or more polynucleic acid molecule with 0 and 1 MM in the human transcriptome (such that only hits allowed are DUX, DUX5, and DBET). Then, the third eliminating step comprises eliminating one or more polynucleic acid molecule with 0 MM in the human intragenic regions (such that only hits allowed are DUX1, DUX5 and DBET pseudogenes). Then, the next eliminating step comprises eliminating one or more polynucleic acid molecule with a MM to DUX4 human sequence used in FLExDUX4 FSHD mouse model. Then, the next step is carrying forward only one or more polynucleic acid molecule with predicted viability ≥ 60 . Next, the eliminating

step comprises eliminating one or more polynucleic acid molecule with a match to a seed region of known miRNAs 1-1000. Then, the eliminating step continues with eliminating one or more polynucleic acid molecule with %GC content 75 and above. Then, the final selection process comprises with 8 or less predicted off-target hits with 2 MM, except for the region 295-1132, for which up to 12 hits are allowed.

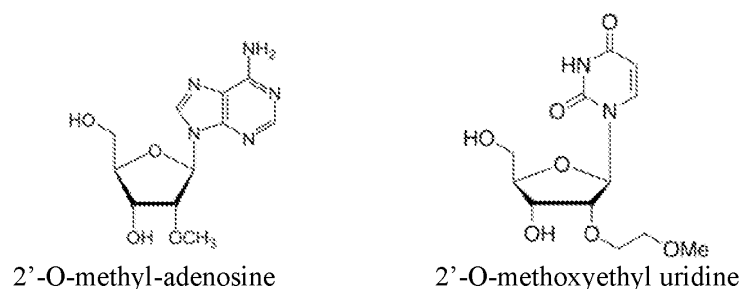
[0066] In some embodiments, the specificity of the polynucleic acid molecule that hybridizes to a target sequence described herein is a 95%, 98%, 99%, 99.5% or 100% sequence complementarity of the polynucleic acid molecule to a target sequence. In some instances, the hybridization is a high stringent hybridization condition.

[0067] In some embodiments, the polynucleic acid molecule has reduced off-target effect. In some instances, “off-target” or “off-target effects” refer to any instance in which a polynucleic acid polymer directed against a given target causes an unintended effect by interacting either directly or indirectly with another mRNA sequence, a DNA sequence or a cellular protein or other moiety. In some instances, an “off-target effect” occurs when there is a simultaneous degradation of other transcripts due to partial homology or complementarity between that other transcript and the sense and/or antisense strand of the polynucleic acid molecule.

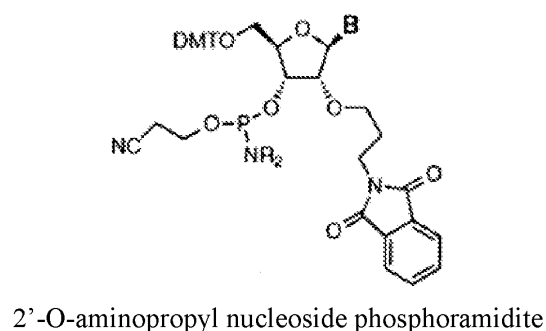
[0068] In some embodiments, the polynucleic acid molecule comprises natural or synthetic or artificial nucleotide analogues or bases. In some cases, the polynucleic acid molecule comprises combinations of DNA, RNA and/or nucleotide analogues. In some instances, the synthetic or artificial nucleotide analogues or bases comprise modifications at one or more of ribose moiety, phosphate moiety, nucleoside moiety, or a combination thereof.

[0069] In some embodiments, nucleotide analogues or artificial nucleotide base comprise a nucleic acid with a modification at a 2' hydroxyl group of the ribose moiety. In some instances, the modification includes an H, OR, R, halo, SH, SR, NH₂, NHR, NR₂, or CN, wherein R is an alkyl moiety. Exemplary alkyl moiety includes, but is not limited to, halogens, sulfurs, thiols, thioethers, thioesters, amines (primary, secondary, or tertiary), amides, ethers, esters, alcohols and oxygen. In some instances, the alkyl moiety further comprises a modification. In some instances, the modification comprises an azo group, a keto group, an aldehyde group, a carboxyl group, a nitro group, a nitroso group, a nitrile group, a heterocycle (*e.g.*, imidazole, hydrazino or hydroxylamino) group, an isocyanate or cyanate group, or a sulfur containing group (*e.g.*, sulfoxide, sulfone, sulfide, and disulfide). In some instances, the alkyl moiety further comprises a hetero substitution. In some instances, the carbon of the heterocyclic group is substituted by a nitrogen, oxygen or sulfur. In some instances, the heterocyclic substitution includes but is not limited to, morpholino, imidazole, and pyrrolidino.

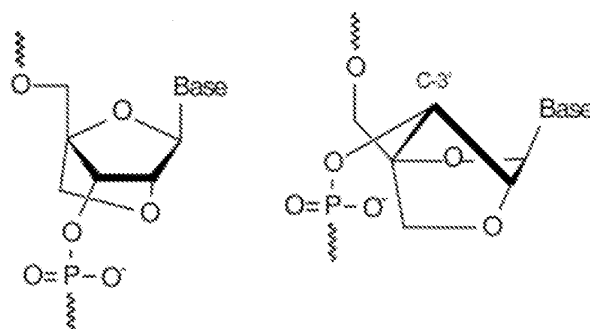
[0070] In some instances, the modification at the 2' hydroxyl group is a 2'-O-methyl modification or a 2'-O-methoxyethyl (2'-O-MOE) modification. In some cases, the 2'-O-methyl modification adds a methyl group to the 2' hydroxyl group of the ribose moiety whereas the 2'-O-methoxyethyl modification adds a methoxyethyl group to the 2' hydroxyl group of the ribose moiety. Exemplary chemical structures of a 2'-O-methyl modification of an adenosine molecule and 2'-O-methoxyethyl modification of an uridine are illustrated below.



[0071] In some instances, the modification at the 2' hydroxyl group is a 2'-O-aminopropyl modification in which an extended amine group comprising a propyl linker binds the amine group to the 2' oxygen. In some instances, this modification neutralizes the phosphate derived overall negative charge of the oligonucleotide molecule by introducing one positive charge from the amine group per sugar and thereby improves cellular uptake properties due to its zwitterionic properties. An exemplary chemical structure of a 2'-O-aminopropyl nucleoside phosphoramidite is illustrated below.

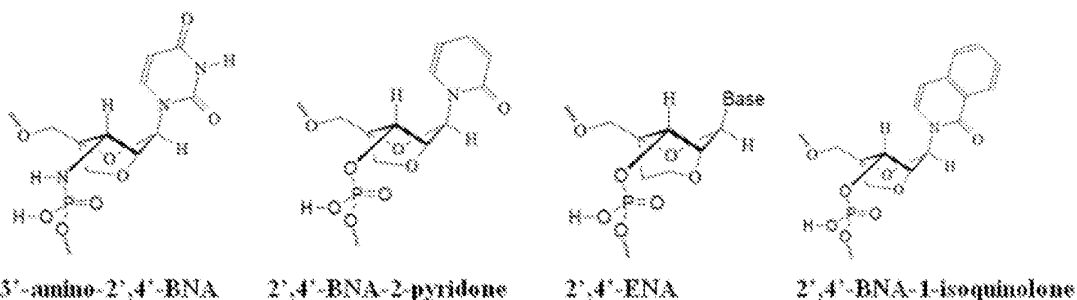


[0072] In some instances, the modification at the 2' hydroxyl group is a locked or bridged ribose modification (*e.g.*, locked nucleic acid or LNA) in which the oxygen molecule bound at the 2' carbon is linked to the 4' carbon by a methylene group, thus forming a 2'-C,4'-C-oxy-methylene-linked bicyclic ribonucleotide monomer. Exemplary representations of the chemical structure of LNA are illustrated below. The representation shown to the left highlights the chemical connectivities of an LNA monomer. The representation shown to the right highlights the locked 3'-endo (³E) conformation of the furanose ring of an LNA monomer.



LNA (Locked Nucleic Acids)

[0073] In some instances, the modification at the 2' hydroxyl group comprises ethylene nucleic acids (ENA) such as for example 2'-4'-ethylene-bridged nucleic acid, which locks the sugar conformation into a C_{3'}'-endo sugar pucker conformation. ENA are part of the bridged nucleic acids class of modified nucleic acids that also comprises LNA. Exemplary chemical structures of the ENA and bridged nucleic acids are illustrated below.

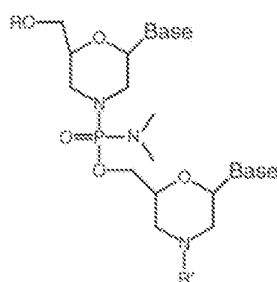


[0074] In some embodiments, additional modifications at the 2' hydroxyl group include 2'-deoxy, 2'-deoxy-2'-fluoro, 2'-O-aminopropyl (2'-O-AP), 2'-O-dimethylaminoethyl (2'-O-DMAOE), 2'-O-dimethylaminopropyl (2'-O-DMAP), 2'-O-dimethylaminoethoxyethyl (2'-O-DMAEOE), or 2'-O-N-methylacetamido (2'-O-NMA).

[0075] In some embodiments, nucleotide analogues comprise modified bases such as, but not limited to, 5-propynyluridine, 5-propynylcytidine, 6-methyladenine, 6-methylguanine, N, N, -dimethyladenine, 2-propyladenine, 2-propylguanine, 2-aminoadenine, 1-methylinosine, 3-methyluridine, 5-methylcytidine, 5-methyluridine and other nucleotides having a modification at the 5 position, 5-(2-amino)propyl uridine, 5-halocytidine, 5-halouridine, 4-acetylcytidine, 1-methyladenosine, 2-methyladenosine, 3-methylcytidine, 6-methyluridine, 2-methylguanosine, 7-methylguanosine, 2, 2-dimethylguanosine, 5-methylaminoethyluridine, 5-methoxyuridine, deazanucleotides such as 7-deaza-adenosine, 6-azouridine, 6-azocytidine, 6-azothymidine, 5-methyl-2-thiouridine, other thio bases such as 2-thiouridine and 4-thiouridine and 2-thiocytidine, dihydrouridine, pseudouridine, queuosine, archaeosine, naphthyl and substituted naphthyl groups, any O- and N-alkylated purines and pyrimidines such as N⁶-methyladenosine, 5-

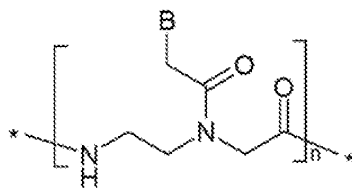
methylcarbonylmethyluridine, uridine 5-oxyacetic acid, pyridine-4-one, pyridine-2-one, phenyl and modified phenyl groups such as aminophenol or 2,4, 6-trimethoxy benzene, modified cytosines that act as G-clamp nucleotides, 8-substituted adenines and guanines, 5-substituted uracils and thymines, azapyrimidines, carboxyhydroxyalkyl nucleotides, carboxyalkylaminoalkyl nucleotides, and alkylcarbonylalkylated nucleotides. Modified nucleotides also include those nucleotides that are modified with respect to the sugar moiety, as well as nucleotides having sugars or analogs thereof that are not ribosyl. For example, the sugar moieties, in some cases are or be based on, mannoses, arabinoses, glucopyranoses, galactopyranoses, 4'-thioribose, and other sugars, heterocycles, or carbocycles. The term nucleotide also includes what are known in the art as universal bases. By way of example, universal bases include but are not limited to 3-nitropyrrole, 5-nitroindole, or nebularine.

[0076] In some embodiments, nucleotide analogues further comprise morpholinos, peptide nucleic acids (PNAs), methylphosphonate nucleotides, thiolphosphonate nucleotides, 2'-fluoro N3-P5'-phosphoramidites, 1', 5'- anhydrohexitol nucleic acids (HNAs), or a combination thereof. Morpholino or phosphorodiamidate morpholino oligo (PMO) comprises synthetic molecules whose structure mimics natural nucleic acid structure by deviates from the normal sugar and phosphate structures. In some instances, the five member ribose ring is substituted with a six member morpholino ring containing four carbons, one nitrogen and one oxygen. In some cases, the ribose monomers are linked by a phosphordiamidate group instead of a phosphate group. In such cases, the backbone alterations remove all positive and negative charges making morpholinos neutral molecules capable of crossing cellular membranes without the aid of cellular delivery agents such as those used by charged oligonucleotides.



Morpholino

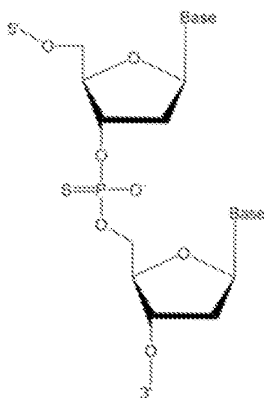
[0077] In some embodiments, peptide nucleic acid (PNA) does not contain sugar ring or phosphate linkage and the bases are attached and appropriately spaced by oligoglycine-like molecules, therefore, eliminating a backbone charge.



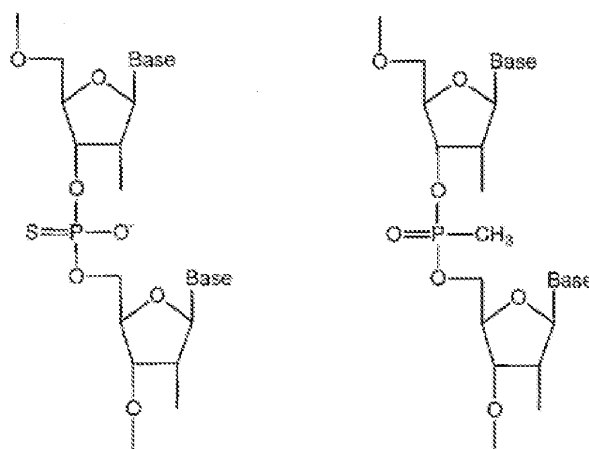
PNA

[0078] In some embodiments, one or more modifications optionally occur at the internucleotide linkage. In some instances, modified internucleotide linkage include, but is not limited to, phosphorothioates, phosphorodithioates, methylphosphonates, 5'-alkylenephosphonates, 5'-methylphosphonate, 3'-alkylene phosphonates, borontrifluoridates, borano phosphate esters and selenophosphates of 3'-5' linkage or 2'-5' linkage, phosphotriesters, thionoalkylphosphotriesters, hydrogen phosphonate linkages, alkyl phosphonates, alkylphosphonothioates, arylphosphonothioates, phosphoroselenoates, phosphorodiselenoates, phosphinates, phosphoramidates, 3'-alkylphosphoramidates, aminoalkylphosphoramidates, thionophosphoramidates, phosphoropiperazidates, phosphoroanilothioates, phosphoroanilidates, ketones, sulfones, sulfonamides, carbonates, carbamates, methylenehydrazos, methylenedimethylhydrazos, formacetals, thioformacetals, oximes, methyleneiminos, methylenemethyliminos, thioamidates, linkages with riboacetyl groups, aminoethyl glycine, silyl or siloxane linkages, alkyl or cycloalkyl linkages with or without heteroatoms of, for example, 1 to 10 carbons that are saturated or unsaturated and/or substituted and/or contain heteroatoms, linkages with morpholino structures, amides, polyamides wherein the bases are attached to the aza nitrogens of the backbone directly or indirectly, and combinations thereof.

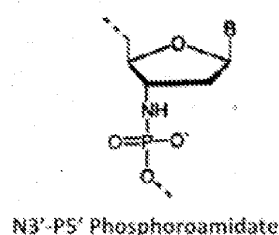
Phosphorothioate antisense oligonucleotides (PS ASO) are antisense oligonucleotides comprising a phosphorothioate linkage. An exemplary PS ASO is illustrated below.



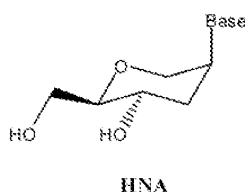
[0079] In some instances, the modification is a methyl or thiol modification such as methylphosphonate or thiolphosphonate modification. Exemplary thiolphosphonate nucleotide (left) and methylphosphonate nucleotide (right) are illustrated below.



[0080] In some instances, a modified nucleotide includes, but is not limited to, 2'-fluoro N3'-P5'-phosphoramidites illustrated as:



[0081] In some instances, a modified nucleotide includes, but is not limited to, hexitol nucleic acid (or 1', 5'- anhydrohexitol nucleic acids (HNA)) illustrated as:



[0082] In some embodiments, one or more modifications further optionally include modifications of the ribose moiety, phosphate backbone and the nucleoside, or modifications of the nucleotide analogues at the 3' or the 5' terminus. For example, the 3' terminus optionally include a 3' cationic group, or by inverting the nucleoside at the 3'-terminus with a 3'-3' linkage. In another alternative, the 3'-terminus is optionally conjugated with an aminoalkyl group, *e.g.*, a 3' C5-aminoalkyl dT. In an additional alternative, the 3'-terminus is optionally conjugated with an abasic site, *e.g.*, with an apurinic or apyrimidinic site. In some instances, the 5'-terminus is conjugated with an aminoalkyl group, *e.g.*, a 5'-O-alkylamino substituent. In

some cases, the 5'-terminus is conjugated with an abasic site, *e.g.*, with an apurinic or apyrimidinic site.

[0083] In some embodiments, the polynucleic acid molecule comprises one or more of the artificial nucleotide analogues described herein. In some instances, the polynucleic acid molecule comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 20, 25, or more of the artificial nucleotide analogues described herein. In some embodiments, the artificial nucleotide analogues include 2'-O-methyl, 2'-O-methoxyethyl (2'-O-MOE), 2'-O-aminopropyl, 2'-deoxy, 2'-deoxy-2'-fluoro, 2'-O-aminopropyl (2'-O-AP), 2'-O-dimethylaminoethyl (2'-O-DMAOE), 2'-O-dimethylaminopropyl (2'-O-DMAP), 2'-O-dimethylaminoethoxyethyl (2'-O-DMAEOE), or 2'-O-N-methylacetamido (2'-O-NMA) modified, LNA, ENA, PNA, HNA, morpholino, methylphosphonate nucleotides, thiophosphonate nucleotides, 2'-fluoro N3-P5'-phosphoramidites, or a combination thereof. In some instances, the polynucleic acid molecule comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 20, 25, or more of the artificial nucleotide analogues selected from 2'-O-methyl, 2'-O-methoxyethyl (2'-O-MOE), 2'-O-aminopropyl, 2'-deoxy, 2'-deoxy-2'-fluoro, 2'-O-aminopropyl (2'-O-AP), 2'-O-dimethylaminoethyl (2'-O-DMAOE), 2'-O-dimethylaminopropyl (2'-O-DMAP), 2'-O-dimethylaminoethoxyethyl (2'-O-DMAEOE), or 2'-O-N-methylacetamido (2'-O-NMA) modified, LNA, ENA, PNA, HNA, morpholino, methylphosphonate nucleotides, thiophosphonate nucleotides, 2'-fluoro N3-P5'-phosphoramidites, or a combination thereof. In some instances, the polynucleic acid molecule comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 20, 25, or more of 2'-O-methyl modified nucleotides. In some instances, the polynucleic acid molecule comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 20, 25, or more of 2'-O-methoxyethyl (2'-O-MOE) modified nucleotides. In some instances, the polynucleic acid molecule comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 20, 25, or more of thiophosphonate nucleotides.

[0084] In some instances, the polynucleic acid molecule comprises at least one of: from about 5% to about 100% modification, from about 10% to about 100% modification, from about 20% to about 100% modification, from about 30% to about 100% modification, from about 40% to about 100% modification, from about 50% to about 100% modification, from about 60% to about 100% modification, from about 70% to about 100% modification, from about 80% to about 100% modification, and from about 90% to about 100% modification.

[0085] In some cases, the polynucleic acid molecule comprises at least one of: from about 10% to about 90% modification, from about 20% to about 90% modification, from about 30% to about 90% modification, from about 40% to about 90% modification, from about 50% to about

90% modification, from about 60% to about 90% modification, from about 70% to about 90% modification, and from about 80% to about 100% modification.

[0086] In some cases, the polynucleic acid molecule comprises at least one of: from about 10% to about 80% modification, from about 20% to about 80% modification, from about 30% to about 80% modification, from about 40% to about 80% modification, from about 50% to about 80% modification, from about 60% to about 80% modification, and from about 70% to about 80% modification.

[0087] In some instances, the polynucleic acid molecule comprises at least one of: from about 10% to about 70% modification, from about 20% to about 70% modification, from about 30% to about 70% modification, from about 40% to about 70% modification, from about 50% to about 70% modification, and from about 60% to about 70% modification.

[0088] In some instances, the polynucleic acid molecule comprises at least one of: from about 10% to about 60% modification, from about 20% to about 60% modification, from about 30% to about 60% modification, from about 40% to about 60% modification, and from about 50% to about 60% modification.

[0089] In some cases, the polynucleic acid molecule comprises at least one of: from about 10% to about 50% modification, from about 20% to about 50% modification, from about 30% to about 50% modification, and from about 40% to about 50% modification.

[0090] In some cases, the polynucleic acid molecule comprises at least one of: from about 10% to about 40% modification, from about 20% to about 40% modification, and from about 30% to about 40% modification.

[0091] In some cases, the polynucleic acid molecule comprises at least one of: from about 10% to about 30% modification, and from about 20% to about 30% modification.

[0092] In some cases, the polynucleic acid molecule comprises from about 10% to about 20% modification.

[0093] In some cases, the polynucleic acid molecule comprises from about 15% to about 90%, from about 20% to about 80%, from about 30% to about 70%, or from about 40% to about 60% modifications.

[0094] In additional cases, the polynucleic acid molecule comprises at least about 15%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or 99% modification.

[0095] In some embodiments, the polynucleic acid molecule comprises at least about 1, about 2, about 3, about 4, about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 21, about 22 or more modifications.

[0096] In some instances, the polynucleic acid molecule comprises at least about 1, about 2, about 3, about 4, about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 21, about 22 or more modified nucleotides.

[0097] In some instances, from about 5 to about 100% of the polynucleic acid molecule comprise the artificial nucleotide analogues described herein. In some instances, about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 100% of the polynucleic acid molecule comprise the artificial nucleotide analogues described herein. In some instances, about 5% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 10% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 15% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 20% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 25% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 30% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 35% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 40% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 45% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 50% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 55% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 60% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 65% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 70% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 75% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 80% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 85% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 90% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 95% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 96% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In

some instances, about 97% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 98% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 99% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some instances, about 100% of the polynucleic acid molecule comprises the artificial nucleotide analogues described herein. In some embodiments, the artificial nucleotide analogues include 2'-O-methyl, 2'-O-methoxyethyl (2'-O-MOE), 2'-O-aminopropyl, 2'-deoxy, 2'-deoxy-2'-fluoro, 2'-O-aminopropyl (2'-O-AP), 2'-O-dimethylaminoethyl (2'-O-DMAOE), 2'-O-dimethylaminopropyl (2'-O-DMAP), 2'-O-dimethylaminoethoxyethyl (2'-O-DMAEOE), or 2'-O-N-methylacetamido (2'-O-NMA) modified, LNA, ENA, PNA, HNA, morpholino, methylphosphonate nucleotides, thiophosphonate nucleotides, 2'-fluoro N3-P5'-phosphoramidites, or a combination thereof.

[0098] In some embodiments, the polynucleic acid molecule comprises from about 1 to about 25 modifications in which the modification comprises an artificial nucleotide analogues described herein. In some embodiments, the polynucleic acid molecule comprises about 1 modification in which the modification comprises an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 2 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 3 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 4 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 5 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 6 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 7 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 8 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 9 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 10 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 11 modifications in which the

modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 12 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 13 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 14 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 15 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 16 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 17 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 18 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 19 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 20 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 21 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 22 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 23 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 24 modifications in which the modifications comprise an artificial nucleotide analogue described herein. In some embodiments, the polynucleic acid molecule comprises about 25 modifications in which the modifications comprise an artificial nucleotide analogue described herein.

[0099] In some embodiments, a polynucleic acid molecule is assembled from two separate polynucleotides wherein one polynucleotide comprises the sense strand and the second polynucleotide comprises the antisense strand of the polynucleic acid molecule. In other embodiments, the sense strand is connected to the antisense strand via a linker molecule, which in some instances is a polynucleotide linker or a non-nucleotide linker.

[0100] In some embodiments, a polynucleic acid molecule comprises a sense strand and antisense strand, wherein pyrimidine nucleotides in the sense strand comprises 2'-O-methylpyrimidine nucleotides and purine nucleotides in the sense strand comprise 2'-deoxy purine nucleotides. In some embodiments, a polynucleic acid molecule comprises a sense strand and antisense strand, wherein pyrimidine nucleotides present in the sense strand comprise 2'-deoxy-2'-fluoro pyrimidine nucleotides and wherein purine nucleotides present in the sense strand comprise 2'-deoxy purine nucleotides.

[0101] In some embodiments, a polynucleic acid molecule comprises a sense strand and antisense strand, wherein the pyrimidine nucleotides when present in said antisense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides when present in said antisense strand are 2'-O-methyl purine nucleotides.

[0102] In some embodiments, a polynucleic acid molecule comprises a sense strand and antisense strand, wherein the pyrimidine nucleotides when present in said antisense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides and wherein the purine nucleotides when present in said antisense strand comprise 2'-deoxy-purine nucleotides.

[0103] In some embodiments, a polynucleic acid molecule comprises a sense strand and antisense strand, and at least one of sense strand and antisense strands has a plurality of (*e.g.*, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, etc) 2'-O-methyl or 2'-deoxy-2'-fluoro modified nucleotides. In some embodiments, where at least two out of the a plurality of 2'-O-methyl or 2'-deoxy-2'-fluoro modified nucleotides are consecutive nucleotides. In some embodiments, where consecutive 2'-O-methyl or 2'-deoxy-2'-fluoro modified nucleotides are located at the 5'-end of the sense strand and/or the antisense strand. In some embodiments, where consecutive 2'-O-methyl or 2'-deoxy-2'-fluoro modified nucleotides are located at the 3'-end of the sense strand and/or the antisense strand. In some embodiments, the sense strand of polynucleic acid molecule includes at least four, at least five, at least six consecutive 2'-O-methyl modified nucleotides at its 5' end and/or 3' end, or both. Optionally, in such embodiments, the sense strand of polynucleic acid molecule includes at least one, at least two, at least three, at least four 2'-deoxy-2'-fluoro modified nucleotides at the 3' end of the at least four, at least five, at least six consecutive 2'-O-methyl modified nucleotides at the polynucleotides' 5' end, or at the 5' end of the at least four, at least five, at least six consecutive 2'-O-methyl modified nucleotides at polynucleotides' 3' end. Also optionally, such at least two, at least three, at least four 2'-deoxy-2'-fluoro modified nucleotides are consecutive nucleotides.

[0104] In some embodiments, a polynucleic acid molecule comprises a sense strand and antisense strand, and at least one of sense strand and antisense strands has 2'-O-methyl modified

nucleotide located at the 5'-end of the sense strand and/or the antisense strand. In some embodiments, at least one of sense strand and antisense strands has 2'-O-methyl modified nucleotide located at the 3'-end of the sense strand and/or the antisense strand. In some embodiments, the 2'-O-methyl modified nucleotide located at the 5'-end of the sense strand and/or the antisense strand is a purine nucleotide. In some embodiments, the 2'-O-methyl modified nucleotide located at the 5'-end of the sense strand and/or the antisense strand is a pyridine nucleotide.

[0105] In some embodiments, a polynucleic acid molecule comprises a sense strand and antisense strand, and the antisense strand has two or more consecutive 2'-deoxy-2'-fluoro modified nucleotides at 5'-end. In some embodiments, a polynucleic acid molecule comprises a sense strand and antisense strand, and the antisense strand has two or more consecutive 2'-O-methyl modified nucleotides at 3'-end. In some embodiments, a polynucleic acid molecule comprises a sense strand and antisense strand, and the antisense strand has at least 2, 3, 4, 5, 6, or 7 consecutive 2'-O-methyl modified nucleotides.

[0106] In some embodiments, a polynucleic acid molecule comprises a sense strand and antisense strand, and the sense strand comprises a nucleic acid of 5'-nsnsnnnnNfNfNfnnnnnnnnsnsa-3' (lower case (n) = 2'-O-Me (methyl), Nf = 2'-F (fluoro); s = phosphorothioate backbone modification). In some embodiments, a polynucleic acid molecule comprises a sense strand and antisense strand, and the antisense strand comprises a nucleic acid of 5'-UfsNfsnnnnNfnnnnnnnNfnNfnnsusu-3' (lower case (n) = 2'-O-Me (methyl), Nf = 2'-F (fluoro); s = phosphorothioate backbone modification). In some embodiments, a polynucleic acid molecule comprises a sense strand and antisense strand, and the sense strand comprises a nucleic acid of 5'-nsnsnnnnNfNfNfnnnnnnnnsnsa-3' (lower case (n) = 2'-O-Me (methyl), Nf = 2'-F (fluoro); s = phosphorothioate backbone modification) and the antisense strand comprises a nucleic acid of 5'-UfsNfsnnnnNfnnnnnnnNfnNfnnsusu-3' (lower case (n) = 2'-O-Me (methyl), Nf = 2'-F (fluoro); s = phosphorothioate backbone modification).

[0107] In some embodiments, a polynucleic acid molecule comprises a sense strand and antisense strand, wherein the sense strand includes a terminal cap moiety at the 5'-end, the 3'-end, or both of the 5' and 3' ends of the sense strand. In other embodiments, the terminal cap moiety is an inverted deoxy abasic moiety.

[0108] In some embodiments, a polynucleic acid molecule comprises a sense strand and an antisense strand, wherein the antisense strand comprises a glyceryl modification at the 3' end of the antisense strand.

[0109] In some embodiments, a polynucleic acid molecule comprises a sense strand and an antisense strand, in which the sense strand comprises one or more, for example, about 1, 2, 3, 4,

5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or about one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and in which the antisense strand comprises about 1 to about 10 or more, specifically about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In other embodiments, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, pyrimidine nucleotides of the sense and/or antisense strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

[0110] In some embodiments, a polynucleic acid molecule comprises a sense strand and an antisense strand, in which the sense strand comprises about 1 to about 25, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and in which the antisense strand comprises about 1 to about 25 or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In other embodiments, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, pyrimidine nucleotides of the sense and/or antisense strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without about 1 to about 25 or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

[0111] In some embodiments, a polynucleic acid molecule comprises a sense strand and an antisense strand, in which the antisense strand comprises one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more phosphorothioate internucleotide linkages, and/or about one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand and/or antisense strand, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand. In some embodiments, the antisense strand comprises about 1 to about 10 or more, specifically about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In other embodiments, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more pyrimidine nucleotides of the sense and/or antisense strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3' and 5'-ends, being present in the same or different strand.

[0112] In some embodiments, a polynucleic acid molecule comprises a sense strand and an antisense strand, in which the antisense strand comprises about 1 to about 25 or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and the antisense strand comprises about 1 to about 25 or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In other embodiments, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more pyrimidine nucleotides of the sense and/or antisense strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without about 1 to about 5, for example about 1, 2, 3, 4, 5 or more

phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

[0113] In some embodiments, a polynucleic acid molecule described herein is a chemically-modified short interfering nucleic acid molecule having about 1 to about 25, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more phosphorothioate internucleotide linkages in each strand of the polynucleic acid molecule. In some embodiments, a polynucleic acid molecule comprises a sense strand and an antisense strand, and the antisense strand comprises a phosphate backbone modification at the 3' end of the antisense strand. Alternatively and/or additionally, a polynucleic acid molecule comprises a sense strand and an antisense strand, and the sense strand comprises a phosphate backbone modification at the 5' end of the antisense strand. In some instances, the phosphate backbone modification is a phosphorothioate. In some embodiments, the sense or antisense strand has three consecutive nucleosides that are coupled via two phosphorothioate backbone.

[0114] In another embodiment, a polynucleic acid molecule described herein comprises 2'-5' internucleotide linkages. In some instances, the 2'-5' internucleotide linkage(s) is at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of one or both sequence strands. In addition instances, the 2'-5' internucleotide linkage(s) is present at various other positions within one or both sequence strands, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more including every internucleotide linkage of a pyrimidine nucleotide in one or both strands of the polynucleic acid molecule comprise a 2'-5' internucleotide linkage, or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more including every internucleotide linkage of a purine nucleotide in one or both strands of the polynucleic acid molecule comprise a 2'-5' internucleotide linkage.

[0115] In some embodiments, a polynucleic acid molecule is a single stranded polynucleic acid molecule that mediates RNAi activity in a cell or reconstituted *in vitro* system, wherein the polynucleic acid molecule comprises a single stranded polynucleotide having complementarity to a target nucleic acid sequence, and wherein one or more pyrimidine nucleotides present in the polynucleic acid are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any purine nucleotides present in the polynucleic acid are 2'-deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides), and a terminal cap modification, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the polynucleic acid molecule optionally further comprising about 1 to about 4 (*e.g.*, about 1, 2, 3, or 4) terminal 2'-deoxynucleotides at the 3'-end of the polynucleic acid molecule, wherein the terminal

nucleotides further comprise one or more (*e.g.*, 1, 2, 3, or 4) phosphorothioate internucleotide linkages, and wherein the polynucleic acid molecule optionally further comprises a terminal phosphate group, such as a 5'-terminal phosphate group.

[0116] In some cases, one or more of the artificial nucleotide analogues described herein are resistant toward nucleases such as for example ribonuclease such as RNase H, deoxyribonuclease such as DNase, or exonuclease such as 5'-3' exonuclease and 3'-5' exonuclease when compared to natural polynucleic acid molecules. In some instances, artificial nucleotide analogues comprising 2'-O-methyl, 2'-O-methoxyethyl (2'-O-MOE), 2'-O-aminopropyl, 2'-deoxy, 2'-deoxy-2'-fluoro, 2'-O-aminopropyl (2'-O-AP), 2'-O-dimethylaminoethyl (2'-O-DMAOE), 2'-O-dimethylaminopropyl (2'-O-DMAP), 2'-O-dimethylaminoethoxyethyl (2'-O-DMAEOE), or 2'-O-N-methylacetamido (2'-O-NMA) modified, LNA, ENA, PNA, HNA, morpholino, methylphosphonate nucleotides, thiolphosphonate nucleotides, 2'-fluoro N3-P5'-phosphoramidites, or combinations thereof are resistant toward nucleases such as for example ribonuclease such as RNase H, deoxyribonuclease such as DNase, or exonuclease such as 5'-3' exonuclease and 3'-5' exonuclease. In some instances, 2'-O-methyl modified polynucleic acid molecule is nuclease resistance (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some instances, 2'-O-methoxyethyl (2'-O-MOE) modified polynucleic acid molecule is nuclease resistance (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some instances, 2'-O-aminopropyl modified polynucleic acid molecule is nuclease resistance (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some instances, 2'-deoxy modified polynucleic acid molecule is nuclease resistance (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some instances, 2'-deoxy-2'-fluoro modified polynucleic acid molecule is nuclease resistance (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some instances, 2'-O-aminopropyl (2'-O-AP) modified polynucleic acid molecule is nuclease resistance (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some instances, 2'-O-dimethylaminoethyl (2'-O-DMAOE) modified polynucleic acid molecule is nuclease resistance (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some instances, 2'-O-dimethylaminopropyl (2'-O-DMAP) modified polynucleic acid molecule is nuclease resistance (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some instances, 2'-O-dimethylaminoethoxyethyl (2'-O-DMAEOE) modified polynucleic acid molecule is nuclease resistance (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some instances, 2'-O-N-methylacetamido (2'-O-NMA) modified polynucleic acid molecule is nuclease resistance (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some

instances, LNA modified polynucleic acid molecule is nuclease resistance (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some instances, ENA modified polynucleic acid molecule is nuclease resistance (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some instances, HNA modified polynucleic acid molecule is nuclease resistance (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some instances, morpholinos is nuclease resistance (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some instances, PNA modified polynucleic acid molecule is resistant to nucleases (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some instances, methylphosphonate nucleotides modified polynucleic acid molecule is nuclease resistance (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some instances, thiophosphonate nucleotides modified polynucleic acid molecule is nuclease resistance (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some instances, polynucleic acid molecule comprising 2'-fluoro N3-P5'-phosphoramidites is nuclease resistance (*e.g.*, RNase H, DNase, 5'-3' exonuclease or 3'-5' exonuclease resistance). In some instances, the 5' conjugates described herein inhibit 5'-3' exonucleolytic cleavage. In some instances, the 3' conjugates described herein inhibit 3'-5' exonucleolytic cleavage.

[0117] In some embodiments, one or more of the artificial nucleotide analogues described herein have increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. The one or more of the artificial nucleotide analogues comprising 2'-O-methyl, 2'-O-methoxyethyl (2'-O-MOE), 2'-O-aminopropyl, 2'-deoxy, 2'-deoxy-2'-fluoro, 2'-O-aminopropyl (2'-O-AP), 2'-O-dimethylaminoethyl (2'-O-DMAOE), 2'-O-dimethylaminopropyl (2'-O-DMAP), 2'-O-dimethylaminoethyloxyethyl (2'-O-DMAEOE), or 2'-O-N-methylacetamido (2'-O-NMA) modified, LNA, ENA, PNA, HNA, morpholino, methylphosphonate nucleotides, thiophosphonate nucleotides, or 2'-fluoro N3-P5'-phosphoramidites have increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some instances, 2'-O-methyl modified polynucleic acid molecule has increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some instances, 2'-O-methoxyethyl (2'-O-MOE) modified polynucleic acid molecule has increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some instances, 2'-O-aminopropyl modified polynucleic acid molecule has increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some instances, 2'-deoxy modified polynucleic acid molecule has increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some instances, 2'-deoxy-2'-fluoro modified polynucleic acid molecule has increased binding affinity toward their mRNA

target relative to an equivalent natural polynucleic acid molecule. In some instances, 2'-O-aminopropyl (2'-O-AP) modified polynucleic acid molecule has increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some instances, 2'-O-dimethylaminoethyl (2'-O-DMAOE) modified polynucleic acid molecule has increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some instances, 2'-O-dimethylaminopropyl (2'-O-DMAP) modified polynucleic acid molecule has increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some instances, 2'-O-dimethylaminoethoxyethyl (2'-O-DMAEOE) modified polynucleic acid molecule has increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some instances, 2'-O-N-methylacetamido (2'-O-NMA) modified polynucleic acid molecule has increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some instances, LNA modified polynucleic acid molecule has increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some instances, ENA modified polynucleic acid molecule has increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some instances, PNA modified polynucleic acid molecule has increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some instances, HNA modified polynucleic acid molecule has increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some instances, morpholino modified polynucleic acid molecule has increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some instances, methylphosphonate nucleotides modified polynucleic acid molecule has increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some instances, thiophosphonate nucleotides modified polynucleic acid molecule has increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some instances, polynucleic acid molecule comprising 2'-fluoro N3-P5'-phosphoramidites has increased binding affinity toward their mRNA target relative to an equivalent natural polynucleic acid molecule. In some cases, the increased affinity is illustrated with a lower K_d, a higher melt temperature (T_m), or a combination thereof.

[0118] In some embodiments, a polynucleic acid molecule described herein is a chirally pure (or stereo pure) polynucleic acid molecule, or a polynucleic acid molecule comprising a single enantiomer. In some instances, the polynucleic acid molecule comprises L-nucleotide. In some instances, the polynucleic acid molecule comprises D-nucleotides. In some instance, a

polynucleic acid molecule composition comprises less than 30%, 25%, 20%, 15%, 10%, 5%, 4%, 3%, 2%, 1%, or less of its mirror enantiomer. In some cases, a polynucleic acid molecule composition comprises less than 30%, 25%, 20%, 15%, 10%, 5%, 4%, 3%, 2%, 1%, or less of a racemic mixture. In some instances, the polynucleic acid molecule is a polynucleic acid molecule described in: U.S. Patent Publication Nos: 2014/194610 and 2015/211006; and PCT Publication No: WO2015107425.

[0119] In some embodiments, a polynucleic acid molecule described herein is further modified to include an aptamer conjugating moiety. In some instances, the aptamer conjugating moiety is a DNA aptamer conjugating moiety. In some instances, the aptamer conjugating moiety is Alphamer (Centauri Therapeutics), which comprises an aptamer portion that recognizes a specific cell-surface target and a portion that presents a specific epitopes for attaching to circulating antibodies. In some instance, a polynucleic acid molecule described herein is further modified to include an aptamer conjugating moiety as described in: U.S. Patent NOs: 8,604,184, 8,591,910, and 7,850,975.

[0120] In additional embodiments, a polynucleic acid molecule described herein is modified to increase its stability. In some embodiment, the polynucleic acid molecule is RNA (*e.g.*, siRNA). In some instances, the polynucleic acid molecule is modified by one or more of the modifications described above to increase its stability. In some cases, the polynucleic acid molecule is modified at the 2' hydroxyl position, such as by 2'-O-methyl, 2'-O-methoxyethyl (2'-O-MOE), 2'-O-aminopropyl, 2'-deoxy, 2'-deoxy-2'-fluoro, 2'-O-aminopropyl (2'-O-AP), 2'-O-dimethylaminoethyl (2'-O-DMAOE), 2'-O-dimethylaminopropyl (2'-O-DMAP), 2'-O-dimethylaminoethoxyethyl (2'-O-DMAEOE), or 2'-O-N-methylacetamido (2'-O-NMA) modification or by a locked or bridged ribose conformation (*e.g.*, LNA or ENA). In some cases, the polynucleic acid molecule is modified by 2'-O-methyl and/or 2'-O-methoxyethyl ribose. In some cases, the polynucleic acid molecule also includes morpholinos, PNAs, HNA, methylphosphonate nucleotides, thiophosphonate nucleotides, and/or 2'-fluoro N3-P5'-phosphoramidites to increase its stability. In some instances, the polynucleic acid molecule is a chirally pure (or stereo pure) polynucleic acid molecule. In some instances, the chirally pure (or stereo pure) polynucleic acid molecule is modified to increase its stability. Suitable modifications to the RNA to increase stability for delivery will be apparent to the skilled person.

[0121] In some instances, the polynucleic acid molecule is a double-stranded polynucleotide molecule comprising self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. In some instances, the

polynucleic acid molecule is assembled from two separate polynucleotides, where one strand is the sense strand and the other is the antisense strand, wherein the antisense and sense strands are self-complementary (*e.g.*, each strand comprises nucleotide sequence that is complementary to nucleotide sequence in the other strand; such as where the antisense strand and sense strand form a duplex or double stranded structure, for example wherein the double stranded region is about 19, 20, 21, 22, 23, or more base pairs); the antisense strand comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense strand comprises nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. Alternatively, the polynucleic acid molecule is assembled from a single oligonucleotide, where the self-complementary sense and antisense regions of the polynucleic acid molecule are linked by means of a nucleic acid based or non-nucleic acid-based linker(s).

[0122] In some cases, the polynucleic acid molecule is a polynucleotide with a duplex, asymmetric duplex, hairpin or asymmetric hairpin secondary structure, having self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a separate target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. In other cases, the polynucleic acid molecule is a circular single-stranded polynucleotide having two or more loop structures and a stem comprising self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof, and wherein the circular polynucleotide is processed either *in vivo* or *in vitro* to generate an active polynucleic acid molecule capable of mediating RNAi. In additional cases, the polynucleic acid molecule also comprises a single-stranded polynucleotide having nucleotide sequence complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof (for example, where such polynucleic acid molecule does not require the presence within the polynucleic acid molecule of nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof), wherein the single stranded polynucleotide further comprises a terminal phosphate group, such as a 5'-phosphate (see for example Martinez et al., 2002, *Cell*, 110, 563-574 and Schwarz et al., 2002, *Molecular Cell*, 10, 537-568), or 5', 3'-diphosphate.

[0123] In some instances, an asymmetric hairpin is a linear polynucleic acid molecule comprising an antisense region, a loop portion that comprises nucleotides or non-nucleotides, and a sense region that comprises fewer nucleotides than the antisense region to the extent that

the sense region has enough complimentary nucleotides to base pair with the antisense region and form a duplex with loop. For example, an asymmetric hairpin polynucleic acid molecule comprises an antisense region having length sufficient to mediate RNAi in a cell or in vitro system (e.g. about 19 to about 22 nucleotides) and a loop region comprising about 4 to about 8 nucleotides, and a sense region having about 3 to about 18 nucleotides that are complementary to the antisense region. In some cases, the asymmetric hairpin polynucleic acid molecule also comprises a 5'-terminal phosphate group that is chemically modified. In additional cases, the loop portion of the asymmetric hairpin polynucleic acid molecule comprises nucleotides, non-nucleotides, linker molecules, or conjugate molecules.

[0124] In some embodiments, an asymmetric duplex is a polynucleic acid molecule having two separate strands comprising a sense region and an antisense region, wherein the sense region comprises fewer nucleotides than the antisense region to the extent that the sense region has enough complimentary nucleotides to base pair with the antisense region and form a duplex. For example, an asymmetric duplex polynucleic acid molecule comprises an antisense region having length sufficient to mediate RNAi in a cell or in vitro system (e.g., about 19 to about 22 nucleotides) and a sense region having about 3 to about 18 nucleotides that are complementary to the antisense region.

[0125] In some cases, a universal base refers to nucleotide base analogs that form base pairs with each of the natural DNA/RNA bases with little discrimination between them. Non-limiting examples of universal bases include C-phenyl, C-naphthyl and other aromatic derivatives, inosine, azole carboxamides, and nitroazole derivatives such as 3-nitropyrrole, 4-nitroindole, 5-nitroindole, and 6-nitroindole as known in the art (see for example Loakes, 2001, *Nucleic Acids Research*, 29, 2437-2447).

Polynucleic Acid Molecule Synthesis

[0126] In some embodiments, a polynucleic acid molecule described herein is constructed using chemical synthesis and/or enzymatic ligation reactions using procedures known in the art. For example, a polynucleic acid molecule is chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the polynucleic acid molecule and target nucleic acids. Exemplary methods include those described in: U.S. Patent NOs. 5,142,047; 5,185,444; 5,889,136; 6,008,400; and 6,111,086; PCT Publication No. WO2009099942; or European Publication NO. 1579015. Additional exemplary methods include those described in: Griffey et al., "2'-O-aminopropyl ribonucleotides: a zwitterionic modification that enhances the exonuclease resistance and biological activity of antisense

oligonucleotides," *J. Med. Chem.* **39**(26):5100-5109 (1997)); Obika, et al. "Synthesis of 2'-O,4'-C-methylenuridine and -cytidine. Novel bicyclic nucleosides having a fixed C3, -endo sugar puckering". *Tetrahedron Letters* **38** (50): 8735 (1997); Koizumi, M. "ENA oligonucleotides as therapeutics". *Current opinion in molecular therapeutics* **8** (2): 144-149 (2006); and Abramova et al., "Novel oligonucleotide analogues based on morpholino nucleoside subunits-antisense technologies: new chemical possibilities," *Indian Journal of Chemistry* **48B**:1721-1726 (2009). Alternatively, the polynucleic acid molecule is produced biologically using an expression vector into which a polynucleic acid molecule has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted polynucleic acid molecule will be of an antisense orientation to a target polynucleic acid molecule of interest).

[0127] In some embodiments, a polynucleic acid molecule is synthesized via a tandem synthesis methodology, wherein both strands are synthesized as a single contiguous oligonucleotide fragment or strand separated by a cleavable linker which is subsequently cleaved to provide separate fragments or strands that hybridize and permit purification of the duplex.

[0128] In some instances, a polynucleic acid molecule is also assembled from two distinct nucleic acid strands or fragments wherein one fragment includes the sense region and the second fragment includes the antisense region of the molecule.

[0129] Additional modification methods for incorporating, for example, sugar, base and phosphate modifications include: Eckstein et al., International Publication PCT No. WO 92/07065; Perrault et al. *Nature*, 1990, 344, 565-568; Pieken et al. *Science*, 1991, 253, 314-317; Usman and Cedergren, *Trends in Biochem. Sci.*, 1992, 17, 334-339; Usman et al. International Publication PCT No. WO 93/15187; Sproat, U.S. Pat. No. 5,334,711 and Beigelman et al., 1995, *J. Biol. Chem.*, 270, 25702; Beigelman et al., International PCT publication No. WO 97/26270; Beigelman et al., U.S. Pat. No. 5,716,824; Usman et al., U.S. Pat. No. 5,627,053; Woolf et al., International PCT Publication No. WO 98/13526; Thompson et al., U.S. Ser. No. 60/082,404 which was filed on Apr. 20, 1998; Karpeisky et al., 1998, *Tetrahedron Lett.*, 39, 1131; Earnshaw and Gait, 1998, *Biopolymers (Nucleic Acid Sciences)*, 48, 39-55; Verma and Eckstein, 1998, *Annu. Rev. Biochem.*, 67, 99-134; and Burlina et al., 1997, *Bioorg. Med. Chem.*, 5, 1999-2010. Such publications describe general methods and strategies to determine the location of incorporation of sugar, base and/or phosphate modifications and the like into nucleic acid molecules without modulating catalysis.

[0130] In some instances, while chemical modification of the polynucleic acid molecule internucleotide linkages with phosphorothioate, phosphorodithioate, and/or 5'-methylphosphonate linkages improves stability, excessive modifications sometimes cause toxicity or decreased activity. Therefore, when designing nucleic acid molecules, the amount of

these internucleotide linkages in some cases is minimized. In such cases, the reduction in the concentration of these linkages lowers toxicity, increases efficacy and higher specificity of these molecules.

Polynucleic Acid Molecule Conjugates

[0131] In some embodiments, a polynucleic acid molecule (B) is further conjugated to a polypeptide (A) for delivery to a site of interest. In some instances, at least one polypeptide A is conjugated to at least one B. In some instances, the at least one polypeptide A is conjugated to the at least one B to form an A-B conjugate. In some embodiments, at least one A is conjugated to the 5' terminus of B, the 3' terminus of B, an internal site on B, or in any combinations thereof. In some instances, the at least one polypeptide A is conjugated to at least two B. In some instances, the at least one polypeptide A is conjugated to at least 2, 3, 4, 5, 6, 7, 8, or more B.

[0132] In some cases, a polynucleic acid molecule is conjugated to a polypeptide (A) and optionally a polymeric moiety (C). In some embodiments, at least one polypeptide A is conjugated at one terminus of at least one B while at least one C is conjugated at the opposite terminus of the at least one B to form an A-B-C conjugate. In some instances, at least one polypeptide A is conjugated at one terminus of the at least one B while at least one of C is conjugated at an internal site on the at least one B. In some instances, at least one polypeptide A is conjugated directly to the at least one C. In some instances, the at least one B is conjugated indirectly to the at least one polypeptide A via the at least one C to form an A-C-B conjugate.

[0133] In some instances, at least one B and/or at least one C, and optionally at least one D are conjugated to at least one polypeptide A. In some instances, the at least one B is conjugated at a terminus (*e.g.*, a 5' terminus or a 3' terminus) to the at least one polypeptide A or are conjugated via an internal site to the at least one polypeptide A. In some cases, the at least one C is conjugated either directly to the at least one polypeptide A or indirectly via the at least one B. If indirectly via the at least one B, the at least one C is conjugated either at the same terminus as the at least one polypeptide A on B, at opposing terminus from the at least one polypeptide A, or independently at an internal site. In some instances, at least one additional polypeptide A is further conjugated to the at least one polypeptide A, to B, or to C. In additional instances, the at least one D is optionally conjugated either directly or indirectly to the at least one polypeptide A, to the at least one B, or to the at least one C. If directly to the at least one polypeptide A, the at least one D is also optionally conjugated to the at least one B to form an A-D-B conjugate or is optionally conjugated to the at least one B and the at least one C to form an A-D-B-C conjugate. In some instances, the at least one D is directly conjugated to the at least one polypeptide A and

indirectly to the at least one B and the at least one C to form a D-A-B-C conjugate. If indirectly to the at least one polypeptide A, the at least one D is also optionally conjugated to the at least one B to form an A-B-D conjugate or is optionally conjugated to the at least one B and the at least one C to form an A-B-D-C conjugate. In some instances, at least one additional D is further conjugated to the at least one polypeptide A, to B, or to C.

Binding Moiety

[0134] In some embodiments, the binding moiety A is a polypeptide. In some instances, the polypeptide is an antibody or its fragment thereof. In some cases, the fragment is a binding fragment. In some instances, the antibody or antigen binding fragment thereof comprises a humanized antibody or antigen binding fragment thereof, murine antibody or antigen binding fragment thereof, chimeric antibody or antigen binding fragment thereof, monoclonal antibody or antigen binding fragment thereof, a binding fragment having a light chain domain and a heavy chain domain, a binding fragment having two light chain domains and two heavy chain domains, a binding fragment having two or more light chain domains and heavy chain domains, monovalent Fab', divalent Fab₂, F(ab')₃ fragments, single-chain variable fragment (scFv), bis-scFv, (scFv)₂, diabody, minibody, nanobody, triabody, tetrabody, disulfide stabilized Fv protein (dsFv), single-domain antibody (sdAb), Ig NAR, camelid antibody or antigen binding fragment thereof, bispecific antibody or binding fragment thereof, or a chemically modified derivative thereof.

[0135] In some embodiments, the binding moiety A is a bispecific antibody or antigen binding fragment thereof. In some instances, the bispecific antibody is a trifunctional antibody or a bispecific mini-antibody. In some cases, the bispecific antibody is a trifunctional antibody. In some instances, the trifunctional antibody is a full length monoclonal antibody comprising binding sites for two different antigens.

[0136] In some cases, the bispecific antibody is a bispecific mini-antibody. In some instances, the bispecific mini-antibody comprises divalent Fab₂, F(ab')₃ fragments, bis-scFv, (scFv)₂, diabody, minibody, triabody, tetrabody or a bi-specific T-cell engager (BiTE). In some embodiments, the bi-specific T-cell engager is a fusion protein that contains two single-chain variable fragments (scFvs) in which the two scFvs target epitopes of two different antigens.

[0137] In some embodiments, the binding moiety A is a bispecific mini-antibody. In some instances, A is a bispecific Fab₂. In some instances, A is a bispecific F(ab')₃ fragment. In some cases, A is a bispecific bis-scFv. In some cases, A is a bispecific (scFv)₂. In some embodiments, A is a bispecific diabody. In some embodiments, A is a bispecific minibody. In

some embodiments, A is a bispecific triabody. In other embodiments, A is a bispecific tetrabody. In other embodiments, A is a bi-specific T-cell engager (BiTE).

[0138] In some embodiments, the binding moiety A is a trispecific antibody. In some instances, the trispecific antibody comprises F(ab)₃ fragments or a triabody. In some instances, A is a trispecific F(ab)₃ fragment. In some cases, A is a triabody. In some embodiments, A is a trispecific antibody as described in Dimas, *et al.*, “Development of a trispecific antibody designed to simultaneously and efficiently target three different antigens on tumor cells,” *Mol. Pharmaceutics*, 12(9): 3490-3501 (2015).

[0139] In some embodiments, the binding moiety A is an antibody or antigen binding fragment thereof that recognizes a cell surface protein. In some instances, the binding moiety A is an antibody or antigen binding fragment thereof that recognizes a cell surface protein on a muscle cell. In some cases, the binding moiety A is an antibody or antigen binding fragment thereof that recognizes a cell surface protein on a skeletal muscle cell.

[0140] In some embodiments, exemplary antibodies include, but are not limited to, an anti-myosin antibody, an anti-transferrin receptor antibody, and an antibody that recognizes Muscle-Specific kinase (MuSK). In some instances, the antibody is an anti-transferrin receptor (anti-CD71) antibody.

[0141] In some embodiments, where the antibody is an anti-transferrin receptor (anti-CD71) antibody, the anti-transferrin antibody specifically binds to a transferrin receptor (TfR), preferably, specifically binds to transferrin receptor 1 (TfR1), or more preferably, specifically binds to human transferrin receptor 1 (TfR1) (or human CD71).

[0142] In some instances, the anti-transferrin receptor antibody comprises a variable heavy chain (VH) region and a variable light chain (VL) region, wherein the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281; HCDR2 sequence EINPIX₁GRSNYAX₂KFQG, wherein X₁ is selected from N or Q and X₂ is selected from Q or E; and HCDR3 sequence comprising SEQ ID NO: 283.

[0143] In some embodiments, the VH region of the anti-transferrin receptor antibody comprises HCDR1, HCDR2, and HCDR3 sequences selected from Table 1.

TABLE 1

Name	HCDR1	SEQ ID NO:	HCDR2	SEQ ID NO:	HCDR3	SEQ ID NO:
13E4_VH1	YTFTNYWMH	281	EINPINGRSNYAQKFQG	282	GTRAMHY	283
13E4_VH2*	YTFTNYWMH	281	EINPINGRSNYAEKFQG	284	GTRAMHY	283
13E4_VH3	YTFTNYWMH	281	EINPIQGRSNYAEKFQG	285	GTRAMHY	283

*13E4_VH2 shares the same HCDR1, HCDR2, and HCDR3 sequences with anti-transferrin receptor antibody 13E4_VH4

[0144] In some embodiments, the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281; HCDR2 sequence comprising SEQ ID NO: 282, 284, or 285; and HCDR3 sequence comprising SEQ ID NO: 283. In some instances, the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 282, and HCDR3 sequence comprising SEQ ID NO: 283. In some instances, the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 284, and HCDR3 sequence comprising SEQ ID NO: 283. In some instances, the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 285, and HCDR3 sequence comprising SEQ ID NO: 283.

[0145] In some embodiments, the VL region of the anti-transferrin receptor antibody comprises LCDR1 sequence RTSENIYX₃NLA, LCDR2 sequence AX₄TNLAX₅, and LCDR3 sequence QHFWGTPLTX₆, wherein X₃ is selected from N or S, X₄ is selected from A or G, X₅ is selected from D or E, and X₆ is present or absence, and if present, is F.

[0146] In some embodiments, the VL region of the anti-transferrin receptor antibody comprises LCDR1, LCDR2, and LCDR3 sequences selected from Table 2.

TABLE 2

Name	LCDR1	SEQ ID NO:	LCDR2	SEQ ID NO:	LCDR3	SEQ ID NO:
13E4_VL1*	RTSENIYNNLA	286	AATNLAD	287	QHFWGTPLT	288
13E4_VL3	RTSENIYNNLA	286	AATNLAE	289	QHFWGTPLTF	290
13E4_VL4	RTSENIYSNLA	291	AGTNLAD	292	QHFWGTPLTF	290

*13E4_VL1 shares the same LCDR1, LCDR2, and LCDR3 sequences with anti-transferrin receptor antibody 13E4_VL2

[0147] In some instances, the VL region comprises LCDR1 sequence RTSENIYX₃NLA, LCDR2 sequence comprising SEQ ID NO: 287, 289, or 292, and LCDR3 sequence comprising SEQ ID NO: 288 or 290, wherein X₃ is selected from N or S.

[0148] In some instances, the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286 or 291, LCDR2 sequence AX₄TNLAX₅, and LCDR3 sequence comprising SEQ ID NO: 288 or 290, wherein X₄ is selected from A or G, and X₅ is selected from D or E.

[0149] In some instances, the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286 or 291, LCDR2 sequence SEQ ID NO: 287, 289, or 292, and LCDR3 sequence QHFWGTPLTX₆, wherein X₆ is present or absence, and if present, is F.

[0150] In some instances, the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286, LCDR2 sequence AATNLAX₅, and LCDR3 sequence QHFWGTPLTX₆, wherein X₅ is selected from D or E and X₆ is present or absence, and if present, is F.

[0151] In some instances, the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286, LCDR2 sequence comprising SEQ ID NO: 287, and LCDR3 sequence comprising SEQ ID NO: 288.

[0152] In some instances, the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286, LCDR2 sequence comprising SEQ ID NO: 289, and LCDR3 sequence comprising SEQ ID NO: 290.

[0153] In some instances, the VL region comprises LCDR1 sequence comprising SEQ ID NO: 291, LCDR2 sequence comprising SEQ ID NO: 292, and LCDR3 sequence comprising SEQ ID NO: 290.

[0154] In some embodiments, the anti-transferrin receptor antibody comprises a VH region and a VL region, wherein the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281; HCDR2 sequence EINPIX₁GRSNYAX₂KFQG, wherein X₁ is selected from N or Q and X₂ is selected from Q or E; and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence RTSENIYX₃NLA, LCDR2 sequence AX₄TNLAX₅, and LCDR3 sequence QHFWGTPLTX₆, wherein X₃ is selected from N or S, X₄ is selected from A or G, X₅ is selected from D or E, and X₆ is present or absence, and if present, is F.

[0155] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, wherein the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281; HCDR2 sequence EINPIX₁GRSNYAX₂KFQG, wherein X₁ is selected from N or Q and X₂ is selected from Q or E; and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence RTSENIYX₃NLA, LCDR2 sequence comprising SEQ ID NO: 287, 289, or 292, and LCDR3 sequence comprising SEQ ID NO: 288 or 290, wherein X₃ is selected from N or S.

[0156] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, wherein the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281; HCDR2 sequence EINPIX₁GRSNYAX₂KFQG, wherein X₁ is selected from N or Q and X₂ is selected from Q or E; and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286 or 291, LCDR2 sequence AX₄TNLAX₅, and LCDR3 sequence comprising SEQ ID NO: 288 or 290, wherein X₄ is selected from A or G, and X₅ is selected from D or E.

[0157] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, wherein the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281; HCDR2 sequence EINPIX₁GRSNYAX₂KFQG, wherein X₁ is selected from N or Q and X₂ is selected from Q or E; and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286 or 291, LCDR2 sequence SEQ ID

NO: 287, 289, or 292, and LCDR3 sequence QHFWGTPLTX₆, wherein X₆ is present or absence, and if present, is F.

[0158] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, wherein the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281; HCDR2 sequence EINPIX₁GRSNYAX₂KFQG, wherein X₁ is selected from N or Q and X₂ is selected from Q or E; and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286, LCDR2 sequence AATNLAX₅, and LCDR3 sequence QHFWGTPLTX₆, wherein X₅ is selected from D or E and X₆ is present or absence, and if present, is F.

[0159] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, wherein the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281; HCDR2 sequence EINPIX₁GRSNYAX₂KFQG, wherein X₁ is selected from N or Q and X₂ is selected from Q or E; and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286, LCDR2 sequence comprising SEQ ID NO: 287, and LCDR3 sequence comprising SEQ ID NO: 288.

[0160] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, wherein the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281; HCDR2 sequence EINPIX₁GRSNYAX₂KFQG, wherein X₁ is selected from N or Q and X₂ is selected from Q or E; and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286, LCDR2 sequence comprising SEQ ID NO: 289, and LCDR3 sequence comprising SEQ ID NO: 290.

[0161] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, wherein the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281; HCDR2 sequence EINPIX₁GRSNYAX₂KFQG, wherein X₁ is selected from N or Q and X₂ is selected from Q or E; and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 291, LCDR2 sequence comprising SEQ ID NO: 292, and LCDR3 sequence comprising SEQ ID NO: 290.

[0162] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 282, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence RTSENIYX₃NLA, LCDR2 sequence comprising SEQ ID NO: 287, 289, or 292, and LCDR3 sequence comprising SEQ ID NO: 288 or 290, wherein X₃ is selected from N or S.

[0163] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281,

HCDR2 sequence comprising SEQ ID NO: 282, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286 or 291, LCDR2 sequence AX₄TNLAX₅, and LCDR3 sequence comprising SEQ ID NO: 288 or 290, wherein X₄ is selected from A or G, and X₅ is selected from D or E.

[0164] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 2, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286 or 291, LCDR2 sequence SEQ ID NO: 287, 289, or 292, and LCDR3 sequence QHFWGTPLTX₆, wherein X₆ is present or absence, and if present, is F.

[0165] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 282, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286, LCDR2 sequence AATNLAX₅, and LCDR3 sequence QHFWGTPLTX₆, wherein X₅ is selected from D or E and X₆ is present or absence, and if present, is F.

[0166] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 282, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286, LCDR2 sequence comprising SEQ ID NO: 287, and LCDR3 sequence comprising SEQ ID NO: 288.

[0167] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 282, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286, LCDR2 sequence comprising SEQ ID NO: 9, and LCDR3 sequence comprising SEQ ID NO: 290.

[0168] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 282, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 291, LCDR2 sequence comprising SEQ ID NO: 292, and LCDR3 sequence comprising SEQ ID NO: 290.

[0169] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 284, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence RTSENIYX₃NLA, LCDR2 sequence

comprising SEQ ID NO: 287, 289, or 292, and LCDR3 sequence comprising SEQ ID NO: 288 or 290, wherein X₃ is selected from N or S.

[0170] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 284, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286 or 291, LCDR2 sequence AX₄TNLAX₅, and LCDR3 sequence comprising SEQ ID NO: 288 or 290, wherein X₄ is selected from A or G, and X₅ is selected from D or E.

[0171] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 284, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286 or 291, LCDR2 sequence SEQ ID NO: 287, 289, or 292, and LCDR3 sequence QHFWGTPLTX₆, wherein X₆ is present or absence, and if present, is F.

[0172] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 284, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286, LCDR2 sequence AATNLAX₅, and LCDR3 sequence QHFWGTPLTX₆, wherein X₅ is selected from D or E and X₆ is present or absence, and if present, is F.

[0173] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 284, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286, LCDR2 sequence comprising SEQ ID NO: 287, and LCDR3 sequence comprising SEQ ID NO: 288.

[0174] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 284, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286, LCDR2 sequence comprising SEQ ID NO: 289, and LCDR3 sequence comprising SEQ ID NO: 290.

[0175] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 284, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 291, LCDR2 sequence comprising SEQ ID NO: 292, and LCDR3 sequence comprising SEQ ID NO: 290.

[0176] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 285, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence RTSENIYX₃NLA, LCDR2 sequence comprising SEQ ID NO: 287, 289, or 29, and LCDR3 sequence comprising SEQ ID NO: 288 or 290, wherein X₃ is selected from N or S.

[0177] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 285, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286 or 291, LCDR2 sequence AX₄TNLAX₅, and LCDR3 sequence comprising SEQ ID NO: 288 or 290, wherein X₄ is selected from A or G, and X₅ is selected from D or E.

[0178] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 285, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286 or 291, LCDR2 sequence SEQ ID NO: 287, 289, or 292, and LCDR3 sequence QHFWGTPLTX₆, wherein X₆ is present or absence, and if present, is F.

[0179] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 285, and HCDR3 sequence comprising SEQ ID NO: 283 and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286, LCDR2 sequence AATNLAX₅, and LCDR3 sequence QHFWGTPLTX₆, wherein X₅ is selected from D or E and X₆ is present or absence, and if present, is F.

[0180] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 285, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286, LCDR2 sequence comprising SEQ ID NO: 287, and LCDR3 sequence comprising SEQ ID NO: 288.

[0181] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 285, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 286, LCDR2 sequence comprising SEQ ID NO: 289, and LCDR3 sequence comprising SEQ ID NO: 290.

[0182] In some instances, the anti-transferrin receptor antibody comprises a VH region and a VL region, in which the VH region comprises HCDR1 sequence comprising SEQ ID NO: 281, HCDR2 sequence comprising SEQ ID NO: 285, and HCDR3 sequence comprising SEQ ID NO: 283; and the VL region comprises LCDR1 sequence comprising SEQ ID NO: 291, LCDR2 sequence comprising SEQ ID NO: 292, and LCDR3 sequence comprising SEQ ID NO: 290.

[0183] In some embodiments, the anti-transferrin receptor antibody comprises a VH region and a VL region in which the sequence of the VH region comprises about 80%, 85%, 90%, 95%, 96% 97%, 98%, 99%, or 100% sequence identity to SEQ ID NOs: 293-296 and the sequence of the VL region comprises about 80%, 85%, 90%, 95%, 96% 97%, 98%, 99%, or 100% sequence identity to SEQ ID NOs: 298-301.

[0184] In some embodiments, the VH region comprises a sequence selected from SEQ ID NOs: 293-296 (Table 3) and the VL region comprises a sequence selected from SEQ ID NOs: 298-301 (Table 4). The underlined regions in Table 3 and Table 4 denote the respective CDR1, CDR2, or CDR3 sequence.

TABLE 3

NAME	VH SEQUENCE	SEQ ID NO:
13E4_VH1	QVQLVQSGAEVKKPGASVKVSCASGYTFTNYWMHWVRQAPGQGLEW MGEINPINGRSNYAQKFQGRVTLTVDTISSTAYMELSRLRSDDTAVYYCA <u>RGTRAMHYWGQGT</u> LVTVSS	293
13E4_VH2	QVQLVQSGAEVKKPGASVKVSCASGYTFTNYWMHWVRQAPGQGLEW IGEINPINGRSNYAEKFQGRVTLTVDTSSSTAYMELSRLRSDDTAVYYCAR <u>GTRAMHYWGQGT</u> LVTVSS	294
13E4_VH3	QVQLVQSGAEVKKPGASVKVSCASGYTFTNYWMHWVRQAPGQGLEW MGEINPIQGRSNYAEKFQGRVTLTVDTSSSTAYMELSSLRSEDATATYYCA <u>RGTRAMHYWGQGT</u> LVTVSS	295
13E4_VH4	QVQLVQSGAEVKKPGASVKVSCASGYTFTNYWMHWVRQAPGQGLEW MGEINPINGRSNYAEKFQGRVTLTVDTSSSTAYMELSSLRSEDATATYYCA <u>RGTRAMHYWGQGT</u> LVTVSS	296
13E4_VH	QVQLQQPGAELVKPGASVKLSCKASGYTFTNYWMHWVKQRPQGGLWEI GEINPINGRSNYGERFKTKATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR <u>GTRAMHYWGQGT</u> SVTVSS	297

TABLE 4

NAME	VL SEQUENCE	SEQ ID NO:
13E4_VL1	DIQMTQSPSSLSASVGDRVTITCRTSENIYNNLAWYQQKPGKSPKLLIYAA <u>TNLA</u> DGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQHFWGTPLTFGGGT KVEIK	298
13E4_VL2	DIQMTQSPSSLSASVGDRVTITCRTSENIYNNLAWYQQKPGKAPKLLIYA <u>ATNLA</u> DGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQHFWGTPLTFGG GTKVEIK	299
13E4_VL3	DIQMTQSPSSLSASVGDRVTITCRTSENIYNNLAWYQQKPGKAPKLLIYA <u>ATNLA</u> EGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQHFWGTPLTFGGG TKVEIK	300

13E4_VL4	DIQMTQSPSSLSASVGDRVITICRTSENIYSNLAWYQQKPGKAPKLLIYAG TNLADGVPSRFSGSGSGTDYTLTISSLQPEDFANYCYQHFWGTPLTFGGG TKVEIK	301
13E4_VL	DIQMTQSPASLSVSVGETVTITCRTSENIYNNLAWYQQKQKGKSPQLLVYA ATNLADGVPSRFSGSGSGTQYSLKINSLSQSEDFGNYYCYQHFWGTPLTFGA GTKLELK	302

[0185] In some embodiments, the anti-transferrin receptor antibody comprises a VH region and a VL region as illustrated in Table 5.

TABLE 5

	13E4_VH1 (SEQ ID NO: 13)	13E4_VH2 (SEQ ID NO: 14)	13E4_VH3 (SEQ ID NO: 15)	13E4_VH4 (SEQ ID NO: 16)
13E4_VL1 (SEQ ID NO: 298)	SEQ ID NO: 293 + SEQ ID NO: 298	SEQ ID NO: 294 + SEQ ID NO: 298	SEQ ID NO: 295 + SEQ ID NO: 298	SEQ ID NO: 296 + SEQ ID NO: 298
13E4_VL2 (SEQ ID NO: 299)	SEQ ID NO: 293 + SEQ ID NO: 299	SEQ ID NO: 294 + SEQ ID NO: 299	SEQ ID NO: 295 + SEQ ID NO: 299	SEQ ID NO: 296 + SEQ ID NO: 299
13E4_VL3 (SEQ ID NO: 300)	SEQ ID NO: 293 + SEQ ID NO: 300	SEQ ID NO: 294 + SEQ ID NO: 300	SEQ ID NO: 295 + SEQ ID NO: 300	SEQ ID NO: 296 + SEQ ID NO: 300
13E4_VL4 (SEQ ID NO: 301)	SEQ ID NO: 293 + SEQ ID NO: 301	SEQ ID NO: 294 + SEQ ID NO: 301	SEQ ID NO: 295 + SEQ ID NO: 301	SEQ ID NO: 296 + SEQ ID NO: 301

[0186] In some embodiments, an anti-transferrin receptor antibody described herein comprises an IgG framework, an IgA framework, an IgE framework, or an IgM framework. In some instances, the anti-transferrin receptor antibody comprises an IgG framework (*e.g.*, IgG1, IgG2, IgG3, or IgG4). In some cases, the anti-transferrin receptor antibody comprises an IgG1 framework. In some cases, the anti-transferrin receptor antibody comprises an IgG2 (*e.g.*, an IgG2a or IgG2b) framework. In some cases, the anti-transferrin receptor antibody comprises an IgG2a framework. In some cases, the anti-transferrin receptor antibody comprises an IgG2b framework. In some cases, the anti-transferrin receptor antibody comprises an IgG3 framework. In some cases, the anti-transferrin receptor antibody comprises an IgG4 framework.

[0187] In some cases, an anti-transferrin receptor antibody comprises one or more mutations in a framework region, *e.g.*, in the CH1 domain, CH2 domain, CH3 domain, hinge region, or a combination thereof. In some instances, the one or more mutations are to stabilize the antibody and/or to increase half-life. In some instances, the one or more mutations are to modulate Fc receptor interactions, to reduce or eliminate Fc effector functions such as FcγR, antibody-dependent cell-mediated cytotoxicity (ADCC), or complement-dependent cytotoxicity (CDC). In additional instances, the one or more mutations are to modulate glycosylation.

[0188] In some embodiments, the one or more mutations are located in the Fc region. In some instances, the Fc region comprises a mutation at residue position L234, L235, or a combination thereof. In some instances, the mutations comprise L234 and L235. In some instances, the mutations comprise L234A and L235A. In some cases, the residue positions are in reference to IgG1.

[0189] In some instances, the Fc region comprises a mutation at residue position L234, L235, D265, N297, K322, L328, or P329, or a combination thereof. In some instances, the mutations comprise L234 and L235 in combination with a mutation at residue position K322, L328, or P329. In some cases, the Fc region comprises mutations at L234, L235, and K322. In some cases, the Fc region comprises mutations at L234, L235, and L328. In some cases, the Fc region comprises mutations at L234, L235, and P329. In some cases, the Fc region comprises mutations at D265 and N297. In some cases, the residue position is in reference to IgG1.

[0190] In some instances, the Fc region comprises L234A, L235A, D265A, N297G, K322G, L328R, or P329G, or a combination thereof. In some instances, the Fc region comprises L234A and L235A in combination with K322G, L328R, or P329G. In some cases, the Fc region comprises L234A, L235A, and K322G. In some cases, the Fc region comprises L234A, L235A, and L328R. In some cases, the Fc region comprises L234A, L235A, and P329G. In some cases, the Fc region comprises D265A and N297G. In some cases, the residue position is in reference to IgG1.

[0191] In some instances, the Fc region comprises a mutation at residue position L235, L236, D265, N297, K322, L328, or P329, or a combination of the mutations. In some instances, the Fc region comprises mutations at L235 and L236. In some instances, the Fc region comprises mutations at L235 and L236 in combination with a mutation at residue position K322, L328, or P329. In some cases, the Fc region comprises mutations at L235, L236, and K322. In some cases, the Fc region comprises mutations at L235, L236, and L328. In some cases, the Fc region comprises mutations at L235, L236, and P329. In some cases, the Fc region comprises mutations at D265 and N297. In some cases, the residue position is in reference to IgG2b.

[0192] In some embodiments, the Fc region comprises L235A, L236A, D265A, N297G, K322G, L328R, or P329G, or a combination thereof. In some instances, the Fc region comprises L235A and L236A. In some instances, the Fc region comprises L235A and L236A in combination with K322G, L328R, or P329G. In some cases, the Fc region comprises L235A, L236A, and K322G. In some cases, the Fc region comprises L235A, L236A, and L328R. In some cases, the Fc region comprises L235A, L236A, and P329G. In some cases, the Fc region comprises D265A and N297G. In some cases, the residue position is in reference to IgG2b.

[0193] In some embodiments, the Fc region comprises a mutation at residue position L233, L234, D264, N296, K321, L327, or P328, wherein the residues correspond to positions 233, 234, 264, 296, 321, 327, and 328 of SEQ ID NO: 303. In some instances, the Fc region comprises mutations at L233 and L234. In some instances, the Fc region comprises mutations at L233 and L234 in combination with a mutation at residue position K321, L327, or P328. In some cases, the Fc region comprises mutations at L233, L234, and K321. In some cases, the Fc region comprises mutations at L233, L234, and L327. In some cases, the Fc region comprises mutations at L233, L234, and K321. In some cases, the Fc region comprises mutations at L233, L234, and P328. In some instances, the Fc region comprises mutations at D264 and N296. In some cases, equivalent positions to residue L233, L234, D264, N296, K321, L327, or P328 in an IgG1, IgG2, IgG3, or IgG4 framework are contemplated. In some cases, mutations to a residue that corresponds to residue L233, L234, D264, N296, K321, L327, or P328 of SEQ ID NO: 303 in an IgG1, IgG2, or IgG4 framework are also contemplated.

[0194] In some embodiments, the Fc region comprises L233A, L234A, D264A, N296G, K321G, L327R, or P328G, wherein the residues correspond to positions 233, 234, 264, 296, 321, 327, and 328 of SEQ ID NO: 303. In some instances, the Fc region comprises L233A and L234A. In some instances, the Fc region comprises L233A and L234A in combination with K321G, L327R, or P328G. In some cases, the Fc region comprises L233A, L234A, and K321G. In some cases, the Fc region comprises L233A, L234A, and L327R. In some cases, the Fc region comprises L233A, L234A, and K321G. In some cases, the Fc region comprises L233A, L234A, and P328G. In some instances, the Fc region comprises D264A and N296G.

[0195] In some embodiments, the human IgG constant region is modified to alter antibody-dependent cellular cytotoxicity (ADCC) and/or complement-dependent cytotoxicity (CDC), *e.g.*, with an amino acid modification described in Natsume *et al.*, 2008 *Cancer Res*, **68**(10): 3863-72; Idusogie *et al.*, 2001 *J Immunol*, **166**(4): 2571-5; Moore *et al.*, 2010 *mAbs*, **2**(2): 181-189; Lazar *et al.*, 2006 *PNAS*, **103**(11): 4005-4010; Shields *et al.*, 2001 *JBC*, **276**(9): 6591-6604; Stavenhagen *et al.*, 2007 *Cancer Res*, **67**(18): 8882-8890; Stavenhagen *et al.*, 2008 *Advan. Enzyme Regul.*, **48**: 152-164; Alegre *et al.*, 1992 *J Immunol*, **148**: 3461-3468; Reviewed in Kaneko and Niwa, 2011 *Biodrugs*, **25**(1): 1-11.

[0196] In some embodiments, an anti-transferrin receptor antibody described herein is a full-length antibody, comprising a heavy chain (HC) and a light chain (LC). In some cases, the heavy chain (HC) comprises a sequence selected from Table 6. In some cases, the light chain (LC) comprises a sequence selected from Table 7. The underlined region denotes the respective CDRs.

TABLE 6

NAME	HC SEQUENCE	SEQ ID NO:
13E4_VH1	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPINGRSNYAQKFQGRVTLTVDTISISTAYMELSRLRSDDTAVY YCARGTRAMHYWGQGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSST LGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPG	303
13E4_VH1_a	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPINGRSNYAQKFQGRVTLTVDTISISTAYMELSRLRSDDTAVY YCARGTRAMHYWGQGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSST LGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVF LFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPG	304
13E4_VH1_b	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPINGRSNYAQKFQGRVTLTVDTISISTAYMELSRLRSDDTAVY YCARGTRAMHYWGQGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSST LGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVF LFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCGVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPG	305
13E4_VH1_c	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPINGRSNYAQKFQGRVTLTVDTISISTAYMELSRLRSDDTAVY YCARGTRAMHYWGQGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSST LGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVF LFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPG	306
13E4_VH1_d	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPINGRSNYAQKFQGRVTLTVDTISISTAYMELSRLRSDDTAVY YCARGTRAMHYWGQGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSST LGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVF LFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPG	307
13E4_VH1_e	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPINGRSNYAQKFQGRVTLTVDTISISTAYMELSRLRSDDTAVY YCARGTRAMHYWGQGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALG	308

	CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSS LGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFL LPPKPKDTLMISRTPEVTCVAVSHEDPEVKFNWYVDGVEVHNAKTK KPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPG	
13E4_VH2	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WIG EIN PINGRSNYAEKFQGRVTLTVDTSSTAYMELSRLRSDDTAVYY CARG TRAMHY WGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSL GTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	309
13E4_VH2_a	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WIG EIN PINGRSNYAEKFQGRVTLTVDTSSTAYMELSRLRSDDTAVYY CARG TRAMHY WGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSL GTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAEEAAGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	310
13E4_VH2_b	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WIG EIN PINGRSNYAEKFQGRVTLTVDTSSTAYMELSRLRSDDTAVYY CARG TRAMHY WGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSL GTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAEEAAGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCGVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	311
13E4_VH2_c	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WIG EIN PINGRSNYAEKFQGRVTLTVDTSSTAYMELSRLRSDDTAVYY CARG TRAMHY WGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSL GTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAEEAAGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	312
13E4_VH2_d	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WIG EIN PINGRSNYAEKFQGRVTLTVDTSSTAYMELSRLRSDDTAVYY CARG TRAMHY WGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSL GTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAEEAAGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALGAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	313

13E4_VH2_e	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WIGEINPIQGRSNYAEKFQGRVTLTVDTSSSTAYMELSLRSDTAVYY CARGTRAMHYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVAVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHN HYTQKSLSLSPG	314
13E4_VH3	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPIQGRSNYAEKFQGRVTLTVDTSSSTAYMELSSLRSEDATYY CARGTRAMHYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHN HYTQKSLSLSPG	315
13E4_VH3_a	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPIQGRSNYAEKFQGRVTLTVDTSSSTAYMELSSLRSEDATYY CARGTRAMHYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHN HYTQKSLSLSPG	316
13E4_VH3_b	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPIQGRSNYAEKFQGRVTLTVDTSSSTAYMELSSLRSEDATYY CARGTRAMHYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCGVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHN HYTQKSLSLSPG	317
13E4_VH3_c	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPIQGRSNYAEKFQGRVTLTVDTSSSTAYMELSSLRSEDATYY CARGTRAMHYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHN HYTQKSLSLSPG	318
13E4_VH3_d	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPIQGRSNYAEKFQGRVTLTVDTSSSTAYMELSSLRSEDATYY CARGTRAMHYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALGAPIEKTISK	319

	AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	
13E4_VH3_e	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPIQGRSNYAEKFQGRVTLTVDTSSTAYMELSSLRSEDATATYY CARGTRAMHYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	320
13E4_VH4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPINGRSNYAEKFQGRVTLTVDTSSTAYMELSSLRSEDATATYY CARGTRAMHYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	321
13E4_VH4_a	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPINGRSNYAEKFQGRVTLTVDTSSTAYMELSSLRSEDATATYY CARGTRAMHYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	322
13E4_VH4_b	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPINGRSNYAEKFQGRVTLTVDTSSTAYMELSSLRSEDATATYY CARGTRAMHYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCGVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	323
13E4_VH4_c	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPINGRSNYAEKFQGRVTLTVDTSSTAYMELSSLRSEDATATYY CARGTRAMHYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	324
13E4_VH4_d	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPINGRSNYAEKFQGRVTLTVDTSSTAYMELSSLRSEDATATYY CARGTRAMHYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL	325

	GTQTYICNVNHNKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALGAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	
13E4_VH4_e	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMHWVRQAPGQGLE WMGEINPINGRSNYAEKFQGRVTLTVDTSSSTAYMELSSLRSEDATYY CARGTRAMHYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSL GTQTYICNVNHNKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	326

TABLE 7

NAME	LC SEQUENCE	SEQ ID NO:
13E4_VL1	DIQMTQSPSSLSASVGDRVTITCRTSENIYNNLAWYQQKPGKSPKLLIYA ATNLADGVPSRFGSGSGTDYTLTISSLQPEDFATYYCQHFWGTPLTFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW KVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEV THQGLSPVTKSFNRGEC	327
13E4_VL2	DIQMTQSPSSLSASVGDRVTITCRTSENIYNNLAWYQQKPGKAPKLLIY AATNLADGVPSRFGSGSGTDYTLTISSLQPEDFATYYCQHFWGTPLTF GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACE VTHQGLSPVTKSFNRGEC	328
13E4_VL3	DIQMTQSPSSLSASVGDRVTITCRTSENIYNNLAWYQQKPGKAPKLLIY AATNLAEVPSRFGSGSGTDYTLTISSLQPEDFATYYCQHFWGTPLTF GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACE VTHQGLSPVTKSFNRGEC	329
13E4_VL4	DIQMTQSPSSLSASVGDRVTITCRTSENIYNNLAWYQQKPGKAPKLLIYA GTNLADGVPSRFGSGSGTDYTLTISSLQPEDFANYCQHFWGTPLTFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW KVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEV THQGLSPVTKSFNRGEC	330

[0197] In some embodiments, an anti-transferrin receptor antibody described herein has an improved serum half-life compared to a reference anti-transferrin receptor antibody. In some instances, the improved serum half-life is at least 30 minutes, 1 hour, 1.5 hour, 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 12 hours, 18 hours, 24 hours, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 14 days, 30 days, or longer than reference anti-transferrin receptor antibody.

[0198] In some embodiments, the binding moiety A is conjugated to a polynucleic acid molecule (B) non-specifically. In some instances, the binding moiety A is conjugated to a polynucleic acid molecule (B) via a lysine residue or a cysteine residue, in a non-site specific

manner. In some instances, the binding moiety A is conjugated to a polynucleic acid molecule (B) via a lysine residue (*e.g.*, lysine residue present in the binding moiety A) in a non-site specific manner. In some cases, the binding moiety A is conjugated to a polynucleic acid molecule (B) via a cysteine residue (*e.g.*, cysteine residue present in the binding moiety A) in a non-site specific manner.

[0199] In some embodiments, the binding moiety A is conjugated to a polynucleic acid molecule (B) in a site-specific manner. In some instances, the binding moiety A is conjugated to a polynucleic acid molecule (B) through a lysine residue, a cysteine residue, at the 5'-terminus, at the 3'-terminus, an unnatural amino acid, or an enzyme-modified or enzyme-catalyzed residue, via a site-specific manner. In some instances, the binding moiety A is conjugated to a polynucleic acid molecule (B) through a lysine residue (*e.g.*, lysine residue present in the binding moiety A) via a site-specific manner. In some instances, the binding moiety A is conjugated to a polynucleic acid molecule (B) through a cysteine residue (*e.g.*, cysteine residue present in the binding moiety A) via a site-specific manner. In some instances, the binding moiety A is conjugated to a polynucleic acid molecule (B) at the 5'-terminus via a site-specific manner. In some instances, the binding moiety A is conjugated to a polynucleic acid molecule (B) at the 3'-terminus via a site-specific manner. In some instances, the binding moiety A is conjugated to a polynucleic acid molecule (B) through an unnatural amino acid via a site-specific manner. In some instances, the binding moiety A is conjugated to a polynucleic acid molecule (B) through an enzyme-modified or enzyme-catalyzed residue via a site-specific manner.

[0200] In some embodiments, one or more polynucleic acid molecule (B) is conjugated to a binding moiety A. In some instances, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or more polynucleic acid molecules are conjugated to one binding moiety A. In some instances, about 1 polynucleic acid molecule is conjugated to one binding moiety A. In some instances, about 2 polynucleic acid molecules are conjugated to one binding moiety A. In some instances, about 3 polynucleic acid molecules are conjugated to one binding moiety A. In some instances, about 4 polynucleic acid molecules are conjugated to one binding moiety A. In some instances, about 5 polynucleic acid molecules are conjugated to one binding moiety A. In some instances, about 6 polynucleic acid molecules are conjugated to one binding moiety A. In some instances, about 7 polynucleic acid molecules are conjugated to one binding moiety A. In some instances, about 8 polynucleic acid molecules are conjugated to one binding moiety A. In some instances, about 9 polynucleic acid molecules are conjugated to one binding moiety A. In some instances, about 10 polynucleic acid molecules are conjugated to one binding moiety A. In some instances, about 11 polynucleic acid molecules are conjugated to one binding moiety A. In

some instances, about 12 polynucleic acid molecules are conjugated to one binding moiety A. In some instances, about 13 polynucleic acid molecules are conjugated to one binding moiety A. In some instances, about 14 polynucleic acid molecules are conjugated to one binding moiety A. In some instances, about 15 polynucleic acid molecules are conjugated to one binding moiety A. In some instances, about 16 polynucleic acid molecules are conjugated to one binding moiety A. In some cases, the one or more polynucleic acid molecules are the same. In other cases, the one or more polynucleic acid molecules are different.

[0201] In some embodiments, the number of polynucleic acid molecule (B) conjugated to a binding moiety A forms a ratio. In some instances, the ratio is referred to as a DAR (drug-to-antibody) ratio, in which the drug as referred to herein is the polynucleic acid molecule (B). In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or greater. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 1 or greater. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 2 or greater. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 3 or greater. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 4 or greater. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 5 or greater. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 6 or greater. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 7 or greater. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 8 or greater. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 9 or greater. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 10 or greater. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 11 or greater. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 12 or greater.

[0202] In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 1. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 2. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 3. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 4. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 5. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 6. In some instances, the DAR ratio of the polynucleic acid molecule (B) to

binding moiety A is about 7. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 8. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 9. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 10. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 11. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 12. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 13. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 14. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 15. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is about 16.

[0203] In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is 1. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is 2. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is 4. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is 6. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is 8. In some instances, the DAR ratio of the polynucleic acid molecule (B) to binding moiety A is 12.

[0204] In some instances, a conjugate comprising polynucleic acid molecule (B) and binding moiety A has improved activity as compared to a conjugate comprising polynucleic acid molecule (B) without a binding moiety A. In some instances, improved activity results in enhanced biologically relevant functions, *e.g.*, improved stability, affinity, binding, functional activity, and efficacy in treatment or prevention of a disease state. In some instances, the disease state is a result of one or more mutated exons of a gene. In some instances, the conjugate comprising polynucleic acid molecule (B) and binding moiety A results in increased exon skipping of the one or more mutated exons as compared to the conjugate comprising polynucleic acid molecule (B) without a binding moiety A. In some instances, exon skipping is increased by at least or about 5%, 10%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or more than 95% in the conjugate comprising polynucleic acid molecule (B) and binding moiety A as compared to the conjugate comprising polynucleic acid molecule (B) without a binding moiety A.

[0205] In some embodiments, an antibody or antigen binding fragment is further modified using conventional techniques known in the art, for example, by using amino acid deletion, insertion, substitution, addition, and/or by recombination and/or any other modification (*e.g.*,

posttranslational and chemical modifications, such as glycosylation and phosphorylation) known in the art either alone or in combination. In some instances, the modification further comprises a modification for modulating interaction with Fc receptors. In some instances, the one or more modifications include those described in, for example, International Publication No.

WO97/34631, which discloses amino acid residues involved in the interaction between the Fc domain and the FcRn receptor. Methods for introducing such modifications in the nucleic acid sequence underlying the amino acid sequence of an antibody or antigen binding fragment is well known to the person skilled in the art.

[0206] In some instances, an antigen binding fragment further encompasses its derivatives and includes polypeptide sequences containing at least one CDR.

[0207] In some instances, the term “single-chain” as used herein means that the first and second domains of a bi-specific single chain construct are covalently linked, preferably in the form of a co-linear amino acid sequence encodable by a single nucleic acid molecule.

[0208] In some instances, a bispecific single chain antibody construct relates to a construct comprising two antibody derived binding domains. In such embodiments, bi-specific single chain antibody construct is tandem bi-scFv or diabody. In some instances, a scFv contains a VH and VL domain connected by a linker peptide. In some instances, linkers are of a length and sequence sufficient to ensure that each of the first and second domains can, independently from one another, retain their differential binding specificities.

[0209] In some embodiments, binding to or interacting with as used herein defines a binding/interaction of at least two antigen-interaction-sites with each other. In some instances, antigen-interaction-site defines a motif of a polypeptide that shows the capacity of specific interaction with a specific antigen or a specific group of antigens. In some cases, the binding/interaction is also understood to define a specific recognition. In such cases, specific recognition refers to that the antibody or its antigen binding fragment is capable of specifically interacting with and/or binding to at least two amino acids of each of a target molecule. For example, specific recognition relates to the specificity of the antibody molecule, or to its ability to discriminate between the specific regions of a target molecule. In additional instances, the specific interaction of the antigen-interaction-site with its specific antigen results in an initiation of a signal, e.g. due to the induction of a change of the conformation of the antigen, an oligomerization of the antigen, etc. In further embodiments, the binding is exemplified by the specificity of a "key-lock-principle". Thus in some instances, specific motifs in the amino acid sequence of the antigen-interaction-site and the antigen bind to each other as a result of their primary, secondary or tertiary structure as well as the result of secondary modifications of said

structure. In such cases, the specific interaction of the antigen-interaction-site with its specific antigen results as well in a simple binding of the site to the antigen.

[0210] In some instances, specific interaction further refers to a reduced cross-reactivity of the antibody or antigen binding fragment or a reduced off-target effect. For example, the antibody or antigen binding fragment that bind to the polypeptide/protein of interest but do not or do not essentially bind to any of the other polypeptides are considered as specific for the polypeptide/protein of interest. Examples for the specific interaction of an antigen-interaction-site with a specific antigen comprise the specificity of a ligand for its receptor, for example, the interaction of an antigenic determinant (epitope) with the antigenic binding site of an antibody.

Additional Binding Moieties

[0211] In some embodiments, the binding moiety is a plasma protein. In some instances, the plasma protein comprises albumin. In some instances, the binding moiety A is albumin. In some instances, albumin is conjugated by one or more of a conjugation chemistry described herein to a polynucleic acid molecule. In some instances, albumin is conjugated by native ligation chemistry to a polynucleic acid molecule. In some instances, albumin is conjugated by lysine conjugation to a polynucleic acid molecule.

[0212] In some instances, the binding moiety is a steroid. Exemplary steroids include cholesterol, phospholipids, di- and triacylglycerols, fatty acids, hydrocarbons that are saturated, unsaturated, comprise substitutions, or combinations thereof. In some instances, the steroid is cholesterol. In some instances, the binding moiety is cholesterol. In some instances, cholesterol is conjugated by one or more of a conjugation chemistry described herein to a polynucleic acid molecule. In some instances, cholesterol is conjugated by native ligation chemistry to a polynucleic acid molecule. In some instances, cholesterol is conjugated by lysine conjugation to a polynucleic acid molecule.

[0213] In some instances, the binding moiety is a polymer, including but not limited to polynucleic acid molecule aptamers that bind to specific surface markers on cells. In this instance the binding moiety is a polynucleic acid that does not hybridize to a target gene or mRNA, but instead is capable of selectively binding to a cell surface marker similarly to an antibody binding to its specific epitope of a cell surface marker.

[0214] In some cases, the binding moiety is a peptide. In some cases, the peptide comprises between about 1 and about 3 kDa. In some cases, the peptide comprises between about 1.2 and about 2.8 kDa, about 1.5 and about 2.5 kDa, or about 1.5 and about 2 kDa. In some instances, the peptide is a bicyclic peptide. In some cases, the bicyclic peptide is a constrained bicyclic

peptide. In some instances, the binding moiety is a bicyclic peptide (*e.g.*, bicycles from Bicycle Therapeutics).

[0215] In additional cases, the binding moiety is a small molecule. In some instances, the small molecule is an antibody-recruiting small molecule. In some cases, the antibody-recruiting small molecule comprises a target-binding terminus and an antibody-binding terminus, in which the target-binding terminus is capable of recognizing and interacting with a cell surface receptor. For example, in some instances, the target-binding terminus comprising a glutamate urea compound enables interaction with PSMA, thereby, enhances an antibody interaction with a cell that expresses PSMA. In some instances, a binding moiety is a small molecule described in Zhang et al., “A remote arene-binding site on prostate specific membrane antigen revealed by antibody-recruiting small molecules,” *J Am Chem Soc.* 132(36): 12711-12716 (2010); or McEnaney, et al., “Antibody-recruiting molecules: an emerging paradigm for engaging immune function in treating human disease,” *ACS Chem Biol.* 7(7): 1139-1151 (2012).

Production of Antibodies or Antigen Binding Fragment Thereof

[0216] In some embodiments, polypeptides described herein (*e.g.*, antibodies and antigen binding fragments) are produced using any method known in the art to be useful for the synthesis of polypeptides (*e.g.*, antibodies), in particular, by chemical synthesis or by recombinant expression, and are preferably produced by recombinant expression techniques.

[0217] In some instances, an antibody or antigen binding fragment thereof is expressed recombinantly, and the nucleic acid encoding the antibody or antigen binding fragment is assembled from chemically synthesized oligonucleotides (*e.g.*, as described in Kutmeier et al., 1994, *BioTechniques* 17:242), which involves the synthesis of overlapping oligonucleotides containing portions of the sequence encoding the antibody, annealing and ligation of those oligonucleotides, and then amplification of the ligated oligonucleotides by PCR.

[0218] Alternatively, a nucleic acid molecule encoding an antibody is optionally generated from a suitable source (*e.g.*, an antibody cDNA library, or cDNA library generated from any tissue or cells expressing the immunoglobulin) by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of the sequence or by cloning using an oligonucleotide probe specific for the particular gene sequence.

[0219] In some instances, an antibody or its antigen binding is optionally generated by immunizing an animal, such as a rabbit, to generate polyclonal antibodies or, more preferably, by generating monoclonal antibodies, *e.g.*, as described by Kohler and Milstein (1975, *Nature* 256:495-497) or, as described by Kozbor et al. (1983, *Immunology Today* 4:72) or Cole et al. (1985 in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96).

Alternatively, a clone encoding at least the Fab portion of the antibody is optionally obtained by screening Fab expression libraries (*e.g.*, as described in Huse et al., 1989, *Science* 246:1275-1281) for clones of Fab fragments that bind the specific antigen or by screening antibody libraries (See, *e.g.*, Clackson et al., 1991, *Nature* 352:624; Hane et al., 1997 *Proc. Natl. Acad. Sci. USA* 94:4937).

[0220] In some embodiments, techniques developed for the production of “chimeric antibodies” (Morrison et al., 1984, *Proc. Natl. Acad. Sci.* 81:851-855; Neuberger et al., 1984, *Nature* 312:604-608; Takeda et al., 1985, *Nature* 314:452-454) by splicing genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity are used. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine monoclonal antibody and a human immunoglobulin constant region, *e.g.*, humanized antibodies.

[0221] In some embodiments, techniques described for the production of single chain antibodies (U.S. Pat. No. 4,694,778; Bird, 1988, *Science* 242:423-42; Huston et al., 1988, *Proc. Natl. Acad. Sci. USA* 85:5879-5883; and Ward et al., 1989, *Nature* 334:544-54) are adapted to produce single chain antibodies. Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide. Techniques for the assembly of functional Fv fragments in *E. coli* are also optionally used (Skerra et al., 1988, *Science* 242:1038-1041).

[0222] In some embodiments, an expression vector comprising the nucleotide sequence of an antibody or the nucleotide sequence of an antibody is transferred to a host cell by conventional techniques (*e.g.*, electroporation, liposomal transfection, and calcium phosphate precipitation), and the transfected cells are then cultured by conventional techniques to produce the antibody. In specific embodiments, the expression of the antibody is regulated by a constitutive, an inducible or a tissue, specific promoter.

[0223] In some embodiments, a variety of host-expression vector systems is utilized to express an antibody or its antigen binding fragment described herein. Such host-expression systems represent vehicles by which the coding sequences of the antibody is produced and subsequently purified, but also represent cells that are, when transformed or transfected with the appropriate nucleotide coding sequences, express an antibody or its antigen binding fragment in situ. These include, but are not limited to, microorganisms such as bacteria (*e.g.*, *E. coli* and *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing an antibody or its antigen binding fragment coding sequences; yeast (*e.g.*, *Saccharomyces Pichia*) transformed with recombinant yeast expression vectors containing an

antibody or its antigen binding fragment coding sequences; insect cell systems infected with recombinant virus expression vectors (*e.g.*, baculovirus) containing an antibody or its antigen binding fragment coding sequences; plant cell systems infected with recombinant virus expression vectors (*e.g.*, cauliflower mosaic virus (CaMV) and tobacco mosaic virus (TMV)) or transformed with recombinant plasmid expression vectors (*e.g.*, Ti plasmid) containing an antibody or its antigen binding fragment coding sequences; or mammalian cell systems (*e.g.*, COS, CHO, BH, 293, 293T, 3T3 cells) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (*e.g.*, metallothionein promoter) or from mammalian viruses (*e.g.* the adenovirus late promoter; the vaccinia virus 7.5K promoter).

[0224] For long-term, high-yield production of recombinant proteins, stable expression is preferred. In some instances, cell lines that stably express an antibody are optionally engineered. Rather than using expression vectors that contain viral origins of replication, host cells are transformed with DNA controlled by appropriate expression control elements (*e.g.*, promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of the foreign DNA, engineered cells are then allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci that in turn are cloned and expanded into cell lines. This method can advantageously be used to engineer cell lines which express the antibody or its antigen binding fragments.

[0225] In some instances, a number of selection systems are used, including but not limited to the herpes simplex virus thymidine kinase (Wigler et al., 1977, *Cell* 11:223), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, 1972, *Proc. Natl. Acad. Sci. USA* 48:202), and adenine phosphoribosyltransferase (Lowy et al., 1980, *Cell* 22:817) genes are employed in tk⁻, hgp⁺ or ap⁺ cells, respectively. Also, antimetabolite resistance are used as the basis of selection for the following genes: dhfr, which confers resistance to methotrexate (Wigler et al., 1980, *Proc. Natl. Acad. Sci. USA* 77:357; O'Hare et al., 1981, *Proc. Natl. Acad. Sci. USA* 78:1527); gpt, which confers resistance to mycophenolic acid (Mulligan & Berg, 1981, *Proc. Natl. Acad. Sci. USA* 78:2072); neo, which confers resistance to the aminoglycoside G-418 (*Clinical Pharmacy* 12:488-505; Wu and Wu, 1991, *Biotherapy* 3:87-95; Tolstoshev, 1993, *Ann. Rev. Pharmacol. Toxicol.* 32:573-596; Mulligan, 1993, *Science* 260:926-932; and Morgan and Anderson, 1993, *Ann. Rev. Biochem.* 62:191-217; May, 1993, *TIB TECH* 11(5):155-215) and hyg⁺, which confers resistance to hygromycin (Santerre et al., 1984, *Gene* 30:147). Methods commonly known in the art of recombinant DNA technology which can be used are described in Ausubel et al. (eds., 1993, *Current Protocols in Molecular Biology*, John Wiley &

Sons, NY; Kriegler, 1990, *Gene Transfer and Expression, A Laboratory Manual*, Stockton Press, NY; and in Chapters 12 and 13, Dracopoli et al. (eds), 1994, *Current Protocols in Human Genetics*, John Wiley & Sons, NY.; Colberre-Garapin et al., 1981, *J. Mol. Biol.* 150:1).

[0226] In some instances, the expression levels of an antibody are increased by vector amplification (for a review, see Bebbington and Hentschel, *The use of vectors based on gene amplification for the expression of cloned genes in mammalian cells in DNA cloning*, Vol. 3. (Academic Press, New York, 1987)). When a marker in the vector system expressing an antibody is amplifiable, an increase in the level of inhibitor present in culture of host cell will increase the number of copies of the marker gene. Since the amplified region is associated with the nucleotide sequence of the antibody, production of the antibody will also increase (Crouse et al., 1983, *Mol. Cell Biol.* 3:257).

[0227] In some instances, any method known in the art for purification or analysis of an antibody or antibody conjugates is used, for example, by chromatography (*e.g.*, ion exchange, affinity, particularly by affinity for the specific antigen after Protein A, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. Exemplary chromatography methods included, but are not limited to, strong anion exchange chromatography, hydrophobic interaction chromatography, size exclusion chromatography, and fast protein liquid chromatography.

Conjugation Chemistry

[0228] In some embodiments, a polynucleic acid molecule B is conjugated to a binding moiety. In some embodiments, a polynucleic acid molecule B is conjugated to a binding moiety in a formula A-X-B (X is a linker conjugating A and B). In some instances, the binding moiety comprises amino acids, peptides, polypeptides, proteins, antibodies, antigens, toxins, hormones, lipids, nucleotides, nucleosides, sugars, carbohydrates, polymers such as polyethylene glycol and polypropylene glycol, as well as analogs or derivatives of all of these classes of substances. Additional examples of binding moiety also include steroids, such as cholesterol, phospholipids, di- and triacylglycerols, fatty acids, hydrocarbons (*e.g.*, saturated, unsaturated, or contains substitutions), enzyme substrates, biotin, digoxigenin, and polysaccharides. In some instances, the binding moiety is an antibody or antigen binding fragment thereof. In some instances, the polynucleic acid molecule is further conjugated to a polymer, and optionally an endosomal lytic moiety.

[0229] In some embodiments, the polynucleic acid molecule is conjugated to the binding moiety by a chemical ligation process. In some instances, the polynucleic acid molecule is conjugated to the binding moiety by a native ligation. In some instances, the conjugation is as described in:

Dawson, et al. "Synthesis of proteins by native chemical ligation," *Science* **1994**, 266, 776–779; Dawson, et al. "Modulation of Reactivity in Native Chemical Ligation through the Use of Thiol Additives," *J. Am. Chem. Soc.* **1997**, 119, 4325–4329; Hackeng, et al. "Protein synthesis by native chemical ligation: Expanded scope by using straightforward methodology.," *Proc. Natl. Acad. Sci. USA* **1999**, 96, 10068–10073; or Wu, et al. "Building complex glycopeptides: Development of a cysteine-free native chemical ligation protocol," *Angew. Chem. Int. Ed.* **2006**, 45, 4116–4125. In some instances, the conjugation is as described in U.S. Patent No. 8,936,910. In some embodiments, the polynucleic acid molecule is conjugated to the binding moiety either site-specifically or non-specifically via native ligation chemistry.

[0230] In some instances, the polynucleic acid molecule is conjugated to the binding moiety by a site-directed method utilizing a "traceless" coupling technology (Philochem). In some instances, the "traceless" coupling technology utilizes an N-terminal 1,2-aminothiol group on the binding moiety which is then conjugate with a polynucleic acid molecule containing an aldehyde group. (see Casi *et al.*, "Site-specific traceless coupling of potent cytotoxic drugs to recombinant antibodies for pharmacodelivery," *JACS* **134**(13): 5887-5892 (2012))

[0231] In some instances, the polynucleic acid molecule is conjugated to the binding moiety by a site-directed method utilizing an unnatural amino acid incorporated into the binding moiety. In some instances, the unnatural amino acid comprises *p*-acetylphenylalanine (pAcPhe). In some instances, the keto group of pAcPhe is selectively coupled to an alkoxy-amine derivatized conjugating moiety to form an oxime bond. (see Axup *et al.*, "Synthesis of site-specific antibody-drug conjugates using unnatural amino acids," *PNAS* **109**(40): 16101-16106 (2012)).

[0232] In some instances, the polynucleic acid molecule is conjugated to the binding moiety by a site-directed method utilizing an enzyme-catalyzed process. In some instances, the site-directed method utilizes SMARTag™ technology (Catalent, Inc.). In some instances, the SMARTag™ technology comprises generation of a formylglycine (FGly) residue from cysteine by formylglycine-generating enzyme (FGE) through an oxidation process under the presence of an aldehyde tag and the subsequent conjugation of FGly to an alkylhydrazine-functionalized polynucleic acid molecule via hydrazino-Pictet-Spengler (HIPS) ligation. (see Wu *et al.*, "Site-specific chemical modification of recombinant proteins produced in mammalian cells by using the genetically encoded aldehyde tag," *PNAS* **106**(9): 3000-3005 (2009); Agarwal, *et al.*, "A Pictet-Spengler ligation for protein chemical modification," *PNAS* **110**(1): 46-51 (2013))

[0233] In some instances, the enzyme-catalyzed process comprises microbial transglutaminase (mTG). In some cases, the polynucleic acid molecule is conjugated to the binding moiety utilizing a microbial transglutaminase-catalyzed process. In some instances, mTG catalyzes the formation of a covalent bond between the amide side chain of a glutamine within the recognition

sequence and a primary amine of a functionalized polynucleic acid molecule. In some instances, mTG is produced from *Streptomyces mobarensis*. (see Strop *et al.*, "Location matters: site of conjugation modulates stability and pharmacokinetics of antibody drug conjugates," *Chemistry and Biology* **20**(2) 161-167 (2013))

[0234] In some instances, the polynucleic acid molecule is conjugated to the binding moiety by a method as described in PCT Publication No. WO2014/140317, which utilizes a sequence-specific transpeptidase.

[0235] In some instances, the polynucleic acid molecule is conjugated to the binding moiety by a method as described in U.S. Patent Publication Nos. 2015/0105539 and 2015/0105540.

Polymer Conjugating Moiety

[0236] In some embodiments, a polymer moiety C is further conjugated to a polynucleic acid molecule described herein, a binding moiety described herein, or in combinations thereof. In some instances, a polymer moiety C is conjugated a polynucleic acid molecule in a formula A-X₁-B-X₂-C (X₁, X₂ as two linkers conjugating A and B, B and C, respectively). In some cases, a polymer moiety C is conjugated to a binding moiety. In other cases, a polymer moiety C is conjugated to a polynucleic acid molecule-binding moiety molecule. In additional cases, a polymer moiety C is conjugated, as illustrated *supra*.

[0237] In some instances, the polymer moiety C is a natural or synthetic polymer, consisting of long chains of branched or unbranched monomers, and/or cross-linked network of monomers in two or three dimensions. In some instances, the polymer moiety C includes a polysaccharide, lignin, rubber, or polyalkylene oxide (*e.g.*, polyethylene glycol). In some instances, the at least one polymer moiety C includes, but is not limited to, alpha-, omega-dihydroxypolyethyleneglycol, biodegradable lactone-based polymer, *e.g.* polyacrylic acid, polylactide acid (PLA), poly(glycolic acid) (PGA), polypropylene, polystyrene, polyolefin, polyamide, polycyanoacrylate, polyimide, polyethylene terephthalate (also known as poly(ethylene terephthalate), PET, PETG, or PETE), polytetramethylene glycol (PTG), or polyurethane as well as mixtures thereof. As used herein, a mixture refers to the use of different polymers within the same compound as well as in reference to block copolymers. In some cases, block copolymers are polymers wherein at least one section of a polymer is build up from monomers of another polymer. In some instances, the polymer moiety C comprises polyalkylene oxide. In some instances, the polymer moiety C comprises PEG. In some instances, the polymer moiety C comprises polyethylene imide (PEI) or hydroxy ethyl starch (HES).

[0238] In some instances, C is a PEG moiety. In some instances, the PEG moiety is conjugated at the 5' terminus of the polynucleic acid molecule while the binding moiety is conjugated at the 3' terminus of the polynucleic acid molecule. In some instances, the PEG moiety is conjugated at the 3' terminus of the polynucleic acid molecule while the binding moiety is conjugated at the 5' terminus of the polynucleic acid molecule. In some instances, the PEG moiety is conjugated to an internal site of the polynucleic acid molecule. In some instances, the PEG moiety, the binding moiety, or a combination thereof, are conjugated to an internal site of the polynucleic acid molecule. In some instances, the conjugation is a direct conjugation. In some instances, the conjugation is via native ligation.

[0239] In some embodiments, the polyalkylene oxide (*e.g.*, PEG) is a polydisperse or monodisperse compound. In some instances, polydisperse material comprises disperse distribution of different molecular weight of the material, characterized by mean weight (weight average) size and dispersity. In some instances, the monodisperse PEG comprises one size of molecules. In some embodiments, C is poly- or monodispersed polyalkylene oxide (*e.g.*, PEG) and the indicated molecular weight represents an average of the molecular weight of the polyalkylene oxide, *e.g.*, PEG, molecules.

[0240] In some embodiments, the molecular weight of the polyalkylene oxide (*e.g.*, PEG) is about 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1450, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, 2500, 2600, 2700, 2800, 2900, 3000, 3250, 3350, 3500, 3750, 4000, 4250, 4500, 4600, 4750, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 10,000, 12,000, 20,000, 35,000, 40,000, 50,000, 60,000, or 100,000 Da.

[0241] In some embodiments, C is polyalkylene oxide (*e.g.*, PEG) and has a molecular weight of about 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1450, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, 2500, 2600, 2700, 2800, 2900, 3000, 3250, 3350, 3500, 3750, 4000, 4250, 4500, 4600, 4750, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 10,000, 12,000, 20,000, 35,000, 40,000, 50,000, 60,000, or 100,000 Da. In some embodiments, C is PEG and has a molecular weight of about 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1450, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, 2500, 2600, 2700, 2800, 2900, 3000, 3250, 3350, 3500, 3750, 4000, 4250, 4500, 4600, 4750, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 10,000, 12,000, 20,000, 35,000, 40,000, 50,000, 60,000, or 100,000 Da. In some instances, the molecular weight of C is about 200 Da. In some instances, the molecular weight of C is about 300 Da. In some instances, the molecular weight of C is about 400 Da. In some instances, the molecular weight of C is about 500 Da. In some instances, the molecular weight of C is about 600 Da. In some instances, the molecular weight of C is about 700 Da. In some instances, the molecular weight of C is about 800 Da. In

some instances, the molecular weight of C is about 900 Da. In some instances, the molecular weight of C is about 1000 Da. In some instances, the molecular weight of C is about 1100 Da. In some instances, the molecular weight of C is about 1200 Da. In some instances, the molecular weight of C is about 1300 Da. In some instances, the molecular weight of C is about 1400 Da. In some instances, the molecular weight of C is about 1450 Da. In some instances, the molecular weight of C is about 1500 Da. In some instances, the molecular weight of C is about 1600 Da. In some instances, the molecular weight of C is about 1700 Da. In some instances, the molecular weight of C is about 1800 Da. In some instances, the molecular weight of C is about 1900 Da. In some instances, the molecular weight of C is about 2000 Da. In some instances, the molecular weight of C is about 2100 Da. In some instances, the molecular weight of C is about 2200 Da. In some instances, the molecular weight of C is about 2300 Da. In some instances, the molecular weight of C is about 2400 Da. In some instances, the molecular weight of C is about 2500 Da. In some instances, the molecular weight of C is about 2600 Da. In some instances, the molecular weight of C is about 2700 Da. In some instances, the molecular weight of C is about 2800 Da. In some instances, the molecular weight of C is about 2900 Da. In some instances, the molecular weight of C is about 3000 Da. In some instances, the molecular weight of C is about 3250 Da. In some instances, the molecular weight of C is about 3350 Da. In some instances, the molecular weight of C is about 3500 Da. In some instances, the molecular weight of C is about 3750 Da. In some instances, the molecular weight of C is about 4000 Da. In some instances, the molecular weight of C is about 4250 Da. In some instances, the molecular weight of C is about 4500 Da. In some instances, the molecular weight of C is about 4600 Da. In some instances, the molecular weight of C is about 4750 Da. In some instances, the molecular weight of C is about 5000 Da. In some instances, the molecular weight of C is about 5500 Da. In some instances, the molecular weight of C is about 6000 Da. In some instances, the molecular weight of C is about 6500 Da. In some instances, the molecular weight of C is about 7000 Da. In some instances, the molecular weight of C is about 7500 Da. In some instances, the molecular weight of C is about 8000 Da. In some instances, the molecular weight of C is about 10,000 Da. In some instances, the molecular weight of C is about 12,000 Da. In some instances, the molecular weight of C is about 20,000 Da. In some instances, the molecular weight of C is about 35,000 Da. In some instances, the molecular weight of C is about 40,000 Da. In some instances, the molecular weight of C is about 50,000 Da. In some instances, the molecular weight of C is about 60,000 Da. In some instances, the molecular weight of C is about 100,000 Da.

[0242] In some embodiments, the polyalkylene oxide (*e.g.*, PEG) comprises discrete ethylene oxide units (*e.g.*, four to about 48 ethylene oxide units). In some instances, the polyalkylene

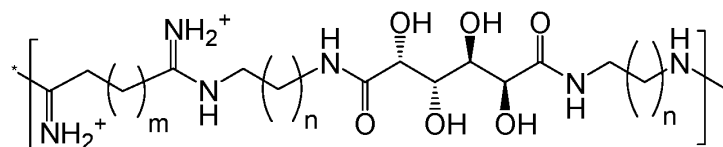
oxide comprising the discrete ethylene oxide units is a linear chain. In other cases, the polyalkylene oxide comprising the discrete ethylene oxide units is a branched chain.

[0243] In some instances, the polymer moiety C is a polyalkylene oxide (*e.g.*, PEG) comprising discrete ethylene oxide units. In some cases, the polymer moiety C comprises between about 4 and about 48 ethylene oxide units. In some cases, the polymer moiety C comprises about 4, about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 21, about 22, about 23, about 24, about 25, about 26, about 27, about 28, about 29, about 30, about 31, about 32, about 33, about 34, about 35, about 36, about 37, about 38, about 39, about 40, about 41, about 42, about 43, about 44, about 45, about 46, about 47, or about 48 ethylene oxide units.

[0244] In some instances, the polymer moiety C is a discrete PEG comprising, *e.g.*, between about 4 and about 48 ethylene oxide units. In some cases, the polymer moiety C is a discrete PEG comprising, *e.g.*, about 4, about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 21, about 22, about 23, about 24, about 25, about 26, about 27, about 28, about 29, about 30, about 31, about 32, about 33, about 34, about 35, about 36, about 37, about 38, about 39, about 40, about 41, about 42, about 43, about 44, about 45, about 46, about 47, or about 48 ethylene oxide units. In some cases, the polymer moiety C is a discrete PEG comprising, *e.g.*, about 4 ethylene oxide units. In some cases, the polymer moiety C is a discrete PEG comprising, *e.g.*, about 5 ethylene oxide units. In some cases, the polymer moiety C is a discrete PEG comprising, *e.g.*, about 6 ethylene oxide units. In some cases, the polymer moiety C is a discrete PEG comprising, *e.g.*, about 7 ethylene oxide units. In some cases, the polymer moiety C is a discrete PEG comprising, *e.g.*, about 8 ethylene oxide units. In some cases, the polymer moiety C is a discrete PEG comprising, *e.g.*, about 9 ethylene oxide units. In some cases, the polymer moiety C is a discrete PEG comprising, *e.g.*, about 10 ethylene oxide units. In some cases, the polymer moiety C is a discrete PEG comprising, *e.g.*, about 11 ethylene oxide units. In some cases, the polymer moiety C is a discrete PEG comprising, *e.g.*, about 12 ethylene oxide units. In some cases, the polymer moiety C is a discrete PEG comprising, *e.g.*, about 13 ethylene oxide units. In some cases, the polymer moiety C is a discrete PEG comprising, *e.g.*, about 14 ethylene oxide units. In some cases, the polymer moiety C is a discrete PEG comprising, *e.g.*, about 15 ethylene oxide units. In some cases, the polymer moiety C is a discrete PEG comprising, *e.g.*, about 16 ethylene oxide units. In some cases, the polymer moiety C is a discrete PEG comprising, *e.g.*, about 17 ethylene oxide units. In some cases, the polymer moiety C is a discrete PEG comprising, *e.g.*, about 18 ethylene oxide units. In some cases, the polymer moiety C is a discrete PEG comprising, *e.g.*, about 19 ethylene oxide units. In some cases, the polymer moiety

[0245] In some cases, the polymer moiety C is dPEG® (Quanta Biodesign Ltd).

[0246] In some embodiments, the polymer moiety C comprises a cationic mucic acid-based polymer (cMAP). In some instances, cMAP comprises one or more subunit of at least one repeating subunit, and the subunit structure is represented as Formula (V):



Formula V

[0247] wherein m is independently at each occurrence 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, preferably 4-6 or 5; and n is independently at each occurrence 1, 2, 3, 4, or 5. In some embodiments, m and n are, for example, about 10.

[0248] In some instances, cMAP is further conjugated to a PEG moiety, generating a cMAP-PEG copolymer, an mPEG-cMAP-PEGm triblock polymer, or a cMAP-PEG-cMAP triblock polymer. In some instances, the PEG moiety is in a range of from about 500 Da to about 50,000 Da. In some instances, the PEG moiety is in a range of from about 500 Da to about 1000 Da, greater than 1000 Da to about 5000 Da, greater than 5000 Da to about 10,000 Da, greater than 10,000 to about 25,000 Da, greater than 25,000 Da to about 50,000 Da, or any combination of two or more of these ranges.

[0249] In some instances, the polymer moiety C is cMAP-PEG copolymer, an mPEG-cMAP-PEGm triblock polymer, or a cMAP-PEG-cMAP triblock polymer. In some cases, the polymer moiety C is cMAP-PEG copolymer. In other cases, the polymer moiety C is an mPEG-cMAP-PEGm triblock polymer. In additional cases, the polymer moiety C is a cMAP-PEG-cMAP triblock polymer.

[0250] In some embodiments, the polymer moiety C is conjugated to the polynucleic acid molecule, the binding moiety, and optionally to the endosomolytic moiety as illustrated *supra*.

Endosomolytic or Cell Membrane Penetration Moiety

[0251] In some embodiments, a molecule of Formula (I): A-X₁-B-X₂-C, further comprises an additional conjugating moiety. In some instances, the additional conjugating moiety is an endosomolytic moiety and/or a cell membrane penetration moiety. In some cases, the endosomolytic moiety is a cellular compartmental release component, such as a compound capable of releasing from any of the cellular compartments known in the art, such as the endosome, lysosome, endoplasmic reticulum (ER), Golgi apparatus, microtubule, peroxisome, or other vesicular bodies with the cell. In some cases, the endosomolytic moiety comprises an endosomolytic polypeptide, an endosomolytic polymer, an endosomolytic lipid, or an endosomolytic small molecule. In some cases, the endosomolytic moiety comprises an

endosomolytic polypeptide. In other cases, the endosomolytic moiety comprises an endosomolytic polymer. In some cases, the cell membrane penetration moiety comprises a cell penetrating peptide (CPP). In other cases, the cell membrane penetration moiety comprises a cell penetrating lipid. In other cases, the cell membrane penetration moiety comprises a cell penetrating small molecule.

Endosomolytic and Cell Membrane Penetration Polypeptides

[0252] In some embodiments, a molecule of Formula (I): A-X₁-B-X₂-C, is further conjugated with an endosomolytic polypeptide. In some cases, the endosomolytic polypeptide is a pH-dependent membrane active peptide. In some cases, the endosomolytic polypeptide is an amphipathic polypeptide. In additional cases, the endosomolytic polypeptide is a peptidomimetic. In some instances, the endosomolytic polypeptide comprises INF, melittin, meucin, or their respective derivatives thereof. In some instances, the endosomolytic polypeptide comprises INF or its derivatives thereof. In other cases, the endosomolytic polypeptide comprises melittin or its derivatives thereof. In additional cases, the endosomolytic polypeptide comprises meucin or its derivatives thereof.

[0253] In some instances, INF7 is a 24 residue polypeptide whose sequence comprises CGIFGEIEELIEEGLNLDWGNA (SEQ ID NO: 331), or GLFEAIEGFIENGWEGMIDGWYGC (SEQ ID NO: 332). In some instances, INF7 or its derivatives comprise a sequence of: GLFEAIEGFIENGWEGMIWDYGS GSCG (SEQ ID NO: 333), GLFEAIEGFIENGWEGMIDG WYG-(PEG)₆-NH₂ (SEQ ID NO: 334), or GLFEAIEGFIENGWEGMIWDYG-SGSC-K(GalNAc)₂ (SEQ ID NO: 335).

[0254] In some cases, melittin is a 26 residue polypeptide whose sequence comprises CLIGAILKVLATGLPTLISWIKNRKQ (SEQ ID NO: 336), or GIGAVLKVLTTGLPALISWIKRKRQQ (SEQ ID NO: 337). In some instances, melittin comprises a polypeptide sequence as described in U.S. Patent No. 8,501,930.

[0255] In some instances, meucin is an antimicrobial peptide (AMP) derived from the venom gland of the scorpion *Mesobuthus eupeus*. In some instances, meucin comprises of meucin-13 whose sequence comprises IFGAIAGLLKNIF-NH₂ (SEQ ID NO: 338) and meucin-18 whose sequence comprises FFGHLFKLATKIIPSLFQ (SEQ ID NO: 339).

[0256] In some instances, the endosomolytic polypeptide comprises a polypeptide in which its sequence is at least 50%, 60%, 70%, 80%, 90%, 95%, or 99% sequence identity to INF7 or its derivatives thereof, melittin or its derivatives thereof, or meucin or its derivatives thereof. In some instances, the endosomolytic moiety comprises INF7 or its derivatives thereof, melittin or its derivatives thereof, or meucin or its derivatives thereof.

[0257] In some instances, the endosomolytic moiety is INF7 or its derivatives thereof. In some cases, the endosomolytic moiety comprises a polypeptide having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NOs: 331-335. In some cases, the endosomolytic moiety comprises a polypeptide having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 331. In some cases, the endosomolytic moiety comprises a polypeptide having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 332-335. In some cases, the endosomolytic moiety comprises SEQ ID NO: 331. In some cases, the endosomolytic moiety comprises SEQ ID NO: 332-335. In some cases, the endosomolytic moiety consists of SEQ ID NO: 331. In some cases, the endosomolytic moiety consists of SEQ ID NO: 332-335.

[0258] In some instances, the endosomolytic moiety is melittin or its derivatives thereof. In some cases, the endosomolytic moiety comprises a polypeptide having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NOs: 336 or 337. In some cases, the endosomolytic moiety comprises a polypeptide having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 336. In some cases, the endosomolytic moiety comprises a polypeptide having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 337. In some cases, the endosomolytic moiety comprises SEQ ID NO: 286. In some cases, the endosomolytic moiety comprises SEQ ID NO: 337. In some cases, the endosomolytic moiety consists of SEQ ID NO: 336. In some cases, the endosomolytic moiety consists of SEQ ID NO: 337.

[0259] In some instances, the endosomolytic moiety is meucin or its derivatives thereof. In some cases, the endosomolytic moiety comprises a polypeptide having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NOs: 338 or 339. In some cases, the endosomolytic moiety comprises a polypeptide having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 338. In some cases, the endosomolytic moiety comprises a polypeptide having at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 339. In some cases, the endosomolytic moiety comprises SEQ ID NO: 338. In some cases, the endosomolytic moiety comprises SEQ ID NO: 339. In some cases, the endosomolytic moiety consists of SEQ ID NO: 338. In some cases, the endosomolytic moiety consists of SEQ ID NO: 339.

[0260] In some instances, the endosomolytic moiety comprises a sequence as illustrated in Table

TABLE 8

NAME	ORIGIN	AMINO ACID SEQUENCE	SEQ ID NO:	TYPE
Pep-1	NLS from Simian Virus 40 large antigen and Reverse transcriptase of HIV	KETWWETWWTEWSQPKKKRKV	340	Primary amphipathic
pVEC	VE-cadherin	LLIILRRRRIRKQAHASK	341	Primary amphipathic
VT5	Synthetic peptide	DPKGDPKGVTVTVTVTGKGDP KPD	342	β -sheet amphipathic
C105Y	1-antitrypsin	CSIPPEVKFNKPFVYLI	343	-
Transportan	Galanin and mastoparan	GWTLNSAGYLLGKINLKALAALA KKIL	344	Primary amphipathic
TP10	Galanin and mastoparan	AGYLLGKINLKALAALAKKIL	345	Primary amphipathic
MPG	A hydrophobic domain from the fusion sequence of HIV gp41 and NLS of SV40 T antigen	GALFLGFLGAAGSTMGA	346	β -sheet amphipathic
gH625	Glycoprotein gH of HSV type I	HGLASTLTRWAHYNALIRAF	347	Secondary amphipathic α -helical
CADY	PPTG1 peptide	GLWRALWRLRLSLWRLWRA	348	Secondary amphipathic α -helical
GALA	Synthetic peptide	WEAALAEALAEALAEHLAEALAE ALEALAA	349	Secondary amphipathic α -helical
INF	Influenza HA2 fusion peptide	GLFEAIEGFIENGWEGMIDGWYGC	350	Secondary amphipathic α -helical/ pH-dependent membrane active peptide
HA2E5-TAT	Influenza HA2 subunit of influenza virus X31 strain fusion peptide	GLFGAIAGFIENGWEGMIDGWYG	351	Secondary amphipathic α -helical/ pH-dependent membrane active peptide
HA2-penetratin	Influenza HA2 subunit of influenza virus X31 strain fusion peptide	GLFGAIAGFIENGWEGMIDGRQIKI WFQNRMMKW KK-amide	352	pH-dependent membrane active peptide

HA-K4	Influenza HA2 subunit of influenza virus X31 strain fusion peptide	GLFGAIAAGFIENGWEGMIDG-SSK KKK	353	pH-dependent membrane active peptide
HA2E4	Influenza HA2 subunit of influenza virus X31 strain fusion peptide	GLFEAIAAGFIENGWEGMIDGGGYC	354	pH-dependent membrane active peptide
H5WYG	HA2 analogue	GLFHAI AHFIHGGWH GLIHGWYG	355	pH-dependent membrane active peptide
GALA-INF3-(PEG)6-NH	INF3 fusion peptide	GLFEAIEGFIENGWEGLAELAEAL EALAA-(PEG)6-NH2	356	pH-dependent membrane active peptide
CM18-TAT11	Cecropin-A-Melittin ₂₋₁₂ (CM ₁₈) fusion peptide	KWKLFKKIGAVLKVLTTG-YGRKKRRQRRR	357	pH-dependent membrane active peptide

[0261] In some cases, the endosomolytic moiety comprises a Bak BH3 polypeptide which induces apoptosis through antagonization of suppressor targets such as Bcl-2 and/or Bcl-x_L. In some instances, the endosomolytic moiety comprises a Bak BH3 polypeptide described in Albarran, *et al.*, “Efficient intracellular delivery of a pro-apoptotic peptide with a pH-responsive carrier,” *Reactive & Functional Polymers* **71**: 261-265 (2011).

[0262] In some instances, the endosomolytic moiety comprises a polypeptide (*e.g.*, a cell-penetrating polypeptide) as described in PCT Publication Nos. WO2013/166155 or WO2015/069587.

Endosomolytic Lipids

[0263] In some embodiments, the endosomolytic moiety is a lipid (*e.g.*, a fusogenic lipid). In some embodiments, a molecule of Formula (I): A-X₁-B-X₂-C, is further conjugated with an endosomolytic lipid (*e.g.*, fusogenic lipid). Exemplary fusogenic lipids include 1,2-dioleoyl-sn-3-phosphoethanolamine (DOPE), phosphatidylethanolamine (POPE), palmitoyloleoylphosphatidylcholine (POPC), (6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,31-tetraen-19-ol (Di-Lin), N-methyl(2,2-di((9Z,12Z)-octadeca-9,12-dienyl)-1,3-dioxolan-4-yl)methanamine (DLin-k-DMA) and N-methyl-2-(2,2-di((9Z,12Z)-octadeca-9,12-dienyl)-1,3-dioxolan-4-yl)ethanamine (XTC).

[0264] In some instances, an endosomolytic moiety is a lipid (*e.g.*, a fusogenic lipid) described in PCT Publication No. WO09/126,933.

Endosomolytic Small Molecules

[0265] In some embodiments, the endosomolytic moiety is a small molecule. In some embodiments, a molecule of Formula (I): A-X₁-B-X₂-C, is further conjugated with an endosomolytic small molecule. Exemplary small molecules suitable as endosomolytic moieties include, but are not limited to, quinine, chloroquine, hydroxychloroquines, amodiaquins (carnoquines), amopyroquines, primaquines, mefloquines, nivaquines, halofantrines, quinone imines, or a combination thereof. In some instances, quinoline endosomolytic moieties include, but are not limited to, 7-chloro-4-(4-diethylamino-1-methylbutyl-amino)quinoline (chloroquine); 7-chloro-4-(4-ethyl-(2-hydroxyethyl)-amino-1-methylbutyl-amino)quinoline (hydroxychloroquine); 7-fluoro-4-(4-diethylamino-1-methylbutyl-amino)quinoline; 4-(4-diethylamino-1-methylbutylamino) quinoline; 7-hydroxy-4-(4-diethyl-amino-1-methylbutylamino)quinoline; 7-chloro-4-(4-diethylamino-1-butylamino)quinoline (desmethylchloroquine); 7-fluoro-4-(4-diethylamino-1-butylamino)quinoline; 4-(4-diethyl-amino-1-butylamino)quinoline; 7-hydroxy-4-(4-diethylamino-1-butylamino)quinoline; 7-chloro-4-(1-carboxy-4-diethylamino-1-butylamino)quinoline; 7-fluoro-4-(1-carboxy-4-diethyl-amino-1-butylamino)quinoline; 4-(1-carboxy-4-diethylamino-1-butylamino) quinoline; 7-hydroxy-4-(1-carboxy-4-diethylamino-1-butylamino)quinoline; 7-chloro-4-(1-carboxy-4-diethylamino-1-methylbutylamino)quinoline; 7-fluoro-4-(1-carboxy-4-diethyl-amino-1-methylbutylamino)quinoline; 4-(1-carboxy-4-diethylamino-1-methylbutylamino)quinoline; 7-hydroxy-4-(1-carboxy-4-diethylamino-1-methylbutylamino)quinoline; 7-fluoro-4-(4-ethyl-(2-hydroxyethyl)-amino-1-methylbutylamino)quinoline; 4-(4-ethyl-(2-hydroxyethyl)-amino-1-methylbutylamino)-quinoline; 7-hydroxy-4-(4-ethyl-(2-hydroxyethyl)-amino-1-methylbutylamino)quinoline; hydroxychloroquine phosphate; 7-chloro-4-(4-ethyl-(2-hydroxyethyl-1)-amino-1-butylamino)quinoline (desmethylhydroxychloroquine); 7-fluoro-4-(4-ethyl-(2-hydroxyethyl)-amino-1-butylamino)quinoline; 4-(4-ethyl-(2-hydroxyethyl)-amino-1-butylamino)quinoline; 7-hydroxy-4-(4-ethyl-(2-hydroxyethyl)-amino-1-butylamino) quinoline; 7-chloro-4-(1-carboxy-4-ethyl-(2-hydroxyethyl)-amino-1-butylamino)quinoline; 7-fluoro-4-(1-carboxy-4-ethyl-(2-hydroxyethyl)-amino-1-butylamino)quinoline; 4-(1-carboxy-4-ethyl-(2-hydroxyethyl)-amino-1-butylamino)quinoline; 7-hydroxy-4-(1-carboxy-4-ethyl-(2-hydroxyethyl)-amino-1-butylamino)quinoline; 7-chloro-4-(1-carboxy-4-ethyl-(2-hydroxyethyl)-amino-1-methylbutylamino)quinoline; 7-fluoro-4-(1-carboxy-4-ethyl-(2-hydroxyethyl)-amino-1-methylbutylamino)quinoline; 4-(1-carboxy-4-ethyl-(2-hydroxyethyl)-amino-1-methylbutylamino)quinoline; 7-hydroxy-4-(1-carboxy-4-ethyl-(2-hydroxyethyl)-amino-1-

methylbutylamino)quinoline; 8-[(4-aminopentyl)amino]-6-methoxydihydrochloride quinoline; 1-acetyl-1,2,3,4-tetrahydroquinoline; 8-[(4-aminopentyl)amino]-6-methoxyquinoline dihydrochloride; 1-butyryl-1,2,3,4-tetrahydroquinoline; 3-chloro-4-(4-hydroxy- α,α' -bis(2-methyl-1-pyrrolidinyl)-2,5-xylidinoquinoline, 4-[(4-diethyl-amino)-1-methylbutyl-amino]-6-methoxyquinoline; 3-fluoro-4-(4-hydroxy- α,α' -bis(2-methyl-1-pyrrolidinyl)-2,5-xylidinoquinoline, 4-[(4-diethylamino)-1-methylbutyl-amino]-6-methoxyquinoline; 4-(4-hydroxy- α,α' -bis(2-methyl-1-pyrrolidinyl)-2,5-xylidinoquinoline; 4-[(4-diethylamino)-1-methylbutyl-amino]-6-methoxyquinoline; 3,4-dihydro-1-(2H)-quinolinecarboxyaldehyde; 1,1'-pentamethylene diquinoleinium diiodide; 8-quinolinol sulfate and amino, aldehyde, carboxylic, hydroxyl, halogen, keto, sulfhydryl and vinyl derivatives or analogs thereof. In some instances, an endosomolytic moiety is a small molecule described in Naisbitt et al (1997, J Pharmacol Exp Therapy 280:884-893) and in U.S. Patent No. 5,736,557.

Cell Penetrating Polypeptide (CPP)

[0266] In some embodiments, cell penetrating polypeptide comprises positively charged short peptides with 5–30 amino acids. In some embodiments, cell penetrating polypeptide comprises arginine or lysine rich amino acid sequences. In some embodiments, cell penetrating polypeptide includes any polypeptide or combination thereof listed in Table 9

TABLE 9

Peptide	Sequence	SEQ ID NO
Antennapedia Penetratin (43–58)	RQIKIWFQNRRMKWKK	358
HIV-1 TAT protein (48–60)	GRKKRRQRRRPPQ	359
pVEC Cadherin (615–632)	LLIILRRRIKQAHAAHSK	360
Transportan Galanine/Mastoparan	GWTLNSAGYLLGKINLKALAALAKKIL	361
MPG HIV-gp41/SV40 T-antigen	GALFLGFLGAAGSTMGAWSQPKKKRKV	362
Pep-1 HIV-reverse transcriptase/SV40 T-antigen	KETWWETWWTEWSQPKKKRKV	363
Polyarginines	R(n); $6 < n < 12$	364
MAP	KLALKLALKALKAAALKLA	365
R6W3	RRWRRRWR	366
NLS	CGYGPKKKRKVGG	367
8-lysines	KKKKKKKK	368
ARF (1–22)	MVRRFLVTLRIRACGPPVRV	369
Azurin-p28	LSTAADMQGVVTDGMASGLDKDYLPDD	370

Linkers

[0267] In some embodiments, a linker described herein is a cleavable linker or a non-cleavable linker. In some instances, the linker is a cleavable linker. In other instances, the linker is a non-cleavable linker.

[0268] In some cases, the linker is a non-polymeric linker. A non-polymeric linker refers to a linker that does not contain a repeating unit of monomers generated by a polymerization process. Exemplary non-polymeric linkers include, but are not limited to, C₁-C₆ alkyl group (*e.g.*, a C₅, C₄, C₃, C₂, or C₁ alkyl group), homobifunctional cross linkers, heterobifunctional cross linkers, peptide linkers, traceless linkers, self-immolative linkers, maleimide-based linkers, or combinations thereof. In some cases, the non-polymeric linker comprises a C₁-C₆ alkyl group (*e.g.*, a C₅, C₄, C₃, C₂, or C₁ alkyl group), a homobifunctional cross linker, a heterobifunctional cross linker, a peptide linker, a traceless linker, a self-immolative linker, a maleimide-based linker, or a combination thereof. In additional cases, the non-polymeric linker does not comprise more than two of the same type of linkers, *e.g.*, more than two homobifunctional cross linkers, or more than two peptide linkers. In further cases, the non-polymeric linker optionally comprises one or more reactive functional groups.

[0269] In some instances, the non-polymeric linker does not encompass a polymer that is described above. In some instances, the non-polymeric linker does not encompass a polymer encompassed by the polymer moiety C. In some cases, the non-polymeric linker does not encompass a polyalkylene oxide (*e.g.*, PEG). In some cases, the non-polymeric linker does not encompass a PEG.

[0270] In some instances, the linker comprises a homobifunctional linker. Exemplary homobifunctional linkers include, but are not limited to, Lomant's reagent dithiobis (succinimidylpropionate) DSP, 3,3'-dithiobis(sulfosuccinimidyl propionate) (DTSSP), disuccinimidyl suberate (DSS), bis(sulfosuccinimidyl)suberate (BS), disuccinimidyl tartrate (DST), disulfosuccinimidyl tartrate (sulfo DST), ethylene glycobis(succinimidylsuccinate) (EGS), disuccinimidyl glutarate (DSG), N,N'-disuccinimidyl carbonate (DSC), dimethyl adipimidate (DMA), dimethyl pimelimidate (DMP), dimethyl suberimidate (DMS), dimethyl-3,3'-dithiobispropionimidate (DTBP), 1,4-di-3'-(2'-pyridyldithio)propionamido)butane (DPDPB), bismaleimido-hexane (BMH), aryl halide-containing compound (DFDNB), such as *e.g.* 1,5-difluoro-2,4-dinitrobenzene or 1,3-difluoro-4,6-dinitrobenzene, 4,4'-difluoro-3,3'-dinitrophenylsulfone (DFDNPS), bis-[β-(4-azidosalicylamido)ethyl]disulfide (BASED), formaldehyde, glutaraldehyde, 1,4-butanediol diglycidyl ether, adipic acid dihydrazide, carbonyldiimidazole, o-toluidine, 3,3'-dimethylbenzidine, benzidine, α,α'-p-diaminodiphenyl, diiodo-

p-xylene sulfonic acid, N,N'-ethylene-bis(iodoacetamide), or N,N'-hexamethylene-bis(iodoacetamide).

[0271] In some embodiments, the linker comprises a heterobifunctional linker. Exemplary heterobifunctional linker include, but are not limited to, amine-reactive and sulfhydryl cross-linkers such as N-succinimidyl 3-(2-pyridyldithio)propionate (SPDP), long-chain N-succinimidyl 3-(2-pyridyldithio)propionate (LC-SPDP), water-soluble-long-chain N-succinimidyl 3-(2-pyridyldithio) propionate (sulfo-LC-SPDP), succinimidylloxycarbonyl- α -methyl- α -(2-pyridyldithio)toluene (sMPT), sulfosuccinimidyl-6-[α -methyl- α -(2-pyridyldithio)toluamido]hexanoate (sulfo-LC-sMPT), succinimidyl-4-(N-maleimidomethyl)cyclohexane-1-carboxylate (sMCC), sulfosuccinimidyl-4-(N-maleimidomethyl)cyclohexane-1-carboxylate (sulfo-sMCC), m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBs), m-maleimidobenzoyl-N-hydroxysulfosuccinimide ester (sulfo-MBs), N-succinimidyl(4-iodoacetyl)aminobenzoate (sIAB), sulfosuccinimidyl(4-iodoacetyl)aminobenzoate (sulfo-sIAB), succinimidyl-4-(p-maleimidophenyl)butyrate (sMPB), sulfosuccinimidyl-4-(p-maleimidophenyl)butyrate (sulfo-sMPB), N-(γ -maleimidobutyryloxy)succinimide ester (GMBs), N-(γ -maleimidobutyryloxy)sulfosuccinimide ester (sulfo-GMBs), succinimidyl 6-((iodoacetyl)amino)hexanoate (sIAX), succinimidyl 6-[6-(((iodoacetyl)amino)hexanoyl)amino]hexanoate (sIAXX), succinimidyl 4-(((iodoacetyl)amino)methyl)cyclohexane-1-carboxylate (sIAC), succinimidyl 6-(((4-iodoacetyl)amino)methyl)cyclohexane-1-carboxylate (sIACX), p-nitrophenyl iodoacetate (NPIA), carbonyl-reactive and sulfhydryl-reactive cross-linkers such as 4-(4-N-maleimidophenyl)butyric acid hydrazide (MPBH), 4-(N-maleimidomethyl)cyclohexane-1-carboxyl-hydrazide-8 (M_2C_2H), 3-(2-pyridyldithio)propionyl hydrazide (PDPH), amine-reactive and photoreactive cross-linkers such as N-hydroxysuccinimidyl-4-azidosalicylic acid (NHs-AsA), N-hydroxysulfosuccinimidyl-4-azidosalicylic acid (sulfo-NHs-AsA), sulfosuccinimidyl-(4-azidosalicylamido)hexanoate (sulfo-NHs-LC-AsA), sulfosuccinimidyl-2-(p-azidosalicylamido)ethyl-1,3'-dithiopropionate (sAsD), N-hydroxysuccinimidyl-4-azidobenzoate (HsAB), N-hydroxysulfosuccinimidyl-4-azidobenzoate (sulfo-HsAB), N-succinimidyl-6-(4'-azido-2'-nitrophenylamino)hexanoate (sANPAH), sulfosuccinimidyl-6-(4'-azido-2'-nitrophenylamino)hexanoate (sulfo-sANPAH), N-5-azido-2-nitrobenzoyloxysuccinimide (ANB-NOs), sulfosuccinimidyl-2-(m-azido-o-nitrobenzamido)-ethyl-1,3'-dithiopropionate (sAND), N-succinimidyl-4(4-azidophenyl)1,3'-dithiopropionate (sADP), N-sulfosuccinimidyl(4-azidophenyl)-1,3'-dithiopropionate (sulfo-sADP), sulfosuccinimidyl 4-(p-azidophenyl)butyrate (sulfo-sAPB), sulfosuccinimidyl 2-(7-azido-4-methylcoumarin-3-acetamide)ethyl-1,3'-dithiopropionate (sAED), sulfosuccinimidyl 7-azido-4-methylcoumain-3-acetate (sulfo-

sAMCA), *p*-nitrophenyl diazopyruvate (*p*NPDP), *p*-nitrophenyl-2-diazo-3,3,3-trifluoropropionate (PNP-DTP), sulfhydryl-reactive and photoreactive cross-linkers such as 1-(*p*-Azidosalicylamido)-4-(iodoacetamido)butane (AsIB), N-[4-(*p*-azidosalicylamido)butyl]-3'-(2'-pyridyldithio)propionamide (APDP), benzophenone-4-iodoacetamide, benzophenone-4-maleimide carbonyl-reactive and photoreactive cross-linkers such as *p*-azidobenzoyl hydrazide (ABH), carboxylate-reactive and photoreactive cross-linkers such as 4-(*p*-azidosalicylamido)butylamine (AsBA), and arginine-reactive and photoreactive cross-linkers such as *p*-azidophenyl glyoxal (APG).

[0272] In some instances, the linker comprises a reactive functional group. In some cases, the reactive functional group comprises a nucleophilic group that is reactive to an electrophilic group present on a binding moiety. Exemplary electrophilic groups include carbonyl groups—such as aldehyde, ketone, carboxylic acid, ester, amide, enone, acyl halide or acid anhydride. In some embodiments, the reactive functional group is aldehyde. Exemplary nucleophilic groups include hydrazide, oxime, amino, hydrazine, thiosemicarbazone, hydrazine carboxylate, and arylhydrazide.

[0273] In some embodiments, the linker comprises a maleimide group. In some instances, the maleimide group is also referred to as a maleimide spacer. In some instances, the maleimide group further encompasses a caproic acid, forming maleimidocaproyl (mc). In some cases, the linker comprises maleimidocaproyl (mc). In some cases, the linker is maleimidocaproyl (mc). In other instances, the maleimide group comprises a maleimidomethyl group, such as succinimidyl-4-(N-maleimidomethyl)cyclohexane-1-carboxylate (sMCC) or sulfosuccinimidyl-4-(N-maleimidomethyl)cyclohexane-1-carboxylate (sulfo-sMCC) described above.

[0274] In some embodiments, the maleimide group is a self-stabilizing maleimide. In some instances, the self-stabilizing maleimide utilizes diaminopropionic acid (DPR) to incorporate a basic amino group adjacent to the maleimide to provide intramolecular catalysis of tiosuccinimide ring hydrolysis, thereby eliminating maleimide from undergoing an elimination reaction through a retro-Michael reaction. In some instances, the self-stabilizing maleimide is a maleimide group described in Lyon *et al.*, “Self-hydrolyzing maleimides improve the stability and pharmacological properties of antibody-drug conjugates,” *Nat. Biotechnol.* **32**(10):1059-1062 (2014). In some instances, the linker comprises a self-stabilizing maleimide. In some instances, the linker is a self-stabilizing maleimide.

[0275] In some embodiments, the linker comprises a peptide moiety. In some instances, the peptide moiety comprises at least 2, 3, 4, 5, or 6 more amino acid residues. In some instances, the peptide moiety comprises at most 2, 3, 4, 5, 6, 7, or 8 amino acid residues. In some instances, the peptide moiety comprises about 2, about 3, about 4, about 5, or about 6 amino acid residues.

In some instances, the peptide moiety is a cleavable peptide moiety (*e.g.*, either enzymatically or chemically). In some instances, the peptide moiety is a non-cleavable peptide moiety. In some instances, the peptide moiety comprises Val-Cit (valine-citrulline), Gly-Gly-Phe-Gly, Phe-Lys, Val-Lys, Gly-Phe-Lys, Phe-Phe-Lys, Ala-Lys, Val-Arg, Phe-Cit, Phe-Arg, Leu-Cit, Ile-Cit, Trp-Cit, Phe-Ala, Ala-Leu-Ala-Leu, or Gly-Phe-Leu-Gly. In some instances, the linker comprises a peptide moiety such as: Val-Cit (valine-citrulline), Gly-Gly-Phe-Gly, Phe-Lys, Val-Lys, Gly-Phe-Lys, Phe-Phe-Lys, Ala-Lys, Val-Arg, Phe-Cit, Phe-Arg, Leu-Cit, Ile-Cit, Trp-Cit, Phe-Ala, Ala-Leu-Ala-Leu, or Gly-Phe-Leu-Gly. In some cases, the linker comprises Val-Cit. In some cases, the linker is Val-Cit.

[0276] In some embodiments, the linker comprises a benzoic acid group, or its derivatives thereof. In some instances, the benzoic acid group or its derivatives thereof comprise paraaminobenzoic acid (PABA). In some instances, the benzoic acid group or its derivatives thereof comprise gamma-aminobutyric acid (GABA).

[0277] In some embodiments, the linker comprises one or more of a maleimide group, a peptide moiety, and/or a benzoic acid group, in any combination. In some embodiments, the linker comprises a combination of a maleimide group, a peptide moiety, and/or a benzoic acid group. In some instances, the maleimide group is maleimidocaproyl (mc). In some instances, the peptide group is val-cit. In some instances, the benzoic acid group is PABA. In some instances, the linker comprises a mc-val-cit group. In some cases, the linker comprises a val-cit-PABA group. In additional cases, the linker comprises a mc-val-cit-PABA group.

[0278] In some embodiments, the linker is a self-immolative linker or a self-elimination linker. In some cases, the linker is a self-immolative linker. In other cases, the linker is a self-elimination linker (*e.g.*, a cyclization self-elimination linker). In some instances, the linker comprises a linker described in U.S. Patent NO. 9,089,614 or PCT Publication NO. WO2015038426.

[0279] In some embodiments, the linker is a dendritic type linker. In some instances, the dendritic type linker comprises a branching, multifunctional linker moiety. In some instances, the dendritic type linker is used to increase the molar ratio of polynucleotide B to the binding moiety A. In some instances, the dendritic type linker comprises PAMAM dendrimers.

[0280] In some embodiments, the linker is a traceless linker or a linker in which after cleavage does not leave behind a linker moiety (*e.g.*, an atom or a linker group) to a binding moiety A, a polynucleotide B, a polymer C, or an endosomolytic moiety D. Exemplary traceless linkers include, but are not limited to, germanium linkers, silicium linkers, sulfur linkers, selenium linkers, nitrogen linkers, phosphorus linkers, boron linkers, chromium linkers, or phenylhydrazide linker. In some cases, the linker is a traceless aryl-triazene linker as described

in Hejesen, *et al.*, "A traceless aryl-triazene linker for DNA-directed chemistry," *Org Biomol Chem* **11**(15): 2493-2497 (2013). In some instances, the linker is a traceless linker described in Blaney, *et al.*, "Traceless solid-phase organic synthesis," *Chem. Rev.* **102**: 2607-2024 (2002). In some instances, a linker is a traceless linker as described in U.S. Patent No. 6,821,783.

[0281] In some instances, the linker is a linker described in U.S. Patent Nos. 6,884,869; 7,498,298; 8,288,352; 8,609,105; or 8,697,688; U.S. Patent Publication NOs. 2014/0127239; 2013/028919; 2014/286970; 2013/0309256; 2015/037360; or 2014/0294851; or PCT Publication NOs. WO2015057699; WO2014080251; WO2014197854; WO2014145090; or WO2014177042.

[0282] In some embodiments, X₁ and X₂ are each independently a bond or a non-polymeric linker. In some instances, X₁ and X₂ are each independently a bond. In some cases, X₁ and X₂ are each independently a non-polymeric linker.

[0283] In some instances, X₁ is a bond or a non-polymeric linker. In some instances, X₁ is a bond. In some instances, X₁ is a non-polymeric linker. In some instances, the linker is a C₁-C₆ alkyl group. In some cases, X₁ is a C₁-C₆ alkyl group, such as for example, a C₅, C₄, C₃, C₂, or C₁ alkyl group. In some cases, the C₁-C₆ alkyl group is an unsubstituted C₁-C₆ alkyl group. As used in the context of a linker, and in particular in the context of X₁, alkyl means a saturated straight or branched hydrocarbon radical containing up to six carbon atoms. In some instances, X₁ includes a homobifunctional linker or a heterobifunctional linker described *supra*. In some cases, X₁ includes a heterobifunctional linker. In some cases, X₁ includes sMCC. In other instances, X₁ includes a heterobifunctional linker optionally conjugated to a C₁-C₆ alkyl group. In other instances, X₁ includes sMCC optionally conjugated to a C₁-C₆ alkyl group. In additional instances, X₁ does not include a homobifunctional linker or a heterobifunctional linker described *supra*.

[0284] In some instances, X₂ is a bond or a linker. In some instances, X₂ is a bond. In other cases, X₂ is a linker. In additional cases, X₂ is a non-polymeric linker. In some embodiments, X₂ is a C₁-C₆ alkyl group. In some instances, X₂ is a homobifunctional linker or a heterobifunctional linker described *supra*. In some instances, X₂ is a homobifunctional linker described *supra*. In some instances, X₂ is a heterobifunctional linker described *supra*. In some instances, X₂ comprises a maleimide group, such as maleimidocaproyl (mc) or a self-stabilizing maleimide group described above. In some instances, X₂ comprises a peptide moiety, such as Val-Cit. In some instances, X₂ comprises a benzoic acid group, such as PABA. In additional instances, X₂ comprises a combination of a maleimide group, a peptide moiety, and/or a benzoic acid group. In additional instances, X₂ comprises a mc group. In additional instances, X₂

comprises a mc-val-cit group. In additional instances, X₂ comprises a val-cit-PABA group. In additional instances, X₂ comprises a mc-val-cit-PABA group.

Methods of Use

[0285] Muscle atrophy refers to a loss of muscle mass and/or to a progressive weakening and degeneration of muscles. In some cases, the loss of muscle mass and/or the progressive weakening and degeneration of muscles occurs due to a high rate of protein degradation, a low rate of protein synthesis, or a combination of both. In some cases, a high rate of muscle protein degradation is due to muscle protein catabolism (i.e., the breakdown of muscle protein in order to use amino acids as substrates for gluconeogenesis).

[0286] In one embodiment, muscle atrophy refers to a significant loss in muscle strength. By significant loss in muscle strength is meant a reduction of strength in diseased, injured, or unused muscle tissue in a subject relative to the same muscle tissue in a control subject. In an embodiment, a significant loss in muscle strength is a reduction in strength of at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, or more relative to the same muscle tissue in a control subject. In another embodiment, by significant loss in muscle strength is meant a reduction of strength in unused muscle tissue relative to the muscle strength of the same muscle tissue in the same subject prior to a period of nonuse. In an embodiment, a significant loss in muscle strength is a reduction of at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, or more relative to the muscle strength of the same muscle tissue in the same subject prior to a period of nonuse.

[0287] In another embodiment, muscle atrophy refers to a significant loss in muscle mass. By significant loss in muscle mass is meant a reduction of muscle volume in diseased, injured, or unused muscle tissue in a subject relative to the same muscle tissue in a control subject. In an embodiment, a significant loss of muscle volume is at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, or more relative to the same muscle tissue in a control subject. In another embodiment, by significant loss in muscle mass is meant a reduction of muscle volume in unused muscle tissue relative to the muscle volume of the same muscle tissue in the same subject prior to a period of nonuse. In an embodiment, a significant loss in muscle tissue is at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, or more relative to the muscle volume of the same muscle tissue in the same subject prior to a period of nonuse. Muscle volume is optionally measured by evaluating the cross-section area of a muscle such as

by Magnetic Resonance Imaging (*e.g.*, by a muscle volume/cross-section area (CSA) MRI method).

[0288] In some embodiments, described herein is a method of treating muscle atrophy in a subject, which comprises providing polynucleic acid molecule described herein and administering to the subject a therapeutically effective amount of a polynucleic acid molecule described herein or a polynucleic acid molecule conjugate described herein to reduces a quantity of the mRNA transcript of human *DUX4*. In some instances, the muscle atrophy is associated with Facioscapulohumeral muscular dystrophy (FSHD). The polynucleic acid moiety mediates RNA interference against the human *DUX4* as to modulating muscle atrophy in a subject. In some embodiments, expression of one or more marker genes that are affected by *DUX4* expression is also altered or modulated (*e.g.*, decreased) by the decreased expression of human *DUX4*. The marker genes includes, but not limited to, MBD3L2, TRIM43, PRAMEF1, ZSCAN4, KHDC1L, and LEUTX. In some embodiments, the expression of one or more marker genes is decreased at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, or 50% compared to untreated cells. In some embodiments, the expression of one or more marker genes, as a group or a composite, is decreased at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, or 50% compared to untreated cells.

[0289] In some embodiments, described herein is a method of treating muscle atrophy in a subject, which comprises providing an siRNAantibody conjugate described herein and administering to the subject a therapeutically effective amount of the siRNAantibody conjugate described herein and reducing the levels of mRNA transcript of human *DUX4* in said subject. In some instances, the muscle atrophy is associated with FSHD. The siRNAantibody conjugate mediates RNA interference against the human *DUX4* mRNA as to treat muscle atrophy in the subject, which comprises administering to the subject a therapeutically effective amount of the siRNAantibody conjugate described herein and reducing the levels of mRNA transcript of human *DUX4* in said subject.

[0290] In some embodiments, described herein is a method of treating muscle atrophy in a subject, which comprises providing a *DUX4*siRNAantibody conjugate (*DUX4* siRNA-conjugate or *DUX4*-AOC) described herein and administering to the subject a therapeutically effective amount of the *DUX4* siRNAantibody conjugate described herein and reducing the levels of mRNA transcript of human *DUX4* in said subject. In some instances, the muscle atrophy is associated with FSHD. The *DUX4* siRNAantibody conjugate mediates RNA interference against the human *DUX4* mRNA as to treat muscle atrophy in the subject, which comprises administering to the subject a therapeutically effective amount of the *DUX4* siRNAantibody

conjugate described herein and reducing the levels of mRNA transcript of human DUX4 in said subject.

[0291] In some embodiments, described herein is a method of treating FSHD in a subject, which comprises providing a DUX4 siRNA antibody conjugate (DUX4 siRNA conjugate or DUX4-AOC) described herein and administering to the subject a therapeutically effective amount of the DUX4 siRNA antibody conjugate described herein and reducing the levels of mRNA transcript of human DUX4 in said subject. In some instances, the FSHD is FSHD type 1 (FSHD1). In some instances, the FSHD is FSHD type 2. The DUX4 siRNA antibody conjugate mediates RNA interference against the human DUX4 mRNA as to treat FSHD in the subject, which comprises administering to the subject a therapeutically effective amount of the DUX4 siRNA-conjugate described herein and reducing the levels of mRNA transcript of human DUX4 in said subject. In some embodiments, expression levels of one or more marker genes that are affected by DUX4 expression are also altered or modulated by the decreased expression levels of human DUX4. The DUX4 biomarker genes include but are not limited to MBD3L2, TRIM43, PRAMEF1, ZSCAN4, KHDC1L, and LEUTX.

[0292] In some embodiments, described herein is a method of alleviating symptoms in a subject with FSHD, which comprises providing a DUX siRNA antibody conjugate (DUX4-siRNA conjugate or DUX4-AOC) described herein and administering to the subject a therapeutically effective amount of the siRNA conjugate described herein by reducing the levels of mRNA transcript of human DUX4. In some instances, the FSHD is FSHD type 1 (FSHD1). In some instances, the FSHD is FSHD type 2. In another embodiment, described herein is a method of alleviating symptoms in a FSHD patient, which comprises providing an siRNA conjugate described herein and administering to the FSHD patient a therapeutically effective amount of the siRNA conjugate described herein by reducing the levels of mRNA transcript of human DUX4 or reducing the levels of DUX4 protein.

[0293] In some instances, the symptoms of FSHD affect skeletal muscles. The skeletal muscles affected by FSHD include muscles around the eyes and mouth, muscle of the shoulders, muscle of the upper arms, muscle of the lower legs, abdominal muscles and hip muscles. In some instances, the symptoms of FSHD also affect vision and hearing. In some instances, the symptoms of FSHD also affect the function of the heart or lungs. In some instances, the symptoms of FSHD include muscle weakness, muscle atrophy, muscle dystrophy, pain inflammation, contractures, scoliosis, lordosis, hypoventilation, abnormalities of the retina, exposure to keratitis, mild hearing loss, and EMG abnormality.

[0294] In some embodiments, described herein is a method of improving skeletal muscle functions in a FSHD patient comprising the step of administering to the FSHD patient a

therapeutically effective amount of the siRNA conjugate described herein by reducing the levels of mRNA transcript of human DUX4 or reducing the levels of DUX4 protein. In some instances, FSHD is FSHD type 1 (FSHD1). In some instances, FSHD is FSHD type 2. In some embodiments, described herein is a method of improving skeletal muscle functions, vision, hearing, heart functions or lung functions in a patient suffering from FSHD comprising the step of administering to the FSHD patient a therapeutically effective amount of the siRNA conjugate described herein by reducing the levels of mRNA transcript of human DUX4 or reducing the levels of DUX4 protein.

[0295] In some embodiments, described herein is a method of treating FSHD in a subject, which comprises providing an antisense oligonucleotide (ASO)antibody conjugate (ASO conjugate) described herein and administering to the subject a therapeutically effective amount of the ASO-antibody conjugate described herein and reducing the levels of mRNA transcript of human DUX4 in said subject. In some instances, FSHD is FSHD type 1 (FSHD1). In some instances, FSHD is FSHD type 2. The ASO-conjugate mediates RNA interference against the human DUX4 mRNA as to treat FSHD in the subject, which comprises administering to the subject a therapeutically effective amount of the ASO-antibody conjugate described herein and reducing the levels of mRNA transcript of human DUX4 in said subject. In some embodiments, expression levels of one or more marker genes that are affected by DUX4 expression is also altered or modulated by the decreased expression levels of human DUX4. The DUX4 biomarker genes include but are not limited to MBD3L2, TRIM43, PRAMEF1, ZSCAN4, KHDC1L, and LEUTX.

[0296] In some embodiments, described herein is a method of treating FSHD in a subject. In some instances, the FSHD subject suffers from FSHD1. In other instances, the FSHD subject suffers from FSHD2. In another embodiment, the FSHD subject has muscle cells abnormally expressing DUX4 protein caused by the genetic and epigenetic molecular changes in the D4Z4 region of the long arm of chromosome 4. The genetic molecular changes in the muscle cells are mutations leading to the contraction of the D4Z4 region containing 1-10 repeats instead of the normal 11 to 100 repeats of chromosome 4 of the FSHD subject. The epigenetic molecular changes in the muscle cells are changes leading to the hypomethylation of the D4Z4 region of chromosome 4 of the FSHD subject. In some instances, the muscle cells are skeletal muscle cells.

Pharmaceutical Formulation

[0297] In some embodiments, the pharmaceutical formulations described herein are administered to a subject by multiple administration routes, including but not limited to,

parenteral (*e.g.*, intravenous, subcutaneous, intramuscular), oral, intranasal, buccal, rectal, or transdermal administration routes. In some instances, the pharmaceutical composition describe herein is formulated for parenteral (*e.g.*, intravenous, subcutaneous, intramuscular, intra-arterial, intraperitoneal, intrathecal, intracerebral, intracerebroventricular, or intracranial) administration. In other instances, the pharmaceutical composition describe herein is formulated for oral administration. In still other instances, the pharmaceutical composition describe herein is formulated for intranasal administration.

[0298] In some embodiments, the pharmaceutical formulations include, but are not limited to, aqueous liquid dispersions, self-emulsifying dispersions, solid solutions, liposomal dispersions, aerosols, solid dosage forms, powders, immediate release formulations, controlled release formulations, fast melt formulations, tablets, capsules, pills, delayed release formulations, extended release formulations, pulsatile release formulations, multiparticulate formulations (*e.g.*, nanoparticle formulations), and mixed immediate and controlled release formulations.

[0299] In some instances, the pharmaceutical formulation includes multiparticulate formulations. In some instances, the pharmaceutical formulation includes nanoparticle formulations. In some instances, nanoparticles comprise cMAP, cyclodextrin, or lipids. In some cases, nanoparticles comprise solid lipid nanoparticles, polymeric nanoparticles, self-emulsifying nanoparticles, liposomes, microemulsions, or micellar solutions. Additional exemplary nanoparticles include, but are not limited to, paramagnetic nanoparticles, superparamagnetic nanoparticles, metal nanoparticles, fullerene-like materials, inorganic nanotubes, dendrimers (such as with covalently attached metal chelates), nanofibers, nanohorns, nano-onions, nanorods, nanoropes and quantum dots. In some instances, a nanoparticle is a metal nanoparticle, *e.g.*, a nanoparticle of scandium, titanium, vanadium, chromium, manganese, iron, cobalt, nickel, copper, zinc, yttrium, zirconium, niobium, molybdenum, ruthenium, rhodium, palladium, silver, cadmium, hafnium, tantalum, tungsten, rhenium, osmium, iridium, platinum, gold, gadolinium, aluminum, gallium, indium, tin, thallium, lead, bismuth, magnesium, calcium, strontium, barium, lithium, sodium, potassium, boron, silicon, phosphorus, germanium, arsenic, antimony, and combinations, alloys or oxides thereof.

[0300] In some instances, a nanoparticle includes a core or a core and a shell, as in a core-shell nanoparticle.

[0301] In some instances, a nanoparticle is further coated with molecules for attachment of functional elements (*e.g.*, with one or more of a polynucleic acid molecule or binding moiety described herein). In some instances, a coating comprises chondroitin sulfate, dextran sulfate, carboxymethyl dextran, alginic acid, pectin, carragheenan, fucoidan, agaropectin, porphyran, karaya gum, gellan gum, xanthan gum, hyaluronic acids, glucosamine, galactosamine, chitin (or

chitosan), polyglutamic acid, polyaspartic acid, lysozyme, cytochrome C, ribonuclease, trypsinogen, chymotrypsinogen, α -chymotrypsin, polylysine, polyarginine, histone, protamine, ovalbumin or dextrin or cyclodextrin. In some instances, a nanoparticle comprises a graphene-coated nanoparticle.

[0302] In some cases, a nanoparticle has at least one dimension of less than about 500nm, 400nm, 300nm, 200nm, or 100nm.

[0303] In some instances, the nanoparticle formulation comprises paramagnetic nanoparticles, superparamagnetic nanoparticles, metal nanoparticles, fullerene-like materials, inorganic nanotubes, dendrimers (such as with covalently attached metal chelates), nanofibers, nanohorns, nano-onions, nanorods, nanoropes or quantum dots. In some instances, a polynucleic acid molecule or a binding moiety described herein is conjugated either directly or indirectly to the nanoparticle. In some instances, at least 1, 5, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100 or more polynucleic acid molecules or binding moieties described herein are conjugated either directly or indirectly to a nanoparticle.

[0304] In some embodiments, the pharmaceutical formulation comprises a delivery vector, *e.g.*, a recombinant vector, the delivery of the polynucleic acid molecule into cells. In some instances, the recombinant vector is DNA plasmid. In other instances, the recombinant vector is a viral vector. Exemplary viral vectors include vectors derived from adeno-associated virus, retrovirus, adenovirus, or alphavirus. In some instances, the recombinant vectors capable of expressing the polynucleic acid molecules provide stable expression in target cells. In additional instances, viral vectors are used that provide for transient expression of polynucleic acid molecules.

[0305] In some embodiments, the pharmaceutical formulation includes a carrier or carrier materials selected on the basis of compatibility with the composition disclosed herein, and the release profile properties of the desired dosage form. Exemplary carrier materials include, *e.g.*, binders, suspending agents, disintegration agents, filling agents, surfactants, solubilizers, stabilizers, lubricants, wetting agents, diluents, and the like. Pharmaceutically compatible carrier materials include, but are not limited to, acacia, gelatin, colloidal silicon dioxide, calcium glycerophosphate, calcium lactate, maltodextrin, glycerine, magnesium silicate, polyvinylpyrrolidone (PVP), cholesterol, cholesterol esters, sodium caseinate, soy lecithin, taurocholic acid, phosphatidylcholine, sodium chloride, tricalcium phosphate, dipotassium phosphate, cellulose and cellulose conjugates, sugars sodium stearyl lactylate, carrageenan, monoglyceride, diglyceride, pregelatinized starch, and the like. See, *e.g.*, *Remington: The Science and Practice of Pharmacy*, Nineteenth Ed (Easton, Pa.: Mack Publishing Company, 1995); Hoover, John E., *Remington's Pharmaceutical Sciences*, Mack Publishing Co., Easton,

Pennsylvania 1975; Liberman, H.A. and Lachman, L., Eds., *Pharmaceutical Dosage Forms*, Marcel Decker, New York, N.Y., 1980; and *Pharmaceutical Dosage Forms and Drug Delivery Systems*, Seventh Ed. (Lippincott Williams & Wilkins 1999).

[0306] In some instances, the pharmaceutical formulation further includes pH adjusting agents or buffering agents which include acids such as acetic, boric, citric, lactic, phosphoric and hydrochloric acids; bases such as sodium hydroxide, sodium phosphate, sodium borate, sodium citrate, sodium acetate, sodium lactate and tris-hydroxymethylaminomethane; and buffers such as citrate/dextrose, sodium bicarbonate and ammonium chloride. Such acids, bases and buffers are included in an amount required to maintain pH of the composition in an acceptable range.

[0307] In some instances, the pharmaceutical formulation includes one or more salts in an amount required to bring osmolality of the composition into an acceptable range. Such salts include those having sodium, potassium or ammonium cations and chloride, citrate, ascorbate, borate, phosphate, bicarbonate, sulfate, thiosulfate or bisulfite anions; suitable salts include sodium chloride, potassium chloride, sodium thiosulfate, sodium bisulfite and ammonium sulfate.

[0308] In some instances, the pharmaceutical formulation further includes diluent which are used to stabilize compounds because they provide a more stable environment. Salts dissolved in buffered solutions (which also provide pH control or maintenance) are utilized as diluents in the art, including, but not limited to a phosphate buffered saline solution. In certain instances, diluents increase bulk of the composition to facilitate compression or create sufficient bulk for homogenous blend for capsule filling. Such compounds include *e.g.*, lactose, starch, mannitol, sorbitol, dextrose, microcrystalline cellulose such as Avicel[®]; dibasic calcium phosphate, dicalcium phosphate dihydrate; tricalcium phosphate, calcium phosphate; anhydrous lactose, spray-dried lactose; pregelatinized starch, compressible sugar, such as Di-Pac[®] (Amstar); mannitol, hydroxypropylmethylcellulose, hydroxypropylmethylcellulose acetate stearate, sucrose-based diluents, confectioner's sugar; monobasic calcium sulfate monohydrate, calcium sulfate dihydrate; calcium lactate trihydrate, dextrates; hydrolyzed cereal solids, amylose; powdered cellulose, calcium carbonate; glycine, kaolin; mannitol, sodium chloride; inositol, bentonite, and the like.

[0309] In some cases, the pharmaceutical formulation includes disintegration agents or disintegrants to facilitate the breakup or disintegration of a substance. The term "disintegrate" include both the dissolution and dispersion of the dosage form when contacted with gastrointestinal fluid. Examples of disintegration agents include a starch, *e.g.*, a natural starch such as corn starch or potato starch, a pregelatinized starch such as National 1551 or Amijel[®], or sodium starch glycolate such as Promogel[®] or Explotab[®], a cellulose such as a wood product,

methylcrystalline cellulose, *e.g.*, Avicel[®], Avicel[®] PH101, Avicel[®] PH102, Avicel[®] PH105, Elcema[®] P100, Emcocel[®], Vivacel[®], Ming Tia[®], and Solka-Floc[®], methylcellulose, croscarmellose, or a cross-linked cellulose, such as cross-linked sodium carboxymethylcellulose (Ac-Di-Sol[®]), cross-linked carboxymethylcellulose, or cross-linked croscarmellose, a cross-linked starch such as sodium starch glycolate, a cross-linked polymer such as crospovidone, a cross-linked polyvinylpyrrolidone, alginate such as alginic acid or a salt of alginic acid such as sodium alginate, a clay such as Veegum[®] HV (magnesium aluminum silicate), a gum such as agar, guar, locust bean, Karaya, pectin, or tragacanth, sodium starch glycolate, bentonite, a natural sponge, a surfactant, a resin such as a cation-exchange resin, citrus pulp, sodium lauryl sulfate, sodium lauryl sulfate in combination starch, and the like.

[0310] In some instances, the pharmaceutical formulation includes filling agents such as lactose, calcium carbonate, calcium phosphate, dibasic calcium phosphate, calcium sulfate, microcrystalline cellulose, cellulose powder, dextrose, dextrans, dextrans, starches, pregelatinized starch, sucrose, xylitol, lactitol, mannitol, sorbitol, sodium chloride, polyethylene glycol, and the like.

[0311] Lubricants and glidants are also optionally included in the pharmaceutical formulations described herein for preventing, reducing or inhibiting adhesion or friction of materials. Exemplary lubricants include, *e.g.*, stearic acid, calcium hydroxide, talc, sodium stearyl fumarate, a hydrocarbon such as mineral oil, or hydrogenated vegetable oil such as hydrogenated soybean oil (Sterotex[®]), higher fatty acids and their alkali-metal and alkaline earth metal salts, such as aluminum, calcium, magnesium, zinc, stearic acid, sodium stearates, glycerol, talc, waxes, Stearowet[®], boric acid, sodium benzoate, sodium acetate, sodium chloride, leucine, a polyethylene glycol (*e.g.*, PEG-4000) or a methoxypolyethylene glycol such as Carbowax[™], sodium oleate, sodium benzoate, glyceryl behenate, polyethylene glycol, magnesium or sodium lauryl sulfate, colloidal silica such as Syloid[™], Cab-O-Sil[®], a starch such as corn starch, silicone oil, a surfactant, and the like.

[0312] Plasticizers include compounds used to soften the microencapsulation material or film coatings to make them less brittle. Suitable plasticizers include, *e.g.*, polyethylene glycols such as PEG 300, PEG 400, PEG 600, PEG 1450, PEG 3350, and PEG 800, stearic acid, propylene glycol, oleic acid, triethyl cellulose and triacetin. Plasticizers also function as dispersing agents or wetting agents.

[0313] Solubilizers include compounds such as triacetin, triethylcitrate, ethyl oleate, ethyl caprylate, sodium lauryl sulfate, sodium docusate, vitamin E TPGS, dimethylacetamide, N-methylpyrrolidone, N-hydroxyethylpyrrolidone, polyvinylpyrrolidone, hydroxypropylmethyl cellulose, hydroxypropyl cyclodextrins, ethanol, n-butanol, isopropyl alcohol, cholesterol, bile

salts, polyethylene glycol 200-600, glycofurol, transcitol, propylene glycol, and dimethyl isosorbide and the like.

[0314] Stabilizers include compounds such as any antioxidation agents, buffers, acids, preservatives and the like.

[0315] Suspending agents include compounds such as polyvinylpyrrolidone, *e.g.*, polyvinylpyrrolidone K12, polyvinylpyrrolidone K17, polyvinylpyrrolidone K25, or polyvinylpyrrolidone K30, vinyl pyrrolidone/vinyl acetate copolymer (S630), polyethylene glycol, *e.g.*, the polyethylene glycol has a molecular weight of about 300 to about 6000, or about 3350 to about 4000, or about 7000 to about 5400, sodium carboxymethylcellulose, methylcellulose, hydroxypropylmethylcellulose, hydroxymethylcellulose acetate stearate, polysorbate-80, hydroxyethylcellulose, sodium alginate, gums, such as, *e.g.*, gum tragacanth and gum acacia, guar gum, xanthans, including xanthan gum, sugars, cellulosics, such as, *e.g.*, sodium carboxymethylcellulose, methylcellulose, sodium carboxymethylcellulose, hydroxypropylmethylcellulose, hydroxyethylcellulose, polysorbate-80, sodium alginate, polyethoxylated sorbitan monolaurate, polyethoxylated sorbitan monolaurate, povidone and the like.

[0316] Surfactants include compounds such as sodium lauryl sulfate, sodium docusate, Tween 60 or 80, triacetin, vitamin E TPGS, sorbitan monooleate, polyoxyethylene sorbitan monooleate, polysorbates, polaxomers, bile salts, glyceryl monostearate, copolymers of ethylene oxide and propylene oxide, *e.g.*, Pluronic[®] (BASF), and the like. Additional surfactants include polyoxyethylene fatty acid glycerides and vegetable oils, *e.g.*, polyoxyethylene (60) hydrogenated castor oil; and polyoxyethylene alkylethers and alkylphenyl ethers, *e.g.*, octoxynol 10, octoxynol 40. Sometimes, surfactants is included to enhance physical stability or for other purposes.

[0317] Viscosity enhancing agents include, *e.g.*, methyl cellulose, xanthan gum, carboxymethyl cellulose, hydroxypropyl cellulose, hydroxypropylmethyl cellulose, hydroxypropylmethyl cellulose acetate stearate, hydroxypropylmethyl cellulose phthalate, carbomer, polyvinyl alcohol, alginates, acacia, chitosans and combinations thereof.

[0318] Wetting agents include compounds such as oleic acid, glyceryl monostearate, sorbitan monooleate, sorbitan monolaurate, triethanolamine oleate, polyoxyethylene sorbitan monooleate, polyoxyethylene sorbitan monolaurate, sodium docusate, sodium oleate, sodium lauryl sulfate, sodium docusate, triacetin, Tween 80, vitamin E TPGS, ammonium salts and the like.

Therapeutic Regimens

[0319] In some embodiments, the pharmaceutical compositions described herein are administered for therapeutic applications. In some embodiments, the pharmaceutical composition is administered once per day, twice per day, three times per day or more. The pharmaceutical composition is administered daily, every day, every alternate day, five days a week, once a week, every other week, two weeks per month, three weeks per month, once a month, twice a month, three times per month, once in two months, once in three months, once in four months, once in five months, once in six months or more. The pharmaceutical composition is administered for at least 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 12 months, 18 months, 2 years, 3 years, or more.

[0320] In some embodiments, one or more pharmaceutical compositions are administered simultaneously, sequentially, or at an interval period of time. In some embodiments, one or more pharmaceutical compositions are administered simultaneously. In some cases, one or more pharmaceutical compositions are administered sequentially. In additional cases, one or more pharmaceutical compositions are administered at an interval period of time (*e.g.*, the first administration of a first pharmaceutical composition is on day one followed by an interval of at least 1, 2, 3, 4, 5, or more days prior to the administration of at least a second pharmaceutical composition).

[0321] In some embodiments, two or more different pharmaceutical compositions are co-administered. In some instances, the two or more different pharmaceutical compositions are co-administered simultaneously. In some cases, the two or more different pharmaceutical compositions are co-administered sequentially without a gap of time between administrations. In other cases, the two or more different pharmaceutical compositions are co-administered sequentially with a gap of about 0.5 hour, 1 hour, 2 hour, 3 hour, 12 hours, 1 day, 2 days, or more between administrations.

[0322] In the case wherein the patient's status does improve, upon the doctor's discretion the administration of the composition is given continuously; alternatively, the dose of the composition being administered is temporarily reduced or temporarily suspended for a certain length of time (*i.e.*, a "drug holiday"). In some instances, the length of the drug holiday varies between 2 days and 1 year, including by way of example only, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 10 days, 12 days, 15 days, 20 days, 28 days, 35 days, 50 days, 70 days, 100 days, 120 days, 150 days, 180 days, 200 days, 250 days, 280 days, 300 days, 320 days, 350 days, or 365 days. The dose reduction during a drug holiday is from 10%-100%, including, by way of example only, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100%.

[0323] Once improvement of the patient's conditions has occurred, a maintenance dose is administered if necessary. Subsequently, the dosage or the frequency of administration, or both, can be reduced, as a function of the symptoms, to a level at which the improved disease, disorder or condition is retained.

[0324] In some embodiments, the amount of a given agent that correspond to such an amount varies depending upon factors such as the particular compound, the severity of the disease, the identity (*e.g.*, weight) of the subject or host in need of treatment, but nevertheless is routinely determined in a manner known in the art according to the particular circumstances surrounding the case, including, *e.g.*, the specific agent being administered, the route of administration, and the subject or host being treated. In some instances, the desired dose is conveniently presented in a single dose or as divided doses administered simultaneously (or over a short period of time) or at appropriate intervals, for example as two, three, four or more sub-doses per day.

[0325] The foregoing ranges are merely suggestive, as the number of variables in regard to an individual treatment regime is large, and considerable excursions from these recommended values are not uncommon. Such dosages is altered depending on a number of variables, not limited to the activity of the compound used, the disease or condition to be treated, the mode of administration, the requirements of the individual subject, the severity of the disease or condition being treated, and the judgment of the practitioner.

[0326] In some embodiments, toxicity and therapeutic efficacy of such therapeutic regimens are determined by standard pharmaceutical procedures in cell cultures or experimental animals, including, but not limited to, the determination of the LD50 (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between the toxic and therapeutic effects is the therapeutic index and it is expressed as the ratio between LD50 and ED50. Compounds exhibiting high therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50 with minimal toxicity. The dosage varies within this range depending upon the dosage form employed and the route of administration utilized.

Kits/Article of Manufacture

[0327] Disclosed herein, in certain embodiments, are kits and articles of manufacture for use with one or more of the compositions and methods described herein. Such kits include a carrier, package, or container that is compartmentalized to receive one or more containers such as vials, tubes, and the like, each of the container(s) comprising one of the separate elements to be used

in a method described herein. Suitable containers include, for example, bottles, vials, syringes, and test tubes. In one embodiment, the containers are formed from a variety of materials such as glass or plastic.

[0328] The articles of manufacture provided herein contain packaging materials. Examples of pharmaceutical packaging materials include, but are not limited to, blister packs, bottles, tubes, bags, containers, bottles, and any packaging material suitable for a selected formulation and intended mode of administration and treatment.

[0329] For example, the container(s) include target nucleic acid molecule described herein. Such kits optionally include an identifying description or label or instructions relating to its use in the methods described herein.

[0330] A kit typically includes labels listing contents and/or instructions for use, and package inserts with instructions for use. A set of instructions will also typically be included.

[0331] In one embodiment, a label is on or associated with the container. In one embodiment, a label is on a container when letters, numbers or other characters forming the label are attached, molded or etched into the container itself; a label is associated with a container when it is present within a receptacle or carrier that also holds the container, *e.g.*, as a package insert. In one embodiment, a label is used to indicate that the contents are to be used for a specific therapeutic application. The label also indicates directions for use of the contents, such as in the methods described herein.

[0332] In certain embodiments, the pharmaceutical compositions are presented in a pack or dispenser device which contains one or more unit dosage forms containing a compound provided herein. The pack, for example, contains metal or plastic foil, such as a blister pack. In one embodiment, the pack or dispenser device is accompanied by instructions for administration. In one embodiment, the pack or dispenser is also accompanied with a notice associated with the container in form prescribed by a governmental agency regulating the manufacture, use, or sale of pharmaceuticals, which notice is reflective of approval by the agency of the form of the drug for human or veterinary administration. Such notice, for example, is the labeling approved by the U.S. Food and Drug Administration for prescription drugs, or the approved product insert. In one embodiment, compositions containing a compound provided herein formulated in a compatible pharmaceutical carrier are also prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

Certain Terminology

[0333] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood by one of skill in the art to which the claimed subject

matter belongs. It is to be understood that the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive of any subject matter claimed. In this application, the use of the singular includes the plural unless specifically stated otherwise. It must be noted that, as used in the specification and the appended claims, the singular forms “a,” “an” and “the” include plural referents unless the context clearly dictates otherwise. In this application, the use of “or” means “and/or” unless stated otherwise. Furthermore, use of the term “including” as well as other forms, such as “include”, “includes,” and “included,” is not limiting.

[0334] As used herein, ranges and amounts can be expressed as “about” a particular value or range. About also includes the exact amount. Hence “about 5 μ L” means “about 5 μ L” and also “5 μ L.” Generally, the term “about” includes an amount that would be expected to be within experimental error.

[0335] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

[0336] As used herein, the terms “individual(s)”, “subject(s)” and “patient(s)” mean any mammal. In some embodiments, the mammal is a human. In some embodiments, the mammal is a non-human. None of the terms require or are limited to situations characterized by the supervision (e.g. constant or intermittent) of a health care worker (e.g. a doctor, a registered nurse, a nurse practitioner, a physician’s assistant, an orderly or a hospice worker).

[0337] The term “therapeutically effective amount” relates to an amount of a polynucleic acid molecule conjugate that is sufficient to provide a desired therapeutic effect in a mammalian subject. In some cases, the amount is single or multiple dose administration to a patient (such as a human) for treating, preventing, preventing the onset of, curing, delaying, reducing the severity of, ameliorating at least one symptom of a disorder or recurring disorder, or prolonging the survival of the patient beyond that expected in the absence of such treatment. Naturally, dosage levels of the particular polynucleic acid molecule conjugate employed to provide a therapeutically effective amount vary in dependence of the type of injury, the age, the weight, the gender, the medical condition of the subject, the severity of the condition, the route of administration, and the particular inhibitor employed. In some instances, therapeutically effective amounts of polynucleic acid molecule conjugate, as described herein, is estimated initially from cell culture and animal models. For example, IC_{50} values determined in cell culture methods optionally serve as a starting point in animal models, while IC_{50} values determined in animal models are optionally used to find a therapeutically effective dose in humans.

[0338] Skeletal muscle, or voluntary muscle, is generally anchored by tendons to bone and is generally used to effect skeletal movement such as locomotion or in maintaining posture.

Although some control of skeletal muscle is generally maintained as an unconscious reflex (*e.g.*, postural muscles or the diaphragm), skeletal muscles react to conscious control. Smooth muscle, or involuntary muscle, is found within the walls of organs and structures such as the esophagus, stomach, intestines, uterus, urethra, and blood vessels.

[0339] Skeletal muscle is further divided into two broad types: Type I (or “slow twitch”) and Type II (or “fast twitch”). Type I muscle fibers are dense with capillaries and are rich in mitochondria and myoglobin, which gives Type I muscle tissue a characteristic red color. In some cases, Type I muscle fibers carries more oxygen and sustain aerobic activity using fats or carbohydrates for fuel. Type I muscle fibers contract for long periods of time but with little force. Type II muscle fibers are further subdivided into three major subtypes (IIa, IIx, and IIb) that vary in both contractile speed and force generated. Type II muscle fibers contract quickly and powerfully but fatigue very rapidly, and therefore produce only short, anaerobic bursts of activity before muscle contraction becomes painful.

[0340] Unlike skeletal muscle, smooth muscle is not under conscious control.

[0341] Cardiac muscle is also an involuntary muscle but more closely resembles skeletal muscle in structure and is found only in the heart. Cardiac and skeletal muscles are striated in that they contain sarcomeres that are packed into highly regular arrangements of bundles. By contrast, the myofibrils of smooth muscle cells are not arranged in sarcomeres and therefore are not striated.

[0342] Muscle cells encompass any cells that contribute to muscle tissue. Exemplary muscle cells include myoblasts, satellite cells, myotubes, and myofibril tissues.

[0343] As used here, muscle force is proportional to the cross-sectional area (CSA), and muscle velocity is proportional to muscle fiber length. Thus, comparing the cross-sectional areas and muscle fibers between various kinds of muscles is capable of providing an indication of muscle atrophy. Various methods are known in the art to measure muscle strength and muscle weight, see, for example, “Musculoskeletal assessment: Joint range of motion and manual muscle strength” by Hazel M. Clarkson, published by Lippincott Williams & Wilkins, 2000. The production of tomographic images from selected muscle tissues by computed axial tomography and sonographic evaluation are additional methods of measuring muscle mass.

[0344] The term antibody oligonucleotide conjugate (AOC) refers to an antibody conjugated to a nucleotide.

[0345] The term siRNA conjugate or siRNAantibody conjugate refers to an antibody conjugated to a siRNA.

[0346] The term DUX4 siRNA-conjugate or DUX4 siRNAantibody conjugate refers to an antibody conjugated to a siRNA hybridizing to a target sequence of the human DUX4 mRNA.

[0347] The term DUX4-AOC refers to an antibody conjugated to an siRNA hybridizing to a target sequence of the human DUX4 mRNA.

EXAMPLES

[0348] These examples are provided for illustrative purposes only and not to limit the scope of the claims provided herein.

Example 1. Bioinformatic siRNA library design against human full length DUX4 transcript

[0349] FIG.2 shows a flowchart of in silico selection process of DUX4 siRNA. Sequences of all siRNAs that can binds to DUX4, or a pre-determined region of the DUX4 are collected to generate a starting set of DUX4 siRNA. From the starting set of DUX siRNAs, the first eliminating step comprises eliminating one or more DUX siRNAs that has single nucleotide polymorphism (SNP) and/or MEF < -5. Then, the second eliminating step comprises eliminating DUX siRNAs with 0 and 1 MM in the human transcriptome (such that only hits allowed are DUX, DUX5, and DBET). Then, the third eliminating step comprises eliminating DUX siRNAs with 0 mismatch (MM) in the human intragenic regions (such that only hits allowed are DUX1, DUX5 and DBET pseudogenes). Then, the next eliminating step comprises eliminating DUX siRNAs with a MM to DUX4 human sequence used in FLExDUX4 FSHD mouse model. Then, the next step is carrying forward only or one or more DUX siRNAs with predicted viability ≥ 60 . Next, the eliminating step comprises eliminating one or more DUX siRNAs with a match to a seed region of known miRNAs 1-1000. Then, the eliminating step continues with eliminating DUX siRNAs molecule with %GC content 75 and above. Then, the final selection process comprises with 8 or less predicted off-target hits with 2 MM, except for the region 295-1132, for which up to 12 hits are allowed. Using such series of selection steps, final 70 candidate DUX siRNAs could be selected from a starting set of 1694 DUX siRNAs. FIG. 3 shows the location and numbers of such selected DUX4 siRNA in the DUX4 mRNA transcript (NM_001306068).

[0350] Identified siRNA candidates share common characteristics in their sequences as shown below Table 10 The identified siRNAs have mostly 2'-O-Me modifications, with 2'-F modifications only located on sense strand at positions 7, 8, 9 and 2'-F only located on antisense strand at positions 1, 2, 6, 14, 16. Also, the identified siRNAs comprises 4 thioate modifications on each strand, located at the final 2 linkages of each 5' and 3' terminus. The identified siRNAs further comprises "Uf" at the first position of 5' end of the antisense strand, regardless of the actual target mRNA sequence (coupled with "a" at the last position at the 3' end of the sense strand). The identified siRNAs further comprises "uu" overhang at the 3' end of the antisense strand only, with no overhang at the 3' end of the sense strand. The optimization of the

identified siRNAs may comprise a vinyl phosphonate nucleotide, an inverted abasic moiety, or an amine linker to the passenger strand or the guide strand.

TABLE 10

duplex name	sense strand sequence (5'-3') (passenger strand)	antisense strand sequence (5'-3') (guide strand)
DUX4 template	nsnsnnnnNfNfNfnnnnnnnnsnsa	UfsNfsnnnNfnnnnnnnNfNfnnnnsusu

vpN = vinyl phosphonate 2'-MOE; upper case (N) = 2'-OH (ribo); lower case (n) = 2'-O-Me (methyl)
dN = 2'-H (deoxy); Nf = 2'-F (fluoro); s = phosphorothioate backbone modification; iB = inverted abasic

[0351] Tables 11, 12, and 13 illustrate identified siRNA candidates for the regulation of human DUX4.

TABLE 11

Name	19mer start site	SEQ ID NO	sense/passenger_seq (5'-3')	SEQ ID NO	antisense/guide_seq (5'-3')
NM_001306068_11_29	11	1	cgacaccctcggacagcac	71	gtgctgtccgagggtctcg
NM_001306068_57_75	57	2	acggcgacggagactcgtt	72	aacgagtctccgtcgccgt
NM_001306068_58_76	58	3	cggcgacggagactcgttt	73	aaacgagtctccgtcgccg
NM_001306068_59_77	59	4	ggcgacggagactcgtttg	74	caaacgagtctccgtcgcc
NM_001306068_60_78	60	5	gcgacggagactcgtttgg	75	ccaaacgagtctccgtcgcc
NM_001306068_61_79	61	6	cgacggagactcgtttgga	76	tccaaacgagtctccgtcg
NM_001306068_62_80	62	7	gacggagactcgtttggac	77	gtccaaacgagtctccgtc
NM_001306068_63_81	63	8	acggagactcgtttggacc	78	ggtccaaacgagtctccgt
NM_001306068_77_95	77	9	ggaccccgagccaaagcga	79	tcgctttggctcgggggtcc
NM_001306068_78_96	78	10	gaccccgagccaaagcgag	80	ctcgtttggctcgggggtc
NM_001306068_79_97	79	11	accccgagccaaagcgagg	81	cctcgtttggctcgggggt
NM_001306068_99_117	99	12	cctcgagcctgctttgag	82	ctcaaacgaggctcgagg
NM_001306068_102_120	102	13	gcgagcctgctttgagcgg	83	ccgctcaaacgaggctcgcc
NM_001306068_137_155	137	14	tcgccaccagagaacggct	84	agccgttctctggtggcga
NM_001306068_160_178	160	15	caggccatcggcattccgg	85	ccggaatgccgatggcctg
NM_001306068_162_180	162	16	ggccatcggcattccggag	86	ctccggaatgccgatggcc
NM_001306068_163_181	163	17	gccatcggcattccggagc	87	gctccggaatgccgatggc
NM_001306068_231_249	231	18	gcaccggcggaatctcgg	88	ccgagattccgcccgtgc
NM_001306068_232_250	232	19	caccggcggaatctcggc	89	gccgagattccgcccgtg
NM_001306068_274_292	274	20	ccagaaggccggcgaaagc	90	gctttcgccggccttctgg
NM_001306068_276_294	276	21	agaaggccggcgaaagcgg	91	ccgctttcgccggccttct
NM_001306068_277_295	277	22	gaaggccggcgaaagcgga	92	tccgctttcgccggccttc
NM_001306068_285_303	285	23	gcgaaagccggaccgctgc	93	gacggcggtccgctttgc
NM_001306068_287_305	287	24	gaaagccggaccgctgcac	94	gtgacggcggtccgctttc
NM_001306068_292_310	292	25	cggaccgctcaccggat	95	atccggtgacggcggtccg
NM_001306068_293_311	293	26	ggaccgctcaccggatc	96	gatccggtgacggcggtcc
NM_001306068_294_312	294	27	gaccgctcaccggatcc	97	ggatccggtgacggcggtc

NM_001306068_389_407	389	28	agacgggctcccgagtc	98	gactccgggaggcccgctct
NM_001306068_524_542	524	29	cctcgtgggtcgcttcgc	99	gcgaaggcgacccacgagg
NM_001306068_525_543	525	30	ctcgtgggtcgcttcgcc	100	ggcgaaggcgacccacgag
NM_001306068_679_697	679	31	gaggggatctcccaactg	101	caggttgggagatcccctc
NM_001306068_704_722	704	32	cgcgcggggatttcgcta	102	taggcgaaatccccgcgcg
NM_001306068_705_723	705	33	gcgcggggatttcgctac	103	gtagcgaaatccccgcgc
NM_001306068_708_726	708	34	cggggatttcgctacgcc	104	ggcgttagcgaaatccccg
NM_001306068_893_911	893	35	tgcttgccaccacgctc	105	gacgtgggtggcgcaagca
NM_001306068_1132_1150	1132	36	ctggcgagcccgagtttc	106	gaaactccggctcgccag
NM_001306068_1134_1152	1134	37	ggcgagcccgagtttctg	107	cagaaactccggctcgcc
NM_001306068_1158_1176	1158	38	ggcgcaacctctcctagaa	108	ttctagagaggttgcgcc
NM_001306068_1159_1177	1159	39	gcgcaacctctcctagaaa	109	ttctagagaggttgcgc
NM_001306068_1163_1181	1163	40	aacctctcctagaaacgga	110	tccgttctagagaggtt
NM_001306068_1236_1254	1236	41	cagcgagggaagaataccgg	111	ccggtattctctcgtc
NM_001306068_1237_1255	1237	42	agcgagggaagaataccggg	112	cccggtattctcctcgt
NM_001306068_1238_1256	1238	43	gcgagggaagaataccgggc	113	gcccgtattctcctcgc
NM_001306068_1284_1302	1284	44	gttgggacggggtcggtg	114	cacccgaccccgcccaac
NM_001306068_1290_1308	1290	45	acgggggtcggtggttcgg	115	ccgaaccacccgaccccg
NM_001306068_1294_1312	1294	46	ggtcgggtggttcggggca	116	tgccccgaaccacccgacc
NM_001306068_1295_1313	1295	47	gtcgggtggttcggggcag	117	ctgccccgaaccacccgac
NM_001306068_1315_1333	1315	48	gcggtggcctctctttcgc	118	gcgaaagagagccaccgc
NM_001306068_1316_1334	1316	49	cgggtggcctctctttcgcg	119	cgcgaaagagaggccaccg
NM_001306068_1317_1335	1317	50	ggtggcctctctttcgcgg	120	ccgcgaagagaggccacc
NM_001306068_1321_1339	1321	51	gcctctctttcgggggaa	121	ttccccgcgaagagaggc
NM_001306068_1340_1358	1340	52	cacctggctggtctacggag	122	ctccgtagccagccaggtg
NM_001306068_1350_1368	1350	53	gtacggaggggcggtgtct	123	agacacgcccctccgtagc
NM_001306068_1351_1369	1351	54	ctacggaggggcggtgtctc	124	gagacacgcccctccgtag
NM_001306068_1539_1557	1539	55	acgtgcaaggagctcgtct	125	agcgagctcccttcacgt
NM_001306068_1540_1558	1540	56	cgtgcaaggagctcgtctg	126	cagcgagctcccttcacg
NM_001306068_1541_1559	1541	57	gtgcaaggagctcgtctgg	127	ccagcgagctcccttcac
NM_001306068_1610_1628	1610	58	caccttcgacgctgtctta	128	tagacagcgtcggaaggtg
NM_001306068_1611_1629	1611	59	accttcgacgctgtcttag	129	ctagacagcgtcggaaggt
NM_001306068_1612_1630	1612	60	ccttcgacgctgtctagg	130	cctagacagcgtcggaagg
NM_001306068_1613_1631	1613	61	cttcgacgctgtctaggc	131	gcctagacagcgtcggaag
NM_001306068_1615_1633	1615	62	tccgacgctgtctaggcaa	132	ttgcctagacagcgtcgga
NM_001306068_1616_1634	1616	63	ccgacgctgtctaggcaaa	133	ttgcctagacagcgtcgg
NM_001306068_1619_1637	1619	64	acgctgtctaggcaaacct	134	aggtttcctagacagcgt
NM_001306068_1632_1650	1632	65	aaacctggattagagttac	135	gtaactctaaccaggttt
NM_001306068_336_354	336	66	ctttgagaaggatcgcttt	136	aaagcgatccttctcaag
NM_001306068_672_690	672	67	gcccgcagaggggatctcc	137	ggagatcccctctgcccgc
NM_001306068_882_900	882	68	gggccaagggtgcttgcg	138	cgcaagcacccttgcccc
NM_001306068_884_902	884	69	gccaagggtgcttgcgcc	139	ggcgcaagcacccttggc
NM_001306068_1045_1063	1045	70	atgcaaggcatcccgcgcc	140	gcgcccggatgcttgcac

TABLE 12

Name	19mer start site	SEQ ID NO	sense/passenger_seq (5'-3')	SEQ ID NO	antisense/guide_seq (5'-3')
NM_001306068_11_29	11	141	csgsacacCfCfUfcggac agcsasa	211	UfsUfsgcuGfuccgagg GfuGfucgsusu
NM_001306068_57_75	57	142	ascsggcgAfCfGfgagac ucgsusa	212	UfsAfsccaGfucuccgu CfGfCfucgsusu
NM_001306068_58_76	58	143	csgsgcgaCfGfGfagacu cgususa	213	UfsAfsacgAfgucuccg UfcGfcccgsusu
NM_001306068_59_77	59	144	gsgscgacGfGfAfgacuc guususa	214	UfsAfsaacGfagucucc GfuCfcccgsusu
NM_001306068_60_78	60	145	gscsgacgGfAfGfagucg uuusgsa	215	UfsCfsaaaCfagucucC fgUfcgcsusu
NM_001306068_61_79	61	146	csgsacggAfGfAfcucgu uugsgsa	216	UfsCfscaaAfcgagucC fcGfucgsusu
NM_001306068_62_80	62	147	gsascggaGfAfCfucguu uggsasa	217	UfsUfscgaAfacgaguc UfcCfucgsusu
NM_001306068_63_81	63	148	ascsggagAfCfUfcguuu ggascsa	218	UfsGfsuccAfaagagu CfuCfucgsusu
NM_001306068_77_95	77	149	gsgsacccCfGfAfgccaa agcsgsa	219	UfsCfsgcuUfuggcucg GfgGfucgsusu
NM_001306068_78_96	78	150	gsasccccGfAfGfcaaaa gcgsasa	220	UfsUfscgcUfuuggcuc GfgGfucgsusu
NM_001306068_79_97	79	151	ascscgcgAfGfCfcaag cgasgsa	221	UfsCfsucgCfuuggcu CfGfGfucgsusu
NM_001306068_99_117	99	152	cscsugcgAfGfCfcugcu uuggsasa	222	UfsUfscgaAfgcaggcu CfGfaggsusu
NM_001306068_102_120	102	153	gscsgagcCfUfGfcuuug agcsgsa	223	UfsCfsgcuCfaagcagG fcUfcgcsusu
NM_001306068_137_155	137	154	uscsgccaCfCfAfgagaa cggscsa	224	UfsGfscggUfucucugg UfgGfcggsusu
NM_001306068_160_178	160	155	csasggccAfUfCfggcau uccsgsa	225	UfsCfsggaAfugccgau GfgCfcggsusu
NM_001306068_162_180	162	156	gsgscgauCfGfGfcauuc cggsasa	226	UfsUfscggGfaugccg AfuGfcccgsusu
NM_001306068_163_181	163	157	gscscaucGfGfCfauucc ggasgsa	227	UfsCfsuccGfgaagcc GfaUfggcsusu
NM_001306068_231_249	231	158	gscsaccgGfCfGfggaau cucsgsa	228	UfsCfsgagAfuucccg CfGfucgsusu
NM_001306068_232_250	232	159	csasccggCfGfGfgaauc ucgsgsa	229	UfsCfscgaGfauucccg fcGfucgsusu
NM_001306068_274_292	274	160	cscsagaaGfGfCfcggcg aaasgsa	230	UfsCfsuuuCfcccggcc UfuCfuggsusu
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NM_001306068_277_295	277	162	gsasaggcCfGfGfgcaaa gcgsgsa	232	UfsCfscgcUfuucggcg GfcCfuucgsusu
NM_001306068_285_303	285	163	gscsgaaaGfCfGfgaccg ccgsusa	233	UfsAfsccgCfgguccgc UfuUfcgcsusu
NM_001306068_287_305	287	164	gsasaagcGfGfAfcggcc guacsasa	234	UfsUfsgacGfgcggucc GfcUfuucgsusu
NM_001306068_292_310	292	165	csgsgaccGfCfCfugcac cggsasa	235	UfsUfscggGfugacggc GfgUfcgcsusu
NM_001306068_293_311	293	166	gsgsaccgCfCfGfucacc ggasusa	236	UfsAfsuccGfgugacgg CfGfucgsusu

NM_001306068_294_312	294	167	gsasccgcCfGfUfcaccg gauscsa	237	UfsGfsaucCfaggugacg GfcGfgucsusu
NM_001306068_389_407	389	168	asgsacggGfCfCfucccg gagsusa	238	UfsAfscucCfaggagggc CfcGfucsusu
NM_001306068_524_542	524	169	cscsucguGfGfGfucgcc uucsgsa	239	UfsCfsgaaGfagcaccA fcGfaggusu
NM_001306068_525_543	525	170	csuscgugGfGfUfcgccu ucgscsa	240	UfsGfscgaAfggcgacc CfaCfagsusu
NM_001306068_679_697	679	171	gsasggggAfUfCfucca accsusa	241	UfsAfsgguUfgggagau CfcCfcucsusu
NM_001306068_704_722	704	172	csagcgcgGfGfGfauuuc gccsusa	242	UfsAfsggcGfaauuccC fgCfagcsusu
NM_001306068_705_723	705	173	gscscggGfGfAfuuuc gccusasa	243	UfsUfsaggCfgaauccC fcGfagcsusu
NM_001306068_708_726	708	174	csaggggaUfUfUfcgccu acgscsa	244	UfsGfscgaAfggcgaaa UfcCfagcsusu
NM_001306068_893_911	893	175	usgscuugCfGfCfacc acgsusa	245	UfsAfscguGfaggugcg CfaAfgcasusu
NM_001306068_1132_1150	1132	176	csusggcgAfGfCfcccga guususa	246	UfsAfsaacUfcccggcu CfcCfagcsusu
NM_001306068_1134_1152	1134	177	gsgscgagCfCfCfaggau uucsusa	247	UfsAfsgaaAfcuccggg CfuCfagcsusu
NM_001306068_1158_1176	1158	178	gsgscgcaAfCfCfucucc uagsasa	248	UfsUfscuaGfagagaggu UfgCfagcsusu
NM_001306068_1159_1177	1159	179	gscsgcaaCfCfUfcuccu agasasa	249	UfsUfsucuAfggagagg UfuGfagcsusu
NM_001306068_1163_1181	1163	180	asascucUfCfCfuagaa acgsgsa	250	UfsCfscguUfucuaagga GfaGfguusu
NM_001306068_1236_1254	1236	181	csasgcgaGfGfAfagaau accsgsa	251	UfsCfsgguAfuucucc UfcGfcgcsusu
NM_001306068_1237_1255	1237	182	asgscgagGfAfAfagaau ccgsgsa	252	UfsCfscggUfauucucc CfuCfagcsusu
NM_001306068_1238_1256	1238	183	gscsgaggAfAfGfaauac cgsgsa	253	UfsCfscggGfuauucuu CfcUfcgcsusu
NM_001306068_1284_1302	1284	184	gsusugggAfCfGfgggg cggsusa	254	UfsAfscggGfagcccgC fcCfaacsusu
NM_001306068_1290_1308	1290	185	ascsggggUfCfGfggug guucsgsa	255	UfsCfsgaaCfaccggaC fcCfcgcsusu
NM_001306068_1294_1312	1294	186	gsgsucggGfUfGfguuc gggscsa	256	UfsGfscggCfagaccacC fcGfagcsusu
NM_001306068_1295_1313	1295	187	gsuscgggUfGfGfuucg gggcsasa	257	UfsUfsgccCfagaaccaC fcCfagcsusu
NM_001306068_1315_1333	1315	188	gscsggugGfCfCfucucu uucsgsa	258	UfsCfsgaaAfgagaggc CfaCfagcsusu
NM_001306068_1316_1334	1316	189	csagsgggCfCfUfcucuu ucgscsa	259	UfsGfscgaAfgagagg CfcAfccgsusu
NM_001306068_1317_1335	1317	190	gsgsuggcCfUfCfucuuu cgscgsa	260	UfsCfsgcgAfaagagag GfcCfagcsusu
NM_001306068_1321_1339	1321	191	gscscucuCfUfUfucgg gggsasa	261	UfsUfscggCfaggaagA fgAfgcsusu
NM_001306068_1340_1358	1340	192	csascugGfCfUfggcua cggsasa	262	UfsUfscggUfagccagcC faGfgugsusu
NM_001306068_1350_1368	1350	193	gscsuacgGfAfGfgggcg ugscsa	263	UfsGfsacaCfagccucC fgUfagcsusu
NM_001306068_1351_1369	1351	194	csusacggAfGfGfggcgu gucsusa	264	UfsAfsgacAfcgccccuC fcGfuagsusu

NM_001306068_1539_1 557	1539	195	ascsgugcAfAfGfggagc ucgscsa	265	UfsGfscgaGfcuccuu GfcAfcgususu
NM_001306068_1540_1 558	1540	196	csgsugcaAfGfGfgagcu cgcsusa	266	UfsAfsagcGfagcuccu UfgCfagcsusu
NM_001306068_1541_1 559	1541	197	gsusgcaaGfGfGfagcuc gcusgsa	267	UfsCfsagcGfagcuccu fuGfcacsusu
NM_001306068_1610_1 628	1610	198	csasccuuCfCfGfagcuc gucsusa	268	UfsAfsagcAfgcgucgg AfaGfgugsusu
NM_001306068_1611_1 629	1611	199	ascscuucCfGfAfcgucg ucusasa	269	UfsUfsagaCfagcgucg GfaAfggususu
NM_001306068_1612_1 630	1612	200	cscsuuccGfAfCfGfcugu cuasgsa	270	UfsCfsuagAfcagcguc GfgAfaggsusu
NM_001306068_1613_1 631	1613	201	csusuccGfAfCfGfcuguc uagsgsa	271	UfsCfscuaGfacagcgC fgGfaagsusu
NM_001306068_1615_1 633	1615	202	uscscgacGfCfUfgucua ggcsasa	272	UfsUfsgccUfagacagc GfuCfaggsusu
NM_001306068_1616_1 634	1616	203	cscscgacGfUfGfucua gcasasa	273	UfsUfsugcCfuagacag CfGfUfcggsusu
NM_001306068_1619_1 637	1619	204	ascsgcugUfCfUfagga aacscsa	274	UfsGfsguuUfgccuaga CfaGfcgususu
NM_001306068_1632_1 650	1632	205	asasaccuGfGfAfuaga guusasa	275	UfsUfsaacUfcuaaaccA fgGfuususu
NM_001306068_336_35 4	336	206	csusuugaGfAfAfggauc gcususa	276	UfsAfsagcGfauccuuc UfcAfaagsusu
NM_001306068_672_69 0	672	207	gscscggcAfGfAfgggga ucuscscsa	277	UfsGfsagaUfccccucu GfcCfaggsusu
NM_001306068_882_90 0	882	208	gsgsgccaAfGfGfggugc uugscsa	278	UfsGfscgaGfaccuccu fgGfcccusu
NM_001306068_884_90 2	884	209	gscscagGfGfGfugcuu gcgscsa	279	UfsGfscgcAfcagccccC fuUfggcsusu
NM_001306068_1045_1 063	1045	210	asusgcaaGfGfCfaucce ggcsgsa	280	UfsCfsgccGfggaugcc UfuGfcausus

vpN = vinyl phosphonate 2'-MOE; upper case (N) = 2'-OH (ribo); lower case (n) = 2'-O-Me (methyl)
dN = 2'-H (deoxy); Nf = 2'-F (fluoro); s = phosphorothioate backbone modification; iB = inverted abasic

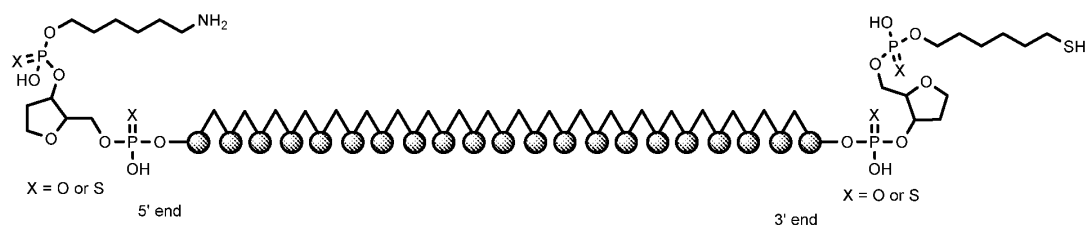
TABLE 13

SEQ ID NO	sense/passenger_seq (5'-3')	SEQ ID NO	antisense/guide_seq (5'-3')
371	CTGCCCTCTCCACCAGCCCA	372	TGGGCTGGTGGAGAGGCAG
373	GCAGAGATGGAGAGAGGAA	374	TTCTCTCTCCATCTCTGC
375	GCGGTTTCCTCCGGGACAA	376	TTGTCCCGGAGGAAACCGC
377	GGACGACGGAGGCGTGATT	378	AATCACGCCTCCGTCTGTC
379	CGGGCACCCGAAACATGCAGGG AA	380	TTCCCTGCATGTTTCCGGGTGCCC G
381	CCGGAAACATGCAGGGAAG	382	CTTCCCTGCATGTTTCCGG
383	GAAATGAACGAGAGCCACA	384	TGTGGCTCTCGTTTCATTT
385	TGGCACACTCAAGACTCCACGG AG	386	CTCCGTGGGAGTCTTGAGTGTGC CA
387	CCACGGAGGTTTCAGTTCCA	388	TGGAACCTGAACCTCCGTGG
389	ACCACCACCACCACCACCA	390	TGGTGGTGGTGGTGGTGGT
391	CGCCATTCATGAAGGGGTG	392	CACCCCTTCATGAATGGCG
393	CATGAAGGGGTGGAGCCTG	394	CAGGCTCCACCCCTTCATG

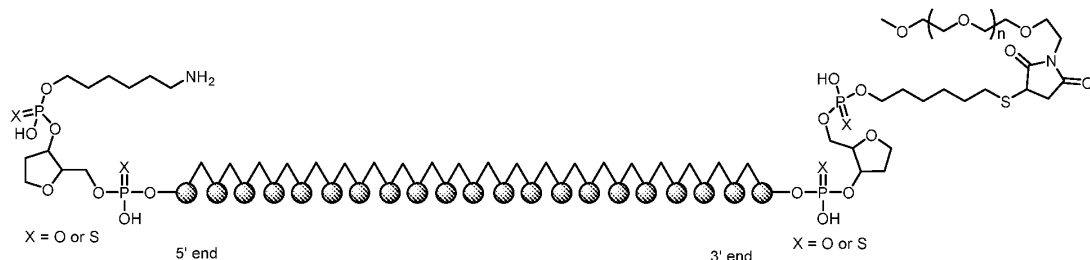
395	GAGCCTGCTTTGAGCGGAA	396	TTCCGCTCAAAGCAGGCTC
397	CCGAGCCTTTGAGAAGGATCGCT TT	398	AAAGCGATCCTTCTCAAAGGCTC GG
399	GGCAGGGCGCCCGCGCAGG	400	CCTGCGCGGGCGCCCTGCC
401	GATGATTAGTTCAGAGATA	402	TATCTCTGAACTAATCATC

Example 2. siRNA sequences and synthesis

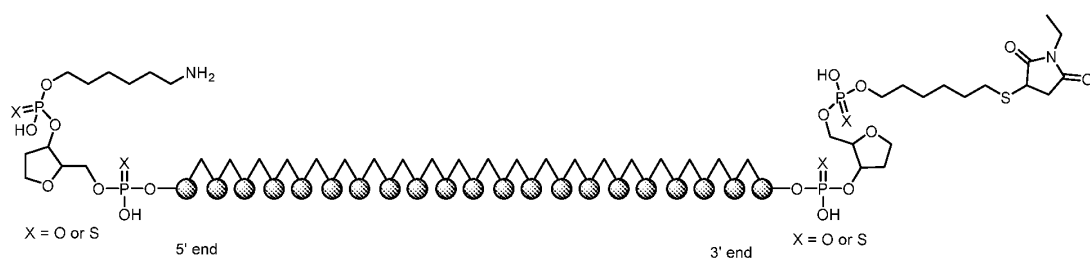
[0352] All siRNA single strands were fully assembled on solid phase using standard phosphoramidite chemistry and purified over HPLC. Purified single strands were duplexed to get the double stranded siRNA. All the siRNA passenger strand contains conjugation handles in different formats, C₆-NH₂ and/or C₆-SH, one at each end of the strand. The conjugation handle or handles were connected to the siRNA passenger strand or siRNA guide strand via inverted abasic phosphodiester or phosphorothioate. Below are representative structures of the formats used in the *in vivo* experiments.



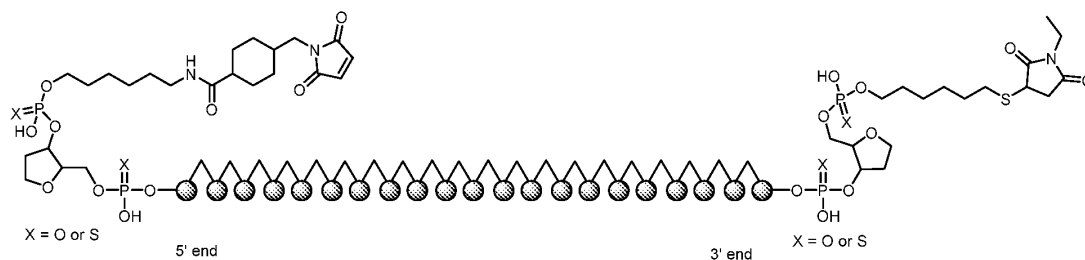
[0353] A representative structure of siRNA with C₆-NH₂ conjugation handle at the 5' end and C₆-SH at 3' end of the passenger strand or guide strand.



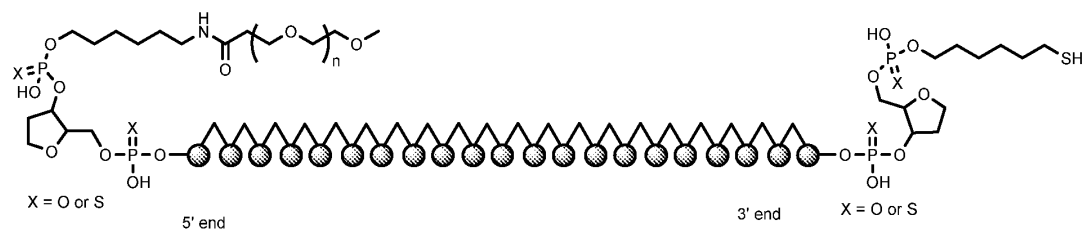
[0354] A representative structure of siRNA passenger strand or guide strand with C₆-NH₂ conjugation handle at the 5' end and C₆-S-PEG at 3' end.



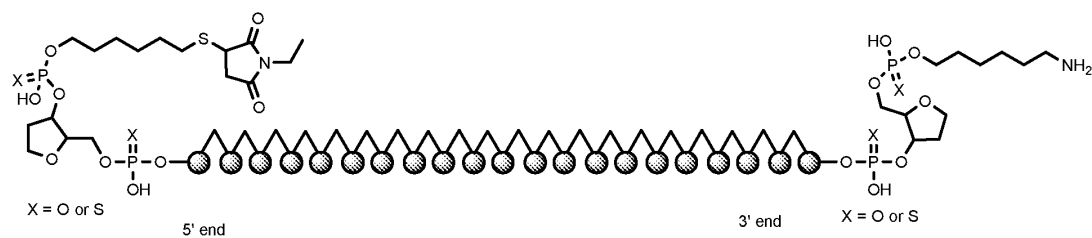
[0355] A representative structure of siRNA passenger strand or guide strand with C₆-NH₂ conjugation handle at the 5' end and C₆-S-NEM at 3' end.



[0356] A representative structure of siRNA passenger strand with C₆-N-SMCC conjugation handle at the 5' end and C₆-S-NEM at 3' end.



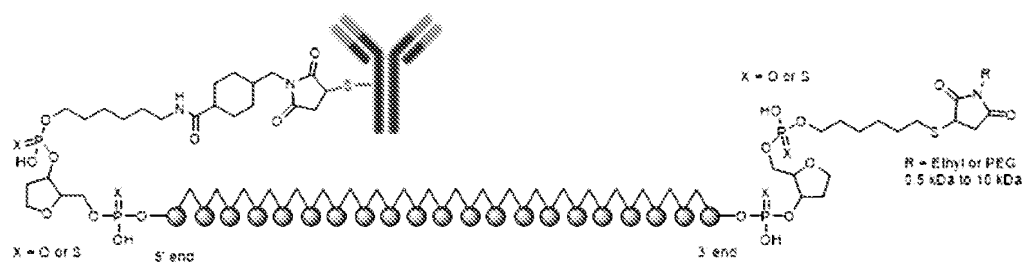
[0357] A representative structure of siRNA passenger strand or guide strand with PEG at the 5' end and C₆-SH at 3' end.



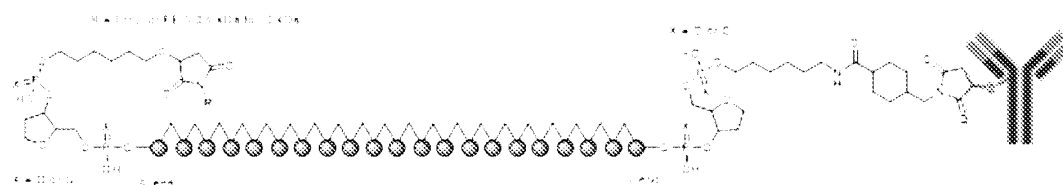
[0358] A representative structure of siRNA passenger strand or guide strand with C₆-S-NEM at the 5' end and C₆-NH₂ conjugation handle at 3' end.

Example 3. Conjugate synthesis

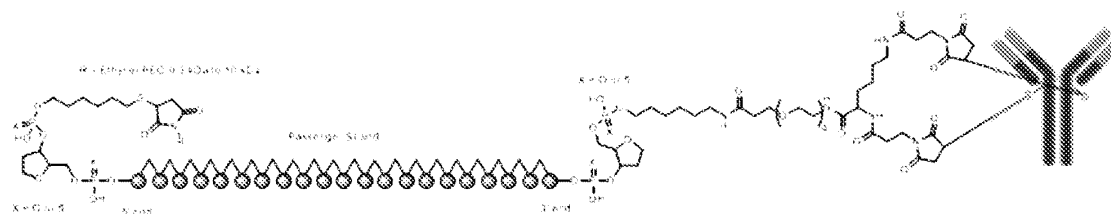
[0359] The following structures illustrate exemplary A-X₁-B-X₂-Y (Formula I) architectures described herein.



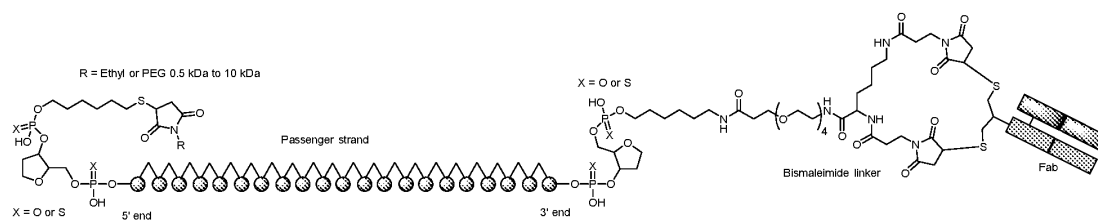
[0360] Architecture-1: Antibody-Cys-SMCC-5'-passenger strand. This conjugate was generated by antibody inter-chain cysteine conjugation to maleimide (SMCC) at the 5' end of passenger strand.



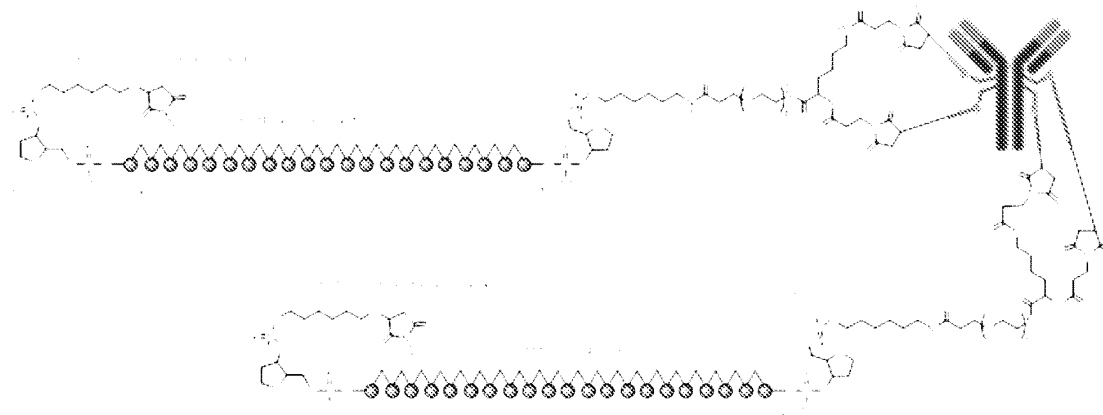
[0361] Architecture-2: Antibody-Cys-SMCC-3'-Passenger strand. This conjugate was generated by antibody inter-chain cysteine conjugation to maleimide (SMCC) at the 3' end of passenger strand.



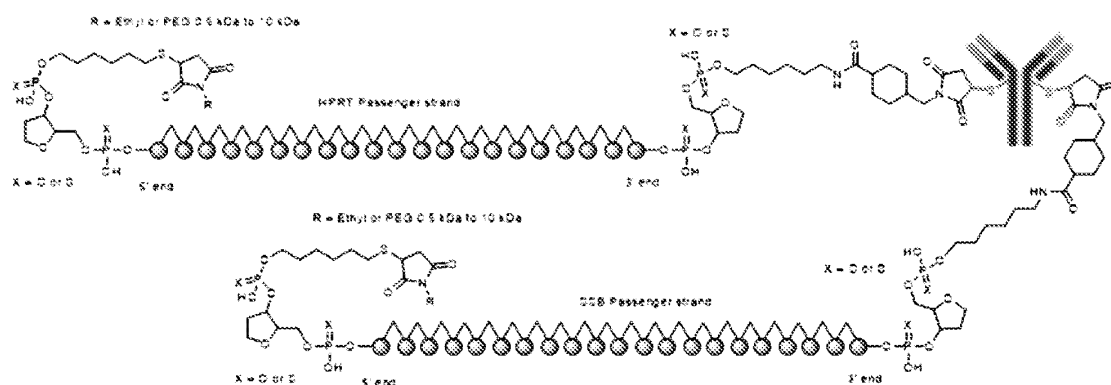
[0362] ASC Architecture-3: Antibody-Cys-bisMal-3'-Passenger strand. This conjugate was generated by antibody inter-chain cysteine conjugation to bismaleimide (bisMal) linker at the 3' end of passenger strand.



[0363] ASC Architecture-4: A model structure of the Fab-Cys-bisMal-3'-Passenger strand. This conjugate was generated by Fab inter-chain cysteine conjugation to bismaleimide (bisMal) linker at the 3' end of passenger strand.

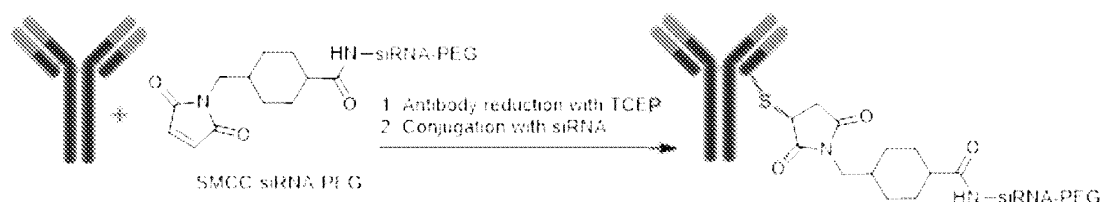


[0364] ASC Architecture-5: A model structure of the antibody siRNA conjugate with two different siRNAs attached to one antibody molecule. This conjugate was generated by conjugating a mixture of SSB and HPRT siRNAs to the reduced mAb inter-chain cysteines to bismaleimide (bisMal) linker at the 3' end of passenger strand of each siRNA.



[0365] ASC Architecture-6: A model structure of the antibody siRNA conjugate with two different siRNAs attached. This conjugate was generated by conjugating a mixture of SSB and HPRT siRNAs to the reduced mAb inter-chain cysteines to maleimide (SMCC) linker at the 3' end of passenger strand of each siRNA.

Example 3.1 Antibody siRNA Conjugate Synthesis using SMCC linker



Synthesis scheme-1: Antibody-Cys-SMCC-siRNA-PEG conjugates via antibody cysteine conjugation

[0366] Step 1: Antibody interchain disulfide reduction with TCEP

[0367] Antibody was buffer exchanged with borax buffer (pH 8) and made up to 10 mg/ml concentration. To this solution, 2 equivalents of TCEP in water was added and rotated for 2 hours at RT. The resultant reaction mixture was buffer exchanged with pH 7.4 PBS containing 5 mM EDTA and added to a solution of SMCC-C6-siRNA or SMCC-C6-siRNA-C6-NHCO-PEG-XkDa (2 equivalents) (X= 0.5 kDa to 10 kDa) in pH 7.4 PBS containing 5 mM EDTA at RT and rotated overnight. Analysis of the reaction mixture by analytical SAX column chromatography showed antibody siRNA conjugate along with unreacted antibody and siRNA.

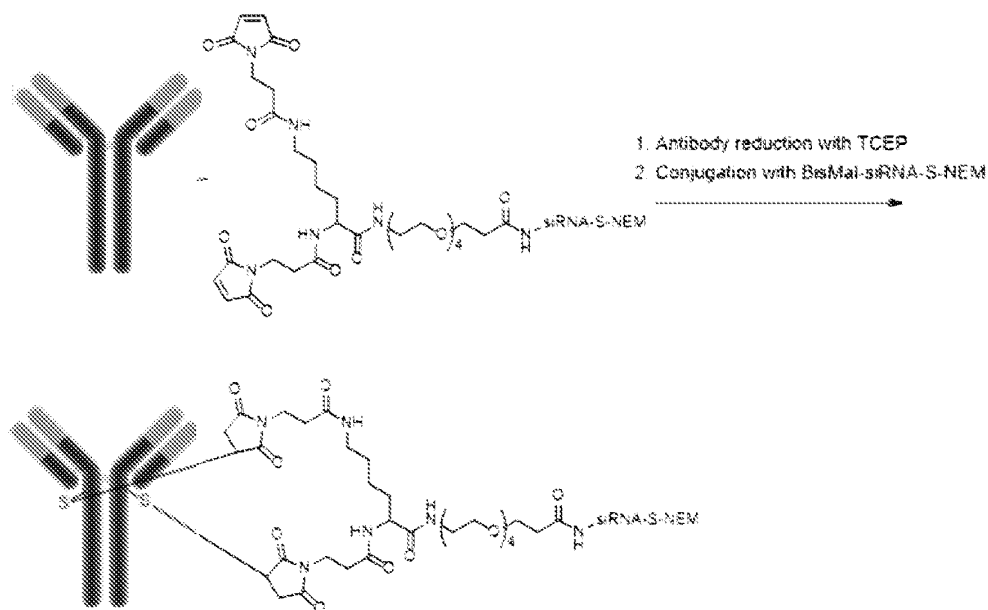
[0368] Step 2: Purification

[0369] The crude reaction mixture was purified by AKTA explorer FPLC using anion exchange chromatography method-1 as described in Example 3.4. Fractions containing DAR1 and DAR>2 antibody-siRNA-PEG conjugates were separated, concentrated and buffer exchanged with pH 7.4 PBS.

[0370] Step 3: Analysis of the purified conjugate

[0371] The isolated conjugates were characterized by SEC, SAX chromatography and SDS-PAGE. The purity of the conjugate was assessed by analytical HPLC using either anion exchange chromatography method-2 or anion exchange chromatography method-3. Both methods are described in Example 3.4. Isolated DAR1 conjugates are typically eluted at 9.0 ± 0.3 min on analytical SAX method and are greater than 90% pure. The typical DAR>2 cysteine conjugate contains more than 85% DAR2 and less than 15% DAR3.

[0372] Example 3.2. Antibody siRNA Conjugate Synthesis using bis-maleimide (BisMal) linker



Synthesis scheme-2: Antibody-Cys-BisMal-siRNA-PEG conjugates

[0373] Step 1: Antibody reduction with TCEP

[0374] Antibody was buffer exchanged with borax buffer (pH 8) and made up to 5mg/ml concentration. To this solution, 2 equivalents of TCEP in water was added and rotated for 2 hours at RT. The resultant reaction mixture was exchanged with pH 7.4 PBS containing 5 mM EDTA and added to a solution of BisMal-C6-siRNA-C6-S-NEM (2 equivalents) in pH 7.4 PBS containing 5 mM EDTA at RT and kept at 4 °C overnight. Analysis of the reaction mixture by analytical SAX column chromatography showed antibody siRNA conjugate along with unreacted antibody and siRNA.

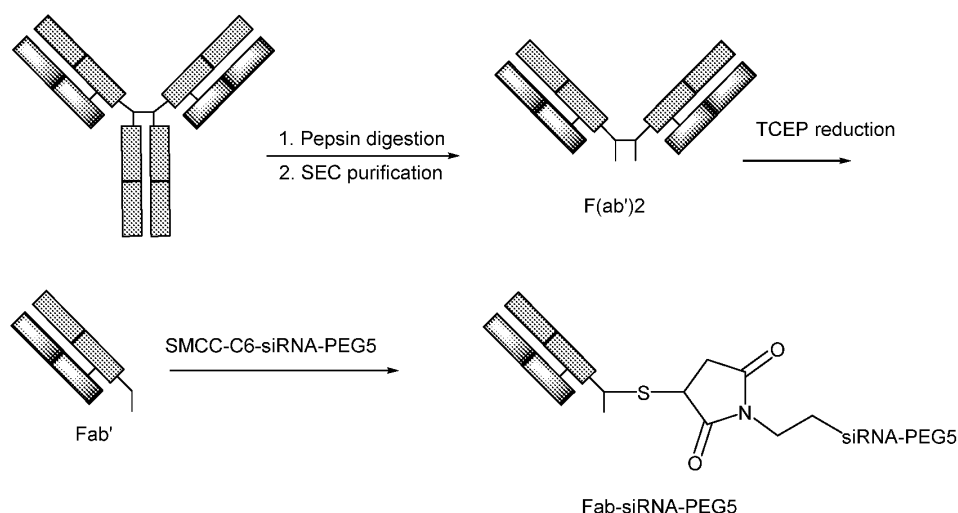
[0375] Step 2: Purification

[0376] The crude reaction mixture was purified by AKTA explorer FPLC using anion exchange chromatography method-1. Fractions containing DAR1 and DAR2 antibody-siRNA conjugates were separated, concentrated and buffer exchanged with pH 7.4 PBS.

[0377] Step-3: Analysis of the purified conjugate

[0378] The isolated conjugates were characterized by either mass spec or SDS-PAGE. The purity of the conjugate was assessed by analytical HPLC using either anion exchange chromatography method-2 or 3 as well as size exclusion chromatography method-1.

[0379] **Example 3.3. Fab' generation from mAb and conjugation to siRNA**



Scheme-3: Fab-siRNA conjugate generation

[0380] Step 1: Antibody digestion with pepsin

[0381] Antibody was buffer exchanged with pH 4.0, 20 mM sodium acetate/acetic acid buffer and made up to 5mg/ml concentration. Immobilized pepsin (Thermo Scientific, Prod#20343) was added and incubated for 3 hours at 37 °C. The reaction mixture was filtered using 30 kDa MWCO Amicon spin filters and pH 7.4 PBS. The retentate was collected and purified using size exclusion chromatography to isolate F(ab')₂. The collected F(ab')₂ was then reduced by 10 equivalents of TCEP and conjugated with SMCC-C₆-siRNA-PEG₅ at room temperature in pH 7.4 PBS. Analysis of reaction mixture on SAX chromatography showed Fab-siRNA conjugate along with unreacted Fab and siRNA-PEG.

[0382] Step 2: Purification

[0383] The crude reaction mixture was purified by AKTA explorer FPLC using anion exchange chromatography method-1. Fractions containing DAR1 and DAR2 Fab-siRNA conjugates were separated, concentrated and buffer exchanged with pH 7.4 PBS.

[0384] Step-3: Analysis of the purified conjugate

[0385] The characterization and purity of the isolated conjugate was assessed by analytical HPLC using anion exchange chromatography method-2 or 3 as well as by SEC method-1.

[0386] Example 3.4. Purification and analytical Methods

[0387] Anion exchange chromatography method (SAX)-1.

1. Column: Tosoh Bioscience, TSKGel SuperQ-5PW, 21.5 mm ID X 15 cm, 13 μm
2. Solvent A: 20 mM TRIS buffer, pH 8.0; Solvent B: 20 mM TRIS, 1.5 M NaCl, pH 8.0; Flow Rate: 6.0 ml/min
3. Gradient:

a.	%A		%B	Column Volume
b.	100		0	1.00
c.	60	40	18.00	
d.	40	60	2.00	
e.	40	60	5.00	
f.	0	100	2.00	
g.	100		0	2.00

[0388] Anion exchange chromatography (SAX) method-2

1. Column: Thermo Scientific, ProPac™ SAX-10, Bio LC™, 4 X 250 mm
2. Solvent A: 80% 10 mM TRIS pH 8, 20% ethanol; Solvent B: 80% 10 mM TRIS pH 8, 20% ethanol, 1.5 M NaCl; Flow Rate: 0.75 ml/min
3. Gradient:

a.	Time	%A	%B
b.	0.0	90	10
c.	3.00	90	10
d.	11.00	40	60
e.	13.00	40	60
f.	15.00	90	10
g.	20.00	90	10

[0389] Anion exchange chromatography (SAX) method-3

1. Column: Thermo Scientific, ProPac™ SAX-10, Bio LCTM, 4 X 250 mm
2. Solvent A: 80% 10 mM TRIS pH 8, 20% ethanol; Solvent B: 80% 10 mM TRIS pH 8, 20% ethanol, 1.5 M NaCl
3. Flow Rate: 0.75 ml/min
4. Gradient:

a.	Time	%A	%B
b.	0.0	90	10
c.	3.00	90	10
d.	11.00	40	60
e.	23.00	40	60
f.	25.00	90	10
g.	30.00	90	10

[0390] Size exclusion chromatography (SEC) method-1

1. Column: TOSOH Biosciences, TSKgelG3000SW XL, 7.8 X 300 mm, 5μM
2. Mobile phase: 150 mM phosphate buffer
3. Flow Rate: 1.0 ml/min for 15 mins

[0391] Example 3.5. Antibody siRNA Conjugate Synthesis using bis-maleimide (BisMal) linker**[0392] Step 1: Antibody reduction with TCEP**

[0393] Antibody was buffer exchanged with 25mM borate buffer (pH 8) with 1mM DTPA and made up to 10mg/ml concentration. To this solution, 4 equivalents of TCEP in the same borate buffer were added and incubated for 2 hours at 37°C. The resultant reaction mixture was

combined with a solution of BisMal-siRNA (1.25 equivalents) in pH 6.0 10 mM acetate buffer at RT and kept at 4 °C overnight. Analysis of the reaction mixture by analytical SAX column chromatography showed antibody siRNA conjugate along with unreacted antibody and siRNA. The reaction mixture was treated with 10 EQ of N-ethylmaleimide (in DMSO at 10 mg/mL) to cap any remaining free cysteine residues.

[0394] Step 2: Purification

[0395] The crude reaction mixture was purified by AKTA Pure FPLC using anion exchange chromatography (SAX) method-1. Fractions containing DAR1 and DAR2 antibody-siRNA conjugates were isolated, concentrated and buffer exchanged with pH 7.4 PBS.

[0396] Anion exchange chromatography method (SAX)-1.

[0397] Column: Tosoh Bioscience, TSKGel SuperQ-5PW, 21.5 mm ID X 15 cm, 13 µm

[0398] Solvent A: 20 mM TRIS buffer, pH 8.0; Solvent B: 20 mM TRIS, 1.5 M NaCl, pH 8.0; Flow Rate: 6.0 ml/min

[0399] Gradient:

a.	%A	%B	Column Volume
b.	100	0	1
c.	81	19	0.5
d.	50	50	13
e.	40	60	0.5
f.	0	100	0.5
g.	100	0	2

[0400] Anion exchange chromatography (SAX) method-2

[0401] Column: Thermo Scientific, ProPac™ SAX-10, Bio LC™, 4 X 250 mm

[0402] Solvent A: 80% 10 mM TRIS pH 8, 20% ethanol; Solvent B: 80% 10 mM TRIS pH 8, 20% ethanol, 1.5 M NaCl; Flow Rate: 0.75 ml/min

[0403] Gradient:

a.	Time	%A	%B
b.	0.0	90	10
c.	3.00	90	10
d.	11.00	40	60
e.	14.00	40	60
f.	15.00	20	80
g.	16.00	90	10
h.	20.00	90	10

Example 4. Expression profile of DUX4 in myonuclei

[0404] Myotubes derived from a healthy individual and FSHD patient were evaluated for DUX4 expression. As shown in FIG. 4, myotubes were immunostained to detect DUX4 expression. Muscle cells' nuclei and cytoplasm were immunostained by labeling DAPI (4',6-diamidino-2-phenylindole) and troponin T. As shown, DUX4 expression could be detected in low and sporadic manner - in less than 1% of myonuclei – indicating that detecting of DUX4 expression directly from the cell can be challenging in determining the effect of DUX4 siRNA activity.

Example 5. Expression profiles of DUX4-dependent marker genes in FSHD donor muscle cells with DUX4 siRNA treatment

[0405] Two DUX4 siRNAs (siDUX4-1 and siDUX4-4 are disclosed in Geng LN et al, *Dev. Cell*, 2012) were used to treat the diseased muscle cells (FSHD donor muscle cells), and RNA expression level of five DUX4-dependent biomarker genes were quantitated, as shown in bar graphs in FIG. 5. As shown, both siDUX4-1 and siDUX4-4 substantially reduced the expression of MBD3L2, TRIM43, PRAMEF1, ZSCAN4, and LEUTX compared to the baseline (100%). More specifically, siDUX4-4 reduced the expression of MBD3L2, TRIM43, PRAMEF1, ZSCAN4, and LEUTX at least ~75% compared to the baseline (100%). DUX4-target genes as biomarkers were sensitive to measure siRNA-mediated downregulation of DUX4.

[0406] Example 6. DUX4 siRNA-mediated reduction of 5 DUX4-target biomarker gene expressions and a FSHD composite of DUX4-target biomarker genes in cultured FSHD primary myotubes

FSHD1 patient-derived primary myoblasts (MB06) were used to validate the FSHD composite as a reliable surrogate biomarker to assess DUX4 siRNA activity with the published 2 DUX4 siRNAs, siDUX4-1 and siDUX4-4 (Geng LN et al, *Dev. Cell*, 2012) in a dose dependent concentration. FSHD primary myoblasts (MB06 (FSHD1)) were grown in recommended media. Prior to seeding, 96-well tissue culture plates (Costar) were coated with 50 μ L of 1% Matrigel per well for at least 2 hours at 37°C and washed 2x with PBS. After coating, myoblasts were seeded in quadruplicate at 4000 cells/well without antibiotics and maintained 24h prior to transfection. On the day of transfection, the DUX4-4 siRNA was formulated with commercially available transfection reagent Lipofectamine RNAiMAX (Life Technologies) and OptiMEM (Life Technologies) according to the manufacturer's "forward transfection" instructions. DUX4-4 siRNA was synthesized by Integrated DNA Technologies (IDT). Myoblasts were transfected with DUX4-4 siRNA at a high concentration of 25 nM with 9-fold serial dilutions. 24 hours post transfection, myogenic differentiation was induced with 15% KOSR-containing differentiation

medium. Myotubes were collected in Trizol 4 days after inducing differentiation and stored at -80°C until processing. RNA isolation was performed using Direct-zol-96 RNA isolation kit (Zymo) according to the manufacturer's instructions. 100-500 ng of purified RNA was converted to cDNA using High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems) using SimpliAmp Thermal Cycler (Applied Biosystems). cDNA was analyzed by qPCR using TaqMan Fast Universal Master Mix II (Thermo Fisher) and TaqMan probes (Thermo Fisher) in duplicates, using QuantStudio 6 or 7 Flex Real-Time PCR instruments (Applied Biosystems). Data were analyzed by QuantStudio™ Real-Time PCR Software v1.3 (Applied Biosystems). The expression levels of 5 DUX4-target genes were evaluated: MBD3L2, ZSCAN4, LEUTX, KHDC1L, and TRIM43. DUX4-target gene expression was normalized to a composite of two reference genes: AHSA1 and RPL27. The percentage of target mRNA expression was determined relative to mock treated cells by using the $2^{-\Delta\Delta C_t}$ method (Livak and Schmittgen, *Methods* 2001). FIG. 6A-B show DUX4 siRNA-mediated reduction of 5 DUX4-target biomarker gene expressions in cultured FSHD primary myotubes. DUX4 siRNA reduced the expression of 5 individual DUX4-target biomarker genes (MBD3L2, ZSCAN4, LEUTX, KHDC1L, and TRIM43) (FIG. 6A) or as a FSHD composite of the 5 DUX4-target biomarker genes (FIG. 6B) in cultured FSHD primary myotubes.

Example 7 . DUX4 siRNA Library Screening - First round at 2 concentrations (10 and 0.5 nM) in MB02 and MB06

[0407] In this example, 70 DUX4 siRNAs were screened for their activity in two FSHD primary myoblast cell lines (MB02 (FSHD1) and MB06 (FSHD1)) to identify more desirable siRNA candidates. Cells were plated at a density of 4,000 cells/well (MW96) and then transfected in four replicates with DUX4 siRNAs, as well as a tool siRNA as control. Transfection was performed 24 hours after plating at 10 nM concentration. Myogenic differentiation was induced 2 days after plating (24 hours after transfection) with 15% KOSR (in DMEM/F-12) medium. Samples were harvested 3 or 4 days after inducing differentiation, depending on the cell line. DUX4-downstream target gene expression was evaluated by RT-qPCR (normalized to a composite AHSA1 and RPL27 housekeeping gene expression value). Data shown in this example are represented as mean FSHD Composite $\pm$ SEM. N=4.

FIG. 7 shows a bar graph of assessment of myotubes differentiation and viability at 10 nM concentration of siDUX4 by monitoring ACTA1 expression in MB02 (FSHD1) and MB06 (FSHD1) cell lines.

FIG. 8 shows a bar graph of screening for activity at 10 nM Concentration of 70 DUX4 siRNAs by measuring FSHD composite expression (Calculations of the FSHD composite: $D_{ct} = (Av. ct$

4 DUX4 target genes) – (Av. ct 2 HKGs), DDct = Dct (siDUX4) – Dct (mock) , Composite = $2^{-DDct} * 100$ (%)).

[0408] FIG. 9 shows a bar graph of screening for activity at 0.5 nM Concentration of 70 DUX4 siRNAs by measuring FSHD composite expression. As used herein, FSHD Composite is made of 4 DUX4-target genes: MBD3L2, ZSCAN4, LEUTX, KHDC1L. As shown in Table 15, downregulation of FSHD composite expression is well correlated with downregulation of individual genes in the composite when normalized to HKG composite (AHSA1, RPL27) (n=4), indicating that the effective downregulation of FSHD composite expression is a good indicator to DUX4 siRNA potency.

TABLE 15

siRNA	MB02							MB06						
	FSHD Composite	KHDC1L	LEUTX	MBD3L2	ZSCAN4	AHSA1	RPL27	FSHD Composite	KHDC1L	LEUTX	MBD3L2	ZSCAN4	AHSA1	RPL27
11	31.76	32.33	27.03	47.47	30.27	109.58	91.38	16.09	6.38	11.09	23.82	13.31	114.06	90.97
57	25.86	22.62	27.70	42.22	20.86	97.29	103.31	14.22	12.16	10.63	18.81	19.54	89.28	116.02
58	9.78	12.44	13.10	5.88	7.31	97.37	103.29	4.10	2.67	2.37	6.05	11.34	101.69	106.66
59	43.49	44.17	43.50	46.55	46.97	106.40	94.78	28.22	22.48	29.71	33.29	32.90	117.04	88.16
60	58.45	59.46	55.13	69.76	57.17	94.97	105.61	140.69	122.45	142.62	155.90	150.70	116.93	94.15
61	6.34	7.32	2.83	11.18	9.93	90.60	113.77	1.73	1.57	1.08	1.78	4.58	98.25	114.58
62	15.44	18.56	12.97	25.33	12.82	100.38	102.07	20.46	10.46	15.63	37.90	32.54	101.13	102.58
63	13.73	29.72	11.40	14.60	10.07	85.09	118.35	17.87	21.42	13.53	24.40	16.06	83.36	122.84
77	37.74	32.95	30.95	47.38	45.61	94.54	106.69	75.08	53.88	68.53	78.07	112.37	111.86	93.58
78	72.97	59.09	58.98	102.78	83.09	100.39	100.53	106.34	79.97	86.79	123.98	154.02	103.95	101.34
79	19.50	12.62	19.46	14.83	24.76	108.94	95.53	5.72	7.19	1.78	5.70	8.23	99.32	104.82
99	22.25	16.43	19.77	36.04	25.06	92.62	109.14	35.72	25.35	26.36	40.42	63.61	99.65	104.80
102	48.17	39.31	49.89	65.85	45.69	101.19	100.20	44.10	57.01	39.64	42.83	40.62	90.72	119.87
137	17.49	14.10	11.62	25.26	31.37	93.65	107.00	17.66	12.44	12.00	21.07	33.17	98.95	106.09
160	201.88	206.62	215.56	241.34	167.58	97.09	103.95	300.78	306.57	304.41	294.44	312.89	108.66	100.20
162	61.62	51.74	58.79	91.54	57.24	106.98	93.68	45.68	29.38	37.70	55.89	73.25	105.10	97.67
163	122.38	116.49	111.83	111.99	164.49	88.53	113.03	79.05	63.62	72.05	62.17	144.47	95.43	109.30
231	91.73	95.05	89.58	106.78	91.32	97.74	102.50	337.97	283.17	379.63	352.81	354.24	115.96	92.45
232	23.56	25.81	22.38	33.70	17.66	102.82	98.35	12.95	11.16	9.33	15.36	17.15	92.25	109.99
274	14.70	12.58	7.62	26.42	21.88	95.39	106.34	34.53	26.94	29.25	37.69	50.61	103.83	99.85
276	366.14	295.05	469.25	349.12	397.99	104.97	96.57	319.52	337.69	319.51	228.18	445.11	99.52	110.28
277	37.91	43.98	41.86	40.48	38.05	108.35	94.03	18.43	17.38	16.75	19.64	22.05	100.75	102.23
285	86.16	108.25	76.64	78.48	98.14	88.18	114.79	65.05	63.72	56.62	72.14	71.66	102.87	103.36
287	339.10	407.16	366.95	331.14	282.13	99.11	101.55	239.05	253.18	231.21	228.18	257.26	101.75	102.15
292	74.54	66.24	70.23	99.22	71.01	99.83	100.24	141.86	143.88	135.19	159.41	136.01	103.00	105.67
293	103.15	93.51	103.54	114.07	115.31	96.28	104.03	55.66	40.83	48.69	71.53	70.82	103.57	100.30
294	104.91	113.06	114.64	112.24	92.48	92.28	108.56	147.19	163.93	152.23	129.50	154.54	104.25	104.91
336	12.62	12.47	13.76	15.54	14.67	100.38	100.64	1.77	1.86	0.74	2.24	3.69	105.87	100.27
389	101.16	143.98	74.83	103.37	105.53	91.60	110.54	87.13	87.19	61.30	80.98	139.82	97.28	110.00
524	10.70	7.90	5.81	18.87	20.05	102.71	97.55	11.57	8.50	7.01	13.83	22.06	125.94	84.71
525	41.37	44.14	45.56	39.27	41.85	100.62	100.49	147.61	131.00	168.62	148.43	149.22	115.00	89.06
672	1105.70	976.91	1558.44	1316.38	778.03	102.53	97.86	876.88	922.45	968.26	747.57	916.32	96.33	105.59
679	126.54	165.55	124.45	112.83	118.55	84.77	118.60	111.13	89.15	108.26	119.11	139.93	108.69	99.35
704	93.68	93.39	94.12	118.64	85.98	100.74	100.94	382.40	346.98	392.66	386.90	415.94	110.04	98.08
705	52.22	62.63	39.24	70.91	49.46	100.96	99.96	37.85	40.55	22.82	47.40	50.42	96.14	108.51

TABLE 15 (Continued)

siRNA	MB02							MB06						
	FSHD Composite	KHDC1L	LEUTX	MDB3L2	ZSCAN4	AHSA1	RPL27	FSHD Composite	KHDC1L	LEUTX	MDB3L2	ZSCAN4	AHSA1	RPL27
708	19.24	17.41	17.79	21.23	14.34	105.74	95.27	11.86	12.61	5.91	21.99	16.45	110.19	98.33
882	65.40	41.13	61.93	118.03	64.59	108.83	93.30	95.03	51.51	92.26	137.90	135.15	126.73	85.08
884	34.58	28.62	25.19	51.92	42.17	106.64	95.66	25.97	22.07	25.24	21.84	35.18	121.69	88.93
893	15.06	12.73	13.13	23.42	14.35	80.16	124.98	25.57	22.57	17.56	14.86	61.47	74.41	151.83
1045	31.86	28.20	32.38	42.01	42.10	102.03	99.58	72.20	55.02	62.24	73.95	110.04	112.74	93.00
1132	3.20	4.19	1.89	4.26	4.64	92.42	110.66	2.37	1.38	1.22	2.33	4.89	110.80	95.16
1134	41.73	31.74	27.87	62.98	58.37	97.67	103.39	165.18	124.57	138.47	238.72	194.16	120.19	96.87
1158	7.01	6.51	4.48	13.31	9.47	91.29	109.76	8.01	6.27	3.33	14.17	16.01	103.69	100.97
1159	226.21	152.73	154.74	292.83	401.40	82.15	126.63	525.79	246.31	419.47	381.92	840.11	109.42	94.92
1163	11.92	15.00	8.01	15.75	10.56	94.55	106.71	0.62	0.71	0.24	1.16	1.49	114.57	93.45
1236	4.22	3.32	1.94	8.35	8.47	82.34	121.73	1.85	1.56	0.70	2.59	4.72	83.65	125.55
1237	32.87	31.02	25.17	43.61	36.79	97.35	102.99	18.02	15.99	12.24	19.83	26.35	86.15	127.14
1238	24.43	25.07	19.03	35.16	24.46	105.02	95.44	29.53	23.79	22.54	35.10	43.41	106.57	101.82
1284	90.11	83.12	84.62	106.45	100.99	98.75	106.13	26.95	26.17	21.71	21.91	47.85	105.06	107.66
1290	104.36	97.53	102.02	118.57	109.73	100.22	101.46	135.73	277.05	410.94	346.25	336.63	129.53	81.28
1294	108.34	91.38	115.59	177.24	78.03	114.67	88.47	210.94	212.54	213.33	192.41	237.66	104.07	108.48
1295	60.35	60.16	43.80	96.21	55.94	69.18	145.68	26.36	19.44	20.39	39.85	31.69	80.55	134.12
1315	92.84	85.02	96.47	111.78	83.44	107.21	93.35	132.47	131.69	120.09	124.25	162.31	102.73	107.96
1316	82.53	68.66	62.91	154.83	71.10	97.30	103.65	170.76	141.70	168.39	207.31	175.30	116.86	93.87
1317	104.92	105.43	101.20	112.07	112.09	97.95	105.07	155.72	136.41	146.45	192.81	163.46	116.80	89.59
1321	23.72	20.71	13.75	44.87	29.79	87.40	115.65	30.38	22.32	20.48	43.92	44.59	91.46	115.30
1340	13.06	14.55	14.52	14.04	12.12	76.27	131.90	12.24	16.78	10.49	8.35	17.48	80.76	135.39
1350	207.49	155.67	224.45	254.19	222.09	103.71	96.95	108.59	73.33	116.32	128.51	130.28	111.71	94.61
1351	221.66	1074.92	2732.04	2200.38	1752.99	135.49	75.80	556.04	409.02	572.93	604.80	690.63	124.43	89.12
1539	85.20	76.82	87.54	121.01	73.71	98.65	102.96	174.37	162.38	150.76	180.05	217.16	105.72	100.85
1540	27.76	27.63	21.74	39.45	27.56	99.84	100.48	5.96	10.19	3.33	8.01	9.77	95.47	111.96
1541	27.45	23.47	21.75	36.77	33.40	94.71	106.55	19.68	13.08	13.66	27.71	34.20	104.27	100.39
1610	28.54	14.04	23.45	56.20	41.60	102.33	98.02	26.04	14.84	20.66	28.45	59.48	111.99	98.08
1611	31.12	23.09	26.42	59.28	27.96	96.38	104.00	148.02	126.75	169.36	178.77	128.62	115.44	90.38
1612	55.31	46.84	46.05	91.02	53.05	104.00	97.07	166.82	149.98	188.56	161.52	174.12	123.98	87.12
1613	5.18	6.53	1.37	8.42	3.97	96.50	106.13	11.55	10.97	6.06	22.26	24.00	110.12	94.54
1615	39.81	36.59	35.01	62.94	35.85	103.77	97.50	15.06	10.29	8.06	20.20	34.44	98.28	107.83
1616	21.13	28.01	32.41	33.99	31.93	94.67	106.96	24.95	15.42	15.30	31.87	59.94	104.72	99.75
1619	16.06	11.42	7.09	38.40	25.85	96.42	104.14	19.69	15.64	10.91	31.63	30.66	103.27	106.14
1632	17.02	21.17	23.00	26.39	8.73	109.10	92.79	4.83	6.04	2.20	7.24	6.80	101.92	104.27

[0409] As shown in FIG. 10, from the DUX4 siRNA library with 70 siRNA candidates, 37 candidates were eliminated that have lower than 70% KD in at least one cell lines at 10 nM. Then, 3 additional siRNA candidates were eliminated that resulted in ACTA1 expression less than 70% in both cell lines. Then, 2 additional siRNA candidates with null activity (<10% KD) at 0.5 nM in both cell lines were eliminated, resulting in total 28 siRNA candidates left for the next screening process. Table 16 lists such selected 28 DUX4 siRNAs and the downregulation of FSHD composite expression in two cell lines at the concentration of 10 nM and 0.5 nM of the selected 28 DUX4 siRNAs (also shown as bar graphs in FIG. 11A and 11B).

TABLE 16

siRNA	FSHD Composite (% Mock)			
	MB02 - 10nM	MB02 - 0.5nM	MB06 - 10nM	MB06 - 0.5nM
11	31.76	51.87	16.09	76.24
57	25.86	64.82	14.22	38.21
58	9.78	40.95	4.10	86.52
61	6.34	34.34	1.73	48.20
62	15.44	45.95	20.46	85.52
63	13.73	52.64	17.87	79.18
79	19.50	56.01	5.72	71.70
99	22.26	63.90	35.72	91.67
137	17.49	39.13	17.66	71.37
277	37.91	76.29	18.43	107.75
336	12.62	31.51	1.77	43.22
524	10.70	53.98	11.57	73.00
708	19.24	73.21	13.86	72.29
1132	5.20	59.37	2.17	66.00
1158	7.01	30.58	6.01	54.40
1163	11.52	48.46	0.62	37.70
1236	4.22	25.00	1.85	16.55
1237	32.87	99.25	18.02	47.65
1238	24.43	60.92	29.53	82.40
1340	13.06	38.81	12.24	47.63
1540	27.76	17.63	6.96	17.57
1541	27.45	34.55	19.68	70.70
1610	28.54	50.65	26.04	76.91
1613	5.18	18.30	13.55	39.25
1615	39.81	45.49	15.05	50.57
1616	31.13	37.63	24.95	32.25
1619	16.06	42.95	19.69	49.95
1632	17.02	20.07	4.83	37.10

[0410] Databases of human polymorphisms are not reliable in repeats and it is possible that polymorphic positions may be missed. Thus, in this round of selection, siRNAs that show poor performance in one of two myoblast cell lines were eliminated for a purpose of validating that selected DUX4 siRNAs are active in a variety of FSHD-patient derived myoblasts. FIG. 12 shows distribution of 70 siRNAs by their efficacies of downregulating FSHD composite in two myoblast cell lines. KD correlation analysis identified ~10% of DUX4 siRNAs that worked only in one of the two FSHD primary myoblast cell lines used in the full library screening.

Example 8 . DUX4 siRNA Library Screening – Second round at 10 nM in four different patient-derived primary myoblast cell lines

[0411] In this example, a total of 9 high quality FSHD patient-derived primary myoblast cell lines (6 FSHD1, 3 FSHD2) were used. Conditions that allow reliable detection of DUX4 target gene expression in FSHD myotubes in-house were established by culturing the cells in Differentiation medium (15% KOSR in DMEM/F-12). Time-point was selected specifically for each cell line. All 9 FSHD cell lines showed a concentration-dependent response to a tool DUX4 siRNA.

[0412] FIG. 13 shows a bar graph of ACTA1 expression levels in four different patient-derived primary myoblast cell lines (MB01, MB05, MB11, MB12). Most of the top 28 DUX4 siRNAs did not effect ACTA1 expression levels in these cell lines, while a few siRNAs showed more

than 30% reduction in ACTA1 expression levels in the additional 4 FSHD primary cell lines tested (8 in MB11, 3 in MB05, 3 in MB12, and none in MB01). In addition, as shown in FIG. 14, the top 28 DUX4 siRNAs showed activity in all four additional FSHD primary cell lines. Several siRNAs showed more than 75% KD in three lines: MB05, MB11, MB12. KD levels were overall lower in MB01. FIG. 15 shows the top 28 DUX4 siRNAs' activity at 10 nM concentration in all FSHD cell lines (MB01, MB02, MB05, MB06, MB11, MB12).

[0413] Top 14 DUX4 siRNAs were selected from top 28 DUX4 siRNAs. Selection of such top 14 DUX4 siRNAs were i) siRNAs that showed no or minimal cell toxicity (visual identification and evaluation of ACTA1 expression levels), and ii) siRNAs that displayed the best activity at both 10nM and 0.5nM concentrations. Table 17 lists the top 14 DUX4 siRNAs and downregulation of FSHD composite expression in six primary FSHD cell lines (MB01, MB02, MB05, MB06, MB11, MB12) at the concentration of 10 nM and 0.5 nM of the selected 14 DUX4 siRNAs, and downregulation of ACTA1 expression in six primary FSHD cell lines at the concentration of 10 nM. Table 18 lists the top 14 DUX4 siRNAs and downregulation of FSHD composite expression in all 9 FSHD primary myotubes.

TABLE 17

siRNA	FSHD Composite (% Mock)								ACTA 1 (% Mock)					
	10nM						0.5nM		10nM					
	MB01	MB02	MB05	MB06	MB11	MB12	MB02	MB06	MB01	MB02	MB05	MB06	MB11	MB12
11	43.10	31.76	15.02	16.09	2.66	13.06	51.87	76.24	182.43	149.99	114.72	134.18	74.18	123.86
57	60.89	25.86	16.05	14.22	29.01	43.75	64.82	38.21	134.81	133.87	77.42	136.08	101.53	122.19
58	47.60	9.78	8.74	4.10	5.00	25.30	40.95	88.53	164.25	152.35	119.96	159.71	89.04	103.74
61	25.54	6.34	6.82	1.73	0.63	4.13	34.34	48.20	161.47	112.20	91.46	95.20	73.28	85.37
137	71.58	17.49	26.43	17.66	7.90	18.69	39.13	71.37	175.58	159.65	113.40	140.40	85.80	114.48
336	36.05	12.62	15.53	1.77	0.96	6.47	31.51	43.22	113.53	92.45	99.88	123.50	159.92	96.08
1132	68.25	3.20	19.20	2.17	13.69	25.30	59.37	66.00	162.91	132.10	98.43	99.33	74.15	125.51
1340	56.58	13.06	21.04	12.24	18.09	22.73	38.81	47.63	237.27	204.96	176.84	146.51	167.31	134.73
1540	73.69	27.76	32.13	6.96	3.91	25.71	17.63	17.57	144.35	114.80	152.76	139.56	103.36	126.51
1613	39.26	5.18	16.04	13.55	14.70	19.28	18.30	39.25	155.21	119.51	107.74	164.23	125.38	122.92
1615	60.45	39.81	17.82	15.05	16.36	20.41	45.49	50.57	127.69	100.20	125.61	125.54	76.09	97.17
1616	81.13	31.13	46.69	24.95	8.98	24.15	37.63	32.25	115.10	74.43	89.58	77.83	52.83	80.73
1619	82.83	16.06	24.32	19.69	12.41	28.99	42.95	49.95	147.16	205.75	165.69	208.77	203.81	172.31
1632	54.74	17.02	11.74	4.83	4.99	12.45	20.07	37.10	151.01	135.47	147.94	162.22	101.99	157.04

TABLE 18

siRNA	FSHD Composite (% Mock)										ACTA 1 (% Mock)									
	10nM										10nM									
	MB01	MB02	MB03	MB04	MB05	MB06	MB10	MB11	MB12	MB02	MB06	MB01	MB02	MB03	MB04	MB05	MB06	MB10	MB11	MB12
11	43.10	31.76	22.90	5.61	15.02	16.09	19.78	2.68	13.06	51.87	26.28	182.43	149.99	94.53	252.83	114.72	134.18	113.25	74.18	123.86
57	60.89	25.86	35.58	81.33	16.05	14.22	33.53	29.01	43.79	64.82	36.21	134.81	133.87	135.56	83.88	77.82	136.08	104.46	101.53	122.19
58	47.80	9.78	17.90	0.72	8.74	4.18	22.25	5.80	25.30	40.95	36.53	164.25	152.35	201.75	146.25	119.96	159.71	82.38	89.04	105.78
61	25.54	6.34	12.59	0.39	6.82	1.73	16.50	0.63	4.13	34.34	46.20	161.47	112.20	170.49	97.32	81.86	95.20	108.30	73.28	85.32
137	71.56	17.49	25.94	0.37	26.43	17.66	26.87	7.90	18.69	39.13	71.37	175.58	159.65	92.10	197.01	113.40	140.40	71.16	85.80	114.48
336	36.05	12.62	15.99	0.13	15.53	1.77	11.35	0.96	6.47	31.51	41.22	113.53	92.45	99.01	476.86	99.88	123.50	93.80	159.92	96.08
1132	68.25	3.20	15.18	6.72	19.20	2.17	34.72	13.69	25.30	59.37	66.08	162.91	132.10	149.30	109.39	96.43	58.33	103.20	74.15	125.51
1340	56.58	13.06	41.13	13.67	21.04	12.24	35.26	18.09	22.79	38.81	47.63	237.27	204.96	182.92	279.19	176.84	346.51	160.47	167.31	134.73
1540	73.69	27.76	39.02	6.94	32.13	6.98	27.94	1.91	25.71	17.63	17.57	144.35	114.80	82.99	101.69	152.76	139.56	88.13	103.36	126.51
1613	39.26	5.18	13.19	76.87	16.04	13.55	88.78	14.70	19.28	18.30	39.25	155.21	119.51	160.42	289.09	107.74	164.23	102.70	125.38	122.92
1615	60.45	39.81	34.04	12.48	17.82	15.05	41.32	16.36	20.41	45.49	50.57	127.69	100.20	97.77	146.44	125.61	125.54	43.69	76.09	97.17
1616	81.11	31.13	36.27	13.95	46.69	24.55	72.30	8.94	24.15	37.63	32.25	115.10	74.43	74.73	84.55	80.52	77.81	46.30	52.83	80.73
1619	82.35	16.06	40.97	3.88	24.32	19.69	41.16	12.41	28.99	42.95	48.85	147.16	205.75	155.05	967.98	165.69	208.77	88.50	203.81	172.31
1632	54.74	17.02	19.15	4.82	11.74	4.83	28.31	4.99	12.45	20.07	37.18	151.03	135.47	113.22	531.53	147.94	162.22	155.60	101.99	157.04

Example 9 . Top 14 DUX4 siRNAs Evaluated for Potency in Concentration Response in MB02, MB05 and MB06

[0414] The goal of the experiments in this example is to select 8 siRNAs with best Emax and potency for off-target analysis. Three FSHD primary myoblast cell lines (MB02, MB05, MB06) were used. Cells were plated at a density of 4,000 cells/well (MW96) and transfected in quadruplicates with selected 14 DUX4 siRNAs. Transfection was performed 24 hours after plating. Myogenic differentiation was induced 2 days after plating (24 hours after transfection) with 15% KOSR (in DMEM/F-12) medium. Samples were harvested 3 or 4 days after inducing differentiation, depending on the cell line. DUX4-downstream target gene expression was evaluated by RT-qPCR (normalized to a composite AHSA1 and RPL27 housekeeping gene expression value). Data represented as mean $\pm$ SEM. N=4.

[0415] FIGs. 16A-C show concentration response of 14 selected DUX4 siRNA in three FSHD patient-derived primary myotubes – MB02, MB05, MB06, respectively. DUX-4-target gene expression was reduced more than 75% by most of the top 14 DUX4 siRNAs in three FSHD patient-derived primary myoblast lines. It was also observed that differences on potency among siRNAs ranged between 60 to 100-fold depending on the cell lines. Tables 19-22 show potency of DUX4 siRNAs evaluated in three FSHD patient-derived primary myotubes based on FSHD composite.

TABLE 19

M802

siRNA	Max KD [%]*	IC50 [nM]
11	95.54	1.506
57	90.06	0.918
58	100.00	1.969
61	100.00	0.639
137	93.90	1.903
336	83.74	0.110
1132	100.00	2.630
1340	83.69	2.137
1540	86.47	0.047
1613	95.09	0.259
1615	76.01	0.166
1616	88.05	0.372
1619	67.10	0.306
1632	91.52	0.082

TABLE 20

M805

siRNA	Max KD [%]*	IC50 [nM]
11	83.78	0.055
57	86.86	0.870
58	89.08	0.375
61	95.24	0.127
137	86.13	0.673
336	94.35	0.127
1132	100.00	2.666
1340	79.53	0.309
1540	91.33	0.075
1613	96.23	0.118
1615	82.43	0.091
1616	81.99	0.130
1619	78.60	0.091
1632	87.59	0.027

TABLE 21

MB06

siRNA	Max KD (%)*	IC50 (nM)
11	90.75	1.923
57	68.18	0.054
58	98.45	1.374
61	100.00	0.665
137	87.25	2.018
336	98.53	0.359
1132	100.00	4.462
1340	100.00	1.090
1540	92.71	0.145
1613	84.07	0.070
1615	80.01	0.457
1616	67.81	0.051
1619	71.63	0.299
1632	93.15	0.243

TABLE 22

All lines together

siRNA	Av. Max KD (%)*	Av. IC50 (nM)
11	90.02	1.161
57	81.70	0.614
58	95.64	1.239
61	98.41	0.477
137	86.89	1.531
336	92.21	0.199
1132	100.00	3.326
1340	87.74	1.179
1540	83.50	0.089
1613	91.60	0.149
1615	79.48	0.238
1616	79.26	0.184
1619	79.18	0.232
1632	90.76	0.117

[0416] Example 11. Antibody-DUX4 siRNA conjugates (DUX4-AOCs) mediated reduction of FSHD composite (composite of DUX4-target biomarker genes) expression in cultured FSHD primary myotubes.

[0417] The *in vitro* concentration-response potency and maximum efficacy of 16 DUX4-AOCs (8 vpUq AOCs or 8 Non-VP AOCs) were assessed in FSHD1 patient-derived primary myotubes (MB06). The guide strand of the DUX4 siRNA of the AOCs was either with vinylphosphonate at the 5' of the strand (vpUq) or without vinylphosphonate at the 5' end of the strand (Non-VP).

[0418] The human IgG1 antibody against human TfR1 was expressed in CHO stable pools, created by transfecting the CHOK1SV GS-KO host cell line with a double gene vector. The antibody was captured from cell culture supernatant using protein A affinity chromatography.

The resultant antibody was further purified using hydrophobic interaction chromatography (to reduce aggregates) and anion exchange chromatography (to reduce host cell DNA & endotoxin). The final antibody was buffer exchanged into either PBS or 50 mM sodium citrate buffer, pH 6.5 at a concentration of 20 mg/mL. The purity of the antibody was assessed by size exclusion chromatography.

[0419] The guide and fully complementary RNA passenger strands were assembled on solid phase using standard phosphoramidite chemistry and purified over HPLC. Purified single strands were duplexed to obtain double stranded siRNA. The guide strand was produced with a vinylphosphonate modified nucleotide structures at the 5' end. The passenger strand had a conjugation handle on the 5' end via a phosphorothioate-inverted abasic-phosphodiester linker.

[0420] Antibody oligonucleotide conjugates (AOCs) were generated using a random cysteine conjugation method. The interchain disulfide bonds of the antibody were partially reduced with TCEP prior to conjugation with a maleimide linker-siRNA. The reaction mixture was purified using strong anion exchange chromatography to ensure a drug-antibody ratio (DAR) equal to 1 (i.e., one siRNA molecule per one antibody molecule). Collected AOC fractions were concentrated, buffer exchanged into PBS and sterile filtered using a 0.2 µm filter. The purity of AOCs was assessed using strong anion exchange chromatography, size exclusion chromatography, and SDS-PAGE.

[0421] FSHD primary myoblasts (MB06 (FSHD1)) were grown in recommended media. Prior to seeding, 96-well tissue culture plates (Costar) were coated with 50 µL of 1% Matrigel per well for at least 2 hours at 37°C and washed 2x with PBS. After coating, myoblasts were seeded in quadruplicate at 4000 cells/well. 2 days after plating, myogenic differentiation was induced with 15% KOSR-containing differentiation medium. 24 hours after inducing differentiation, siDUX4-AOCs were added in the medium at a high concentration of 100 nM with 10-fold serial dilutions. Untreated cells were maintained as a relative control. After 3 days of incubation with DUX4-AOCs, myotubes were collected in Trizol and stored at -80°C until processing. RNA isolation was performed using Direct-zol-96 RNA isolation kit (Zymo) according to the manufacturer's instructions. 100-500 ng of purified RNA was converted to cDNA using High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems) using SimpliAmp Thermal Cycler (Applied Biosystems). cDNA was analyzed by qPCR using TaqMan Fast Universal Master Mix II (Thermo Fisher) and TaqMan probes (Thermo Fisher) in duplicates, using QuantStudio 6 or 7 Flex Real-Time PCR instruments (Applied Biosystems). Data were analyzed by QuantStudio™ Real-Time PCR Software v1.3 (Applied Biosystems). DUX4-target gene expression levels were evaluated by calculating the FSHD Composite score, which integrated

the expression levels of 4 DUX4-target genes (MBD3L2, ZSCAN4, LEUTX, and KHDC1L) normalized to two reference genes (AHSA1 and RPL27).

[0422] FIGs. 18A-B show the dose response curve of DUX4-AOCs mediated reduction of DUX4-target biomarker gene expressions in cultured FSHD primary myotubes. Most DUX4-AOCs with vinylphosphonate (FIG. 18A) and several DUX4-AOCs without vinylphosphonate (FIG. 18B) reduced the expression of the FSHD composite of 4 DUX4-target biomarker genes (MBD3L2, ZSCAN4, LEUTX, and KHDC1L) in FSHD1 patient-derived primary myotubes. Overall, DUX4-AOCs reduced the expression of DUX4-target biomarker gene expressions and the presence of vinylphosphonate on the DUX4 siRNA in the AOCs facilitated the reduction of the DUX4-target biomarker gene expressions.

Example 12. Malat1-siRNA AOC mediated *in vivo* reduction of nuclear localized lnc-RNA Malat1 mRNA levels in 3 different murine skeletal muscles

[0423] Wild type female CD-1 mice (approximately 6-8 weeks old) were dosed once by a single IV bolus injection in the tail vein at 5 mL/kg body weight, of either *Malat1* or Scramble AOCs, in which the siRNA was conjugated to murine anti-Transferrin Receptor (mTfR1) antibody, at doses 0.3, 1, 3, 6 mg/kg body weight (siRNA amount). Muscle tissue samples were collected 2 weeks post treatment in tubes containing ceramic beads, flash frozen in liquid nitrogen, and then homogenized in 1 mL cold Trizol using a FastPrep-24 (MP Biomedicals). Homogenate supernatants were used for RNA isolation using Direct-zol-96 RNA isolation kit (Zymo) according to the manufacturer's instructions. 100-500 ng of purified RNA was converted to cDNA using High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems) using SimpliAmp Thermal Cycler (Applied Biosystems). cDNA was analyzed by qPCR using TaqMan Fast Universal Master Mix II (Thermo Fisher) and TaqMan probes (Thermo Fisher) in duplicates, using QuantStudio 6 or 7 Flex Real-Time PCR instruments (Applied Biosystems). Data were analyzed by QuantStudio™ Real-Time PCR Software v1.3 (Applied Biosystems). The target gene expression was normalized to a reference gene *Ppib*. The percentage of target mRNA expression in treatment samples was determined relative to the control treatment using the $2^{-\Delta\Delta Ct}$ method. Data are represented as % of PBS control (mean $\pm$ SEM; N=4 for siMalat1 and siScramble AOCs, N=5 for PBS groups).

[0424] FIG. 19 shows *Malat1* siRNA-AOC-mediated *in vivo* reduction of nuclear localized lnc-RNA Malat1 levels in skeletal muscles in mice. A single administration of up to 6 mg/kg of *Malat1* siRNA-AOC (siRNA dose) in mice reduced nuclear *Malat1* expression up to 80% in skeletal muscle 2 weeks post-dose. The reduction of nuclear *Malat1* mRNA expression levels indicate the *in vivo* ability of AOCs to target nuclear RNAs for degradation.

Example 13. Sustained AOC-mediated *in vivo* reduction of SSB mRNA levels in murine skeletal muscles with a single dose of 3mg/kg siRNA AOC during an 8-week period

[0425] Wild type male C57BL/6 mice (approximately 12-16 weeks old) were dosed once by a single IV bolus injection in the tail vein at 5 mL/kg body weight of either without vinylphosphonate (Non-VP) or with vinylphosphonate (vpUq) *Ssb* siRNA conjugated to murine anti-TfR1 (mTfR1) antibody at 3 mg/kg body weight (siRNA amount) dose. Gastrocnemius muscles were collected at the following time-points after dosing: day 1, 7, 14, 28, 43 and 57. Muscles were placed in tubes containing ceramic beads, flash frozen in liquid nitrogen, and then homogenized in 1 mL cold Trizol using a FastPrep-24 (MP Biomedicals). Homogenate supernatants were used for RNA isolation using Direct-zol-96 RNA isolation kit (Zymo) according to the manufacturer's instructions. 100-500 ng of purified RNA was converted to cDNA using High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems) using SimpliAmp Thermal Cycler (Applied Biosystems). cDNA was analyzed by qPCR using TaqMan Fast Universal Master Mix II (Thermo Fisher) and TaqMan probes (Thermo Fisher) in duplicates, using QuantStudio 6 or 7 Flex Real-Time PCR instruments (Applied Biosystems). Data were analyzed by QuantStudio™ Real-Time PCR Software v1.3 (Applied Biosystems). *Ssb* gene expression was normalized to the reference gene *Ppib*. The percentage of target mRNA expression in treatment samples was determined relative to the control treatment (PBS) using the $2^{-\Delta\Delta C_t}$ method. Data are represented as % of PBS control (mean $\pm$ SEM; N=4 for siSsb-AOCs, N=3-5 for PBS groups).

[0426] FIG. 20 shows SSB siRNA-AOC-mediated *in vivo* reduction of SSB mRNA levels in murine skeletal muscles with a single dose of 3mg/kg siRNA during an 8-week period. The sustained AOC-mediated *in vivo* reduction of SSB mRNA expression levels was achieved in a mouse skeletal muscle after a 3 mg/kg (siRNA dose) single administration of both without vinylphosphonate (non-VP) and with vinylphosphonate (vpUq) SSB siRNA-AOCs.

[0427] While preferred embodiments of the present disclosure have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the disclosure. It should be understood that various alternatives to the embodiments of the disclosure described herein may be employed in practicing the disclosure. It is intended that the following claims define the scope of the disclosure and that methods and structures within the scope of these claims and their equivalents be covered thereby.