MUSCLE TARGETING COMPLEXES AND USES THEREOF FOR TREATING DYSTROPHINOPATHIES

RELATED APPLICATIONS

[0001] This application claims priority under 35 U.S.C. § 119(e) to U.S. Provisional Application Serial No. 63/219999, entitled "MUSCLE TARGETING COMPLEXES AND USES THEREOF FOR TREATING DYSTROPHINOPATHIES", filed on July 9, 2021, the contents of which are incorporated herein by reference in their entirety.

FIELD OF THE INVENTION

[0002] The present application relates to targeting complexes for delivering molecular payloads (e.g., oligonucleotides) to cells and uses thereof, particularly uses relating to treatment of disease.

REFERENCE TO AN ELECTRONIC SEQUENCE LISTING

[0003] The contents of the electronic sequence listing (D082470065WO00-SEQ-COB.xml; Size: 2,801,833 bytes; and Date of Creation: July 7, 2022) is herein incorporated by reference in its entirety.

BACKGROUND OF INVENTION

[0004] Dystrophinopathies are a group of distinct neuromuscular diseases that result from mutations in the gene encoding dystrophin. Dystrophinopathies include Duchenne muscular dystrophy, Becker muscular dystrophy, and X-linked dilated cardiomyopathy. The DMD gene ("DMD"), which encodes dystrophin, is a large gene, containing 79 exons and about 2.6 million total base pairs. Numerous mutations in DMD, including exonic frameshift, deletion, substitution, and duplicative mutations, are able to diminish the expression of functional dystrophin, leading to dystrophinopathies. Several agents that target exons of human DMD have been approved by the U.S. Food and Drug Administration (FDA), including casimersen, viltolarsen, golodirsen, and eteplirsen.

SUMMARY OF INVENTION

[0005] According to some aspects, the disclosure provides complexes that target muscle cells for purposes of delivering molecular payloads to those cells, as well as molecular payloads that can be used therein. In some embodiments, complexes provided herein are particularly useful for delivering molecular payloads that increase or restore expression or activity of functional

dystrophin protein. In some embodiments, complexes comprise oligonucleotide based molecular payloads that promote expression of functional dystrophin protein through an in-frame exon skipping mechanism or suppression of stop codons, such as by facilitating skipping of DMD exon 55. In some embodiments, molecular payloads provided herein are useful for facilitating exon skipping in a DMD sequence, such as skipping of DMD exon 55. Accordingly, in some embodiments, complexes provided herein comprise muscle-targeting agents (e.g., muscle targeting antibodies) that specifically bind to receptors on the surface of muscle cells for purposes of delivering molecular payloads to the muscle cells. In some embodiments, the complexes are taken up into the cells via a receptor mediated internalization, following which the molecular payload may be released to perform a function inside the cells. For example, complexes engineered to deliver oligonucleotides may release the oligonucleotides such that the oligonucleotides can promote expression of functional dystrophin protein (e.g., through an exon skipping mechanism, such as by facilitating skipping of DMD exon 55) in the muscle cells. In some embodiments, the oligonucleotides are released by endosomal cleavage of covalent linkers connecting oligonucleotides and muscle-targeting agents of the complexes. Complexes and molecular payloads provided herein can be used for treating subjects having a mutated DMD gene, such as a mutated DMD gene that is amenable to exon 55 skipping.

[0006] According to some aspects, complexes comprising an anti-transferrin receptor 1 (TfR1) antibody covalently linked to an oligonucleotide configured for inducing skipping of exon 55 in a DMD pre-mRNA are provided herein, wherein the oligonucleotide comprises a region of complementarity that is complementary with at least 8 consecutive nucleotides of any one of SEQ ID NOs: 160-779.

[0007] In some embodiments, the anti-TfR1 antibody comprises:

(i) a heavy chain complementarity determining region 1 (CDR-H1) of SEQ ID NO: 33, a heavy chain complementarity determining region 2 (CDR-H2) of SEQ ID NO: 34, a heavy chain complementarity determining region 3 (CDR-H3) of SEQ ID NO: 35, a light chain complementarity determining region 1 (CDR-L1) of SEQ ID NO: 36, a light chain complementarity determining region 2 (CDR-L2) of SEQ ID NO: 37, and a light chain complementarity determining region 3 (CDR-L3) of SEQ ID NO: 32;

(ii) a CDR-H1 of SEQ ID NO: 7, a CDR-H2 of SEQ ID NO: 8, a CDR-H3 of SEQ ID NO: 9, a CDR-L1 of SEQ ID NO: 10, a CDR-L2 of SEQ ID NO: 11, and a CDR-L3 of SEQ ID NO: 6;

(iii) a CDR-H1 of SEQ ID NO: 7, a CDR-H2 of SEQ ID NO: 20, a CDR-H3 of SEQ ID NO: 9, a CDR-L1 of SEQ ID NO: 10, a CDR-L2 of SEQ ID NO: 11, and a CDR-L3 of SEQ ID NO: 6;

(iv) a CDR-H1 of SEQ ID NO: 7, a CDR-H2 of SEQ ID NO: 24, a CDR-H3 of SEQ ID NO: 9, a CDR-L1 of SEQ ID NO: 10, a CDR-L2 of SEQ ID NO: 11, and a CDR-L3 of SEQ ID NO: 6;

(v) a CDR-H1 of SEQ ID NO: 51, a CDR-H2 of SEQ ID NO: 52, a CDR-H3 of SEQ ID NO: 53, a CDR-L1 of SEQ ID NO: 54, a CDR-L2 of SEQ ID NO: 55, and a CDR-L3 of SEQ ID NO: 50;

(vi) a CDR-H1 of SEQ ID NO: 64, a CDR-H2 of SEQ ID NO: 52, a CDR-H3 of SEQ ID NO: 53, a CDR-L1 of SEQ ID NO: 54, a CDR-L2 of SEQ ID NO: 55, and a CDR-L3 of SEQ ID NO: 50; or

(vii) a CDR-H1 of SEQ ID NO: 67, a CDR-H2 of SEQ ID NO: 52, a CDR-H3 of SEQ ID NO: 53, a CDR-L1 of SEQ ID NO: 54, a CDR-L2 of SEQ ID NO: 55, and a CDR-L3 of SEQ ID NO: 50.

[0008] In some embodiments, the anti-TfR1 antibody comprises:

(i) a heavy chain variable region (VH) comprising an amino acid sequence at least 85% identical to SEQ ID NO: 76; and/or a light chain variable region (VL) comprising an amino acid sequence at least 85% identical to SEQ ID NO: 75;

(ii) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 69; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 70;

(iii) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 71; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 70;

(iv) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 72; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 70;

(v) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 73; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 74;

(vi) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 73; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 75;

(vii) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 76; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 74;

(viii) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 77; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 78;

(ix) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 79; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 80; or

(x) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 77; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 80.

[0009] In some embodiments, the anti-TfR1 antibody comprises:

(i) a VH comprising the amino acid sequence of SEQ ID NO: 76 and a VL comprising the amino acid sequence of SEQ ID NO: 75;

(ii) a VH comprising the amino acid sequence of SEQ ID NO: 69 and a VL comprising the amino acid sequence of SEQ ID NO: 70;

(iii) a VH comprising the amino acid sequence of SEQ ID NO: 71and a VL comprising the amino acid sequence of SEQ ID NO: 70;

(iv) a VH comprising the amino acid sequence of SEQ ID NO: 72 and a VL comprising the amino acid sequence of SEQ ID NO: 70;

(v) a VH comprising the amino acid sequence of SEQ ID NO: 73 and a VL comprising the amino acid sequence of SEQ ID NO: 74;

(vi) a VH comprising the amino acid sequence of SEQ ID NO: 73 and a VL comprising the amino acid sequence of SEQ ID NO: 75;

(vii) a VH comprising the amino acid sequence of SEQ ID NO: 76 and a VL comprising the amino acid sequence of SEQ ID NO: 74;

(viii) a VH comprising the amino acid sequence of SEQ ID NO: 77 and a VL comprising the amino acid sequence of SEQ ID NO: 78;

(ix) a VH comprising the amino acid sequence of SEQ ID NO: 79 and a VL comprising the amino acid sequence of SEQ ID NO: 80; or

(x) a VH comprising the amino acid sequence of SEQ ID NO: 77 and a VL comprising the amino acid sequence of SEQ ID NO: 80.

[00010] In some embodiments, the anti-TfR1 antibody is a Fab fragment, a Fab' fragment, a F(ab')2 fragment, an scFv, an Fv, or a full-length IgG.

[00011] In some embodiments, the anti-TfR1 antibody is a Fab fragment.

[00012] In some embodiments, the anti-TfR1 antibody comprises:

(i) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 101; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 90;

(ii) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 97; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 85;

(iii) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 98; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 85;

(iv) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID

NO: 99; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 85;

(v) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 100; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 89;

(vi) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 100; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 90;

(vii) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 101; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 89;

(viii) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 102; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 93;

(ix) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 103; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 95; or

(x) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 102; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 95.

[00013] In some embodiments, the anti-TfR1 antibody comprises:

(i) a heavy chain comprising the amino acid sequence of SEQ ID NO: 101; and a light chain comprising the amino acid sequence of SEQ ID NO: 90;

(ii) a heavy chain comprising the amino acid sequence of SEQ ID NO: 97; and a light chain comprising the amino acid sequence of SEQ ID NO: 85;

(iii) a heavy chain comprising the amino acid sequence of SEQ ID NO: 98; and a light chain comprising the amino acid sequence of SEQ ID NO: 85;

(iv) a heavy chain comprising the amino acid sequence of SEQ ID NO: 99; and a light chain comprising the amino acid sequence of SEQ ID NO: 85;

(v) a heavy chain comprising the amino acid sequence of SEQ ID NO: 100; and a light chain comprising the amino acid sequence of SEQ ID NO: 89;

(vi) a heavy chain comprising the amino acid sequence of SEQ ID NO: 100; and a light chain comprising the amino acid sequence of SEQ ID NO: 90;

(vii) a heavy chain comprising the amino acid sequence of SEQ ID NO: 101; and a light chain comprising the amino acid sequence of SEQ ID NO: 89;

(viii) a heavy chain comprising the amino acid sequence of SEQ ID NO: 102; and a light chain comprising the amino acid sequence of SEQ ID NO: 93;

(ix) a heavy chain comprising the amino acid sequence of SEQ ID NO: 103; and a light chain comprising the amino acid sequence of SEQ ID NO: 95; or

(x) a heavy chain comprising the amino acid sequence of SEQ ID NO: 102; and a light chain comprising the amino acid sequence of SEQ ID NO: 95.

[00014] In some embodiments, the anti-TfR1 antibody does not specifically bind to the transferrin binding site of the transferrin receptor 1 and/or the anti-TfR1 antibody does not inhibit binding of transferrin to the transferrin receptor 1.

[00015] In some embodiments, the oligonucleotide comprises a region of complementarity to at least 4 consecutive nucleotides of a splicing feature of the DMD pre-mRNA.

[00016] In some embodiments, the splicing feature is an exonic splicing enhancer (ESE) in exon 55 of the DMD pre-mRNA, optionally wherein the ESE comprises a sequence of any one of SEQ ID NOs: 2031-2061.

[00017] In some embodiments, the splicing feature is a branch point, a splice donor site, or a splice acceptor site, optionally wherein the splicing feature is across the junction of exon 54 and intron 54, in intron 54, across the junction of intron 54 and exon 55, across the junction of exon 55 and intron 55, in intron 55, or across the junction of intron 55 and exon 56 of the DMD pre-mRNA, and further optionally wherein the splicing feature comprises a sequence of any one of SEQ ID NOs: 2028-2030, 2062, and 2063.

[00018] In some embodiments, the oligonucleotide comprises a sequence complementary to any one of SEQ ID NOs: 160-779 or comprises a sequence of any one of SEQ ID NOs: 780-2019, wherein each thymine base (T) may independently and optionally be replaced with a uracil base (U), and each U may independently and optionally be replaced with a T.

[00019] In some embodiments, the oligonucleotide comprises a sequence of any one of SEQ ID NOs: 1400, 1402-1406, 1408, 1409, 1413, 1418-1420, 1483-1491, 1493, 1495, 1496, 1502-1506, 1508, 1510-1512, 1514, 1522-1524, 1529-1531, 1534, 1535, 1559, 1583, 1587, 1591, 1596, 1597, 1598, 1604, 1606, 1607, 1638, 1641, 1693-1695, 1702, 1703, 1766, 1813, 1988, and 1995, wherein each thymine base (T) may independently and optionally be replaced with a uracil base (U), and each U may independently and optionally be replaced with a T.

[00020] In some embodiments, the oligonucleotide comprises one or more phosphorodiamidate morpholinos, optionally wherein the oligonucleotide is a phosphorodiamidate morpholino oligomer (PMO).

[00021] In some embodiments, the anti-TfR1 antibody is covalently linked to the oligonucleotide via a cleavable linker, optionally wherein the cleavable linker comprises a valine-citrulline sequence.

[00022] In some embodiments, the anti-TfR1 antibody is covalently linked to the oligonucleotide via conjugation to a lysine residue or a cysteine residue of the antibody.

[00023] According to some aspects, oligonucleotides that target DMD are provided herein, wherein the oligonucleotide comprises a region of complementarity to any one of SEQ ID NOs: 160-779, optionally wherein the region of complementarity comprises at least 15 consecutive nucleosides complementary to any one of SEQ ID NOs: 160-779.

[00024] In some embodiments, the oligonucleotide comprises at least 15 consecutive nucleosides of any one of SEQ ID NOs: 780-2019, optionally wherein the oligonucleotide comprises a sequence of any one of SEQ ID NOs: 780-2019, wherein each thymine base (T) may independently and optionally be replaced with a uracil base (U), and each U may independently and optionally be replaced with a T.

[00025] According to some aspects, methods of delivering an oligonucleotide to a cell are provided herein, the method comprising contacting the cell with a complex disclosed herein or with an oligonucleotide disclosed herein.

[00026] According to some aspects, methods of promoting the expression or activity of a dystrophin protein in a cell are provided herein, the method comprising contacting the cell with a complex disclosed herein or with an oligonucleotide disclosed herein in an amount effective for promoting internalization of the oligonucleotide to the cell, optionally wherein the cell is a muscle cell.

[00027] In some embodiments, the cell comprises a DMD gene that is amenable to skipping of exon 55.

[00028] In some embodiments, the dystrophin protein is a truncated dystrophin protein.

BRIEF DESCRIPTION OF THE DRAWINGS

[00029] **FIG. 1** shows data illustrating that conjugates containing anti-TfR1 Fab (3M12 VH4/Vκ3) conjugated to a DMD exon-skipping oligonucleotide resulted in enhanced exon skipping compared to the naked DMD exon skipping oligo in Duchenne muscular dystrophy patient myotubes.

DETAILED DESCRIPTION OF INVENTION

[00030] Aspects of the disclosure relate to a recognition that while certain molecular payloads (*e.g.*, oligonucleotides, peptides, small molecules) can have beneficial effects in muscle

cells, it has proven challenging to effectively target such cells. Accordingly, as described herein, the present disclosure provides complexes comprising muscle-targeting agents covalently linked to molecular payloads in order to overcome such challenges. In some embodiments, the complexes are particularly useful for delivering molecular payloads that modulate (e.g., promote) the expression or activity of dystrophin protein (*e.g.*, a truncated dystrophin protein) or DMD (*e.g.*, a mutated DMD allele). In some embodiments, complexes provided herein may comprise oligonucleotides that promote expression and activity of dystrophin protein or DMD, such as by facilitating in-frame exon skipping and/or suppression of premature stop codons. For example, complexes may comprise oligonucleotides that induce skipping of exon(s) of DMD RNA (*e.g.*, pre-mRNA), such as oligonucleotides that induce skipping of exon 55. In some embodiments, synthetic nucleic acid payloads (*e.g.*, DNA or RNA payloads) may be used that express one or more proteins that promote normal expression and activity of dystrophin protein or DMD.

[00031] Duchenne muscular dystrophy is an X-linked muscular disorder caused by one or more mutations in the DMD gene located on Xp21. Dystrophin protein typically forms the dystrophin-associated glycoprotein complex (DGC) at the sarcolemma, which links the muscle sarcomeric structure to the extracellular matrix and protects the sarcolemma from contraction-induced injury. In patients with Duchenne muscular dystrophy, the dystrophin protein is generally absent and muscle fibers typically become damaged due to mechanical overextension. Mutations in the DMD gene are associated with two types of muscular dystrophy, Duchenne muscular dystrophy and Becker muscular dystrophy, depending on whether the translational reading frame is lost or maintained. Becker muscular dystrophy is a clinically milder form of Duchenne muscular dystrophy, and is characterized by features similar to Duchenne muscular dystrophy. In some embodiments, exon skipping induced by oligonucleotides (e.g., delivered using complexes provided herein) can be used to restore the reading frame of a mutated DMD allele resulting in production of a truncated dystrophin protein that is sufficiently functional to improve muscle function. In some embodiments, such exon skipping converts a Duchenne muscular dystrophy phenotype into a milder Becker muscular dystrophy phenotype.

[00032] Further aspects of the disclosure, including a description of defined terms, are provided below.

I. Definitions

[00033] **Administering**: As used herein, the terms "administering" or "administration" means to provide a complex to a subject in a manner that is physiologically and/or (e.g., and) pharmacologically useful (*e.g.*, to treat a condition in the subject).

[00034] **Approximately:** As used herein, the term "approximately" or "about," as applied to one or more values of interest, refers to a value that is similar to a stated reference value. In certain embodiments, the term "approximately" or "about" refers to a range of values that fall within 15%, 14%, 13%, 12%, 11%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, or less in either direction (greater than or less than) of the stated reference value unless otherwise stated or otherwise evident from the context (except where such number would exceed 100% of a possible value).

[00035] **Antibody:** As used herein, the term "antibody" refers to a polypeptide that includes at least one immunoglobulin variable domain or at least one antigenic determinant, e.g., paratope that specifically binds to an antigen. In some embodiments, an antibody is a full-length antibody. In some embodiments, an antibody is a chimeric antibody. In some embodiments, an antibody is a humanized antibody. However, in some embodiments, an antibody is a Fab fragment, a Fab' fragment, a F(ab')2 fragment, a Fv fragment or a scFv fragment. In some embodiments, an antibody is a nanobody derived from a camelid antibody or a nanobody derived from shark antibody. In some embodiments, an antibody is a diabody. In some embodiments, an antibody comprises a framework having a human germline sequence. In another embodiment, an antibody comprises a heavy chain constant domain selected from the group consisting of IgG, IgG1, IgG2, IgG2A, IgG2B, IgG2C, IgG3, IgG4, IgA1, IgA2, IgD, IgM, and IgE constant domains. In some embodiments, an antibody comprises a heavy (H) chain variable region (abbreviated herein as VH), and/or (e.g., and) a light (L) chain variable region (abbreviated herein as VL). In some embodiments, an antibody comprises a constant domain, e.g., an Fc region. An immunoglobulin constant domain refers to a heavy or light chain constant domain. Human IgG heavy chain and light chain constant domain amino acid sequences and their functional variations are known. With respect to the heavy chain, in some embodiments, the heavy chain of an antibody described herein can be an alpha (α), delta (Δ), epsilon (ε), gamma (γ) or mu (μ) heavy chain. In some embodiments, the heavy chain of an antibody described herein can comprise a human alpha (α), delta (Δ), epsilon (ε), gamma (γ) or mu (μ) heavy chain. In a particular embodiment, an antibody described herein comprises a human gamma 1 CH1, CH2, and/or (e.g., and) CH3 domain. In some embodiments, the amino acid sequence of the VH domain comprises the amino acid sequence of a human gamma (γ) heavy chain constant region, such as any known in the art. Non-limiting examples of human constant region sequences have been described in the art, e.g., see U.S. Pat. No. 5,693,780 and Kabat E A et al., (1991) supra. In some embodiments, the VH domain comprises an amino acid sequence that is at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or at least 99% identical to any of the variable chain constant regions provided herein. In some embodiments, an antibody is

modified, e.g., modified via glycosylation, phosphorylation, sumoylation, and/or (e.g., and) methylation. In some embodiments, an antibody is a glycosylated antibody, which is conjugated to one or more sugar or carbohydrate molecules. In some embodiments, the one or more sugar or carbohydrate molecule are conjugated to the antibody via N-glycosylation, O-glycosylation, C-glycosylation, glypiation (GPI anchor attachment), and/or (e.g., and) phosphoglycosylation. In some embodiments, the one or more sugar or carbohydrate molecule are monosaccharides, disaccharides, oligosaccharides, or glycans. In some embodiments, the one or more sugar or carbohydrate molecule is a branched oligosaccharide or a branched glycan. In some embodiments, the one or more sugar or carbohydrate molecule includes a mannose unit, a glucose unit, an N-acetylglucosamine unit, an N-acetylgalactosamine unit, a galactose unit, a fucose unit, or a phospholipid unit. In some embodiments, an antibody is a construct that comprises a polypeptide comprising one or more antigen binding fragments of the disclosure linked to a linker polypeptide or an immunoglobulin constant domain. Linker polypeptides comprise two or more amino acid residues joined by peptide bonds and are used to link one or more antigen binding portions. Examples of linker polypeptides have been reported (see e.g., Holliger, P., et al. (1993) Proc. Natl. Acad. Sci. USA 90:6444-6448; Poljak, R. J., et al. (1994) Structure 2:1121-1123). Still further, an antibody may be part of a larger immunoadhesion molecule, formed by covalent or noncovalent association of the antibody or antibody portion with one or more other proteins or peptides. Examples of such immunoadhesion molecules include use of the streptavidin core region to make a tetrameric scFv molecule (Kipriyanov, S. M., et al. (1995) Human Antibodies and Hybridomas 6:93-101) and use of a cysteine residue, a marker peptide and a C-terminal polyhistidine tag to make bivalent and biotinylated scFv molecules (Kipriyanov, S. M., et al. (1994) Mol. Immunol. 31:1047-1058).

[00036] **Branch point:** As used herein, the term "branch point" or "branch site" refers to a nucleic acid sequence motif within an intron of a gene or pre-mRNA that is involved in splicing of pre-mRNA into mRNA (*i.e.*, removing introns from the pre-mRNA), and can be referred to as a splicing feature. A branch point is typically located 18 to 40 nucleotides from the 3' end of an intron, and contains an adenine but is otherwise relatively unrestricted in sequence. Common sequence motifs for branch points are YNYYRAY, YTRAC, and YNYTRAY, where Y is a pyrimidine, N is any nucleotide, R is any purine, and A is adenine. During splicing, the pre-mRNA is cleaved at the 5' end of the intron, which then attaches to the branch point region downstream through transesterification bonding between guanines and adenines from the 5' end and the branch point, respectively, to form a looped lariat structure.

[00037] **CDR:** As used herein, the term "CDR" refers to the complementarity determining region within antibody variable sequences. A typical antibody molecule comprises a heavy

chain variable region (VH) and a light chain variable region (VL), which are usually involved in antigen binding. The VH and VL regions can be further subdivided into regions of hypervariability, also known as "complementarity determining regions" ("CDR"), interspersed with regions that are more conserved, which are known as "framework regions" ("FR"). Each VH and VL is typically composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. The extent of the framework region and CDRs can be precisely identified using methodology known in the art, for example, by the Kabat definition, the IMGT definition, the Chothia definition, the AbM definition, and/or (e.g., and) the contact definition, all of which are well known in the art. See, e.g., Kabat, E.A., et al. (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242; IMGT®, the international ImMunoGeneTics information system® www.imgt.org, Lefranc, M.-P. et al., Nucleic Acids Res., 27:209-212 (1999); Ruiz, M. et al., Nucleic Acids Res., 28:219-221 (2000); Lefranc, M.-P., Nucleic Acids Res., 29:207-209 (2001); Lefranc, M.-P., Nucleic Acids Res., 31:307-310 (2003); Lefranc, M.-P. et al., In Silico Biol., 5, 0006 (2004) [Epub], 5:45-60 (2005); Lefranc, M.-P. et al., Nucleic Acids Res., 33:D593-597 (2005); Lefranc, M.-P. et al., Nucleic Acids Res., 37:D1006-1012 (2009); Lefranc, M.-P. et al., Nucleic Acids Res., 43:D413-422 (2015); Chothia et al., (1989) Nature 342:877; Chothia, C. et al. (1987) J. Mol. Biol. 196:901-917, Al-lazikani et al (1997) J. Molec. Biol. 273:927-948; and Almagro, J. Mol. Recognit. 17:132-143 (2004). See also bioinf.org.uk/abs. As used herein, a CDR may refer to the CDR defined by any method known in the art. Two antibodies having the same CDR means that the two antibodies have the same amino acid sequence of that CDR as determined by the same method, for example, the IMGT definition.

[00038] There are three CDRs in each of the variable regions of the heavy chain and the light chain, which are designated CDR1, CDR2 and CDR3, for each of the variable regions. The term "CDR set" as used herein refers to a group of three CDRs that occur in a single variable region capable of binding the antigen. The exact boundaries of these CDRs have been defined differently according to different systems. The system described by Kabat (Kabat *et al.,* Sequences of Proteins of Immunological Interest (National Institutes of Health, Bethesda, Md. (1987) and (1991)) not only provides an unambiguous residue numbering system applicable to any variable region of an antibody, but also provides precise residue boundaries defining the three CDRs. These CDRs may be referred to as Kabat CDRs. Sub-portions of CDRs may be designated as L1, L2 and L3 or H1, H2 and H3 where the "L" and the "H" designates the light chain and the heavy chains regions, respectively. These regions may be referred to as Chothia CDRs, which have boundaries that overlap with Kabat CDRs. Other boundaries defining CDRs

overlapping with the Kabat CDRs have been described by Padlan (FASEB J. 9:133-139 (1995)) and MacCallum (J Mol Biol 262(5):732-45 (1996)). Still other CDR boundary definitions may not strictly follow one of the above systems, but will nonetheless overlap with the Kabat CDRs, although they may be shortened or lengthened in light of prediction or experimental findings that particular residues or groups of residues or even entire CDRs do not significantly impact antigen binding. The methods used herein may utilize CDRs defined according to any of these systems. Examples of CDR definition systems are provided in Table 1.

Table 1. CDR Definitions

	IMGT[1]	Kabat[2]	Chothia[3]
CDR-H1	27-38	31-35	26-32
CDR-H2	56-65	50-65	53-55
CDR-H3	105-116/117	95-102	96-101
CDR-L1	27-38	24-34	26-32
CDR-L2	56-65	50-56	50-52
CDR-L3	105-116/117	89-97	91-96

[1] IMGT®, the international ImMunoGeneTics information system®, imgt.org, Lefranc, M.-P. et al., Nucleic Acids Res., 27:209-212 (1999)
[2] Kabat et al. (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242
[3] Chothia et al., J. Mol. Biol. 196:901-917 (1987))

[00039] **CDR-grafted antibody:** The term "CDR-grafted antibody" refers to antibodies which comprise heavy and light chain variable region sequences from one species but in which the sequences of one or more of the CDR regions of VH and/or (e.g., and) VL are replaced with CDR sequences of another species, such as antibodies having murine heavy and light chain variable regions in which one or more of the murine CDRs (*e.g.*, CDR3) has been replaced with human CDR sequences.

[00040] **Chimeric antibody:** The term "chimeric antibody" refers to antibodies which comprise heavy and light chain variable region sequences from one species and constant region sequences from another species, such as antibodies having murine heavy and light chain variable regions linked to human constant regions.

[00041] **Complementary:** As used herein, the term "complementary" refers to the capacity for precise pairing between two nucleosides or two sets of nucleosides. In particular, complementary is a term that characterizes an extent of hydrogen bond pairing that brings about binding between two nucleosides or two sets of nucleosides. For example, if a base at one position of an oligonucleotide is capable of hydrogen bonding with a base at the corresponding position of a target nucleic acid (e.g., an mRNA), then the bases are considered to be complementary to each other at that position. Base pairings may include both canonical Watson-Crick base pairing and non-Watson-Crick base pairing (e.g., Wobble base pairing and Hoogsteen base pairing). For example, in some embodiments, for complementary base pairings,

adenosine-type bases (A) are complementary to thymidine-type bases (T) or uracil-type bases (U), that cytosine-type bases (C) are complementary to guanosine-type bases (G), and that universal bases such as 3-nitropyrrole or 5-nitroindole can hybridize to and are considered complementary to any A, C, U, or T. Inosine (I) has also been considered in the art to be a universal base and is considered complementary to any A, C, U or T.

[00042] **Conservative amino acid substitution:** As used herein, a "conservative amino acid substitution" refers to an amino acid substitution that does not alter the relative charge or size characteristics of the protein in which the amino acid substitution is made. Variants can be prepared according to methods for altering polypeptide sequence known to one of ordinary skill in the art such as are found in references which compile such methods, e.g. Molecular Cloning: A Laboratory Manual, J. Sambrook, et al., eds., Fourth Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 2012, or Current Protocols in Molecular Biology, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. Conservative substitutions of amino acids include substitutions made amongst amino acids within the following groups: (a) M, I, L, V; (b) F, Y, W; (c) K, R, H; (d) A, G; (e) S, T; (f) Q, N; and (g) E, D.

[00043] **Covalently linked:** As used herein, the term "covalently linked" refers to a characteristic of two or more molecules being linked together via at least one covalent bond. In some embodiments, two molecules can be covalently linked together by a single bond, e.g., a disulfide bond or disulfide bridge, that serves as a linker between the molecules. However, in some embodiments, two or more molecules can be covalently linked together via a molecule that serves as a linker that joins the two or more molecules together through multiple covalent bonds. In some embodiments, a linker may be a cleavable linker. However, in some embodiments, a linker may be a non-cleavable linker.

[00044] **Cross-reactive:** As used herein and in the context of a targeting agent (e.g., antibody), the term "cross-reactive," refers to a property of the agent being capable of specifically binding to more than one antigen of a similar type or class (e.g., antigens of multiple homologs, paralogs, or orthologs) with similar affinity or avidity. For example, in some embodiments, an antibody that is cross-reactive against human and non-human primate antigens of a similar type or class (e.g., a human transferrin receptor and non-human primate transferrin receptor) is capable of binding to the human antigen and non-human primate antigens with a similar affinity or avidity. In some embodiments, an antibody is cross-reactive against a human antigen and a rodent antigen of a similar type or class. In some embodiments, an antibody is cross-reactive against a rodent antigen and a non-human primate antigen of a similar type or class. In some embodiments, an antibody is cross-reactive against a human antigen, a non-human primate antigen, and a rodent antigen of a similar type or class.

[00045] **DMD:** As used herein, the term "DMD" refers to a gene that encodes dystrophin protein, a key component of the dystrophin-glycoprotein complex, which bridges the inner cytoskeleton and the extracellular matrix in muscle cells, particularly muscle fibers. Deletions, duplications, and point mutations in DMD may cause dystrophinopathies, such as Duchenne muscular dystrophy, Becker muscular dystrophy, or cardiomyopathy. Alternative promoter usage and alternative splicing result in numerous distinct transcript variants and protein isoforms for this gene. In some embodiments, a dystrophin gene (DMD or DMD gene) may be a human (Gene ID: 1756), non-human primate (e.g., Gene ID: 465559), or rodent gene (e.g., Gene ID: 13405; Gene ID: 24907). In addition, multiple human transcript variants (e.g., as annotated under GenBank RefSeq Accession Numbers: NM_000109.3, NM_004006.2, NM_004009.3, NM_004010.3 and NM_004011.3) have been characterized that encode different protein isoforms.

[00046] **DMD allele:** As used herein, the term "DMD allele" refers to any one of alternative forms (e.g., wild-type or mutant forms) of a DMD gene. In some embodiments, a DMD allele may encode for dystrophin that retains its normal and typical functions. In some embodiments, a DMD allele may comprise one or more mutations that results in muscular dystrophy. Common mutations that lead to Duchenne muscular dystrophy involve frameshift, deletion, substitution, and duplicative mutations of one or more of 79 exons present in a dystrophin allele, *e.g.*, exon 8, exon 23, exon 41, exon 44, exon 45, exon 50, exon 51, exon 52, exon 53, or exon 55. Further examples of DMD mutations are disclosed, for example, in Flanigan KM, et al., *Mutational spectrum of DMD mutations in dystrophinopathy patients: application of modern diagnostic techniques to a large cohort.* Hum Mutat. 2009 Dec; 30 (12):1657-66, the contents of which are incorporated herein by reference in its entirety.

[00047] **Dystrophinopathy:** As used herein, the term "dystrophinopathy" refers to a muscle disease results from one or more mutated DMD alleles. Dystrophinopathies include a spectrum of conditions (ranging from mild to severe) that includes Duchenne muscular dystrophy, Becker muscular dystrophy, and DMD-associated dilated cardiomyopathy (DCM). In some embodiments, at one end of the spectrum, dystrophinopathy is phenotypically associated with an asymptomatic increase in serum concentration of creatine phosphokinase (CK) and/or (e.g., and) muscle cramps with myoglobinuria. In some embodiments, at the other end of the spectrum, dystrophinopathy is phenotypically associated with progressive muscle diseases that are generally classified as Duchenne or Becker muscular dystrophy when skeletal muscle is primarily affected and as DMD-associated dilated cardiomyopathy (DCM) when the heart is primarily affected. Symptoms of Duchenne muscular dystrophy include muscle loss or degeneration, diminished muscle function, pseudohypertrophy of the tongue and calf muscles,

higher risk of neurological abnormalities, and a shortened lifespan. Duchenne muscular dystrophy is associated with Online Mendelian Inheritance in Man (OMIM) Entry # 310200. Becker muscular dystrophy is associated with OMIM Entry # 300376. Dilated cardiomyopathy is associated with OMIM Entry X# 302045.

[00048] Exonic splicing enhancer (ESE): As used herein, the term "exonic splicing enhancer" or "ESE" refers to a nucleic acid sequence motif within an exon of a gene, pre-mRNA, or mRNA that directs or enhances splicing of pre-mRNA into mRNA, e.g., as described in Blencowe et al., Trends Biochem Sci 25, 106-10. (2000), incorporated herein by reference. ESEs can be referred to as splicing features. ESEs may direct or enhance splicing, for example, to remove one or more introns and/or one or more exons from a gene transcript. ESE motifs are typically 6-8 nucleobases in length. SR proteins (e.g., proteins encoded by the gene SRSF1, SRSF2, SRSF3, SRSF4, SRSF5, SRSF6, SRSF7, SRSF8, SRSF9, SRSF10, SRSF11, SRSF12, TRA2A or TRA2B) bind to ESEs through their RNA recognition motif region to facilitate splicing. ESE motifs can be identified through a number of methods, including those described in Cartegni et al., Nucleic Acids Research, 2003, Vol. 31, No. 13, 3568–3571, incorporated herein by reference.

[00049] Framework: As used herein, the term "framework" or "framework sequence" refers to the remaining sequences of a variable region minus the CDRs. Because the exact definition of a CDR sequence can be determined by different systems, the meaning of a framework sequence is subject to correspondingly different interpretations. The six CDRs (CDR-L1, CDR-L2, and CDR-L3 of light chain and CDR-H1, CDR-H2, and CDR-H3 of heavy chain) also divide the framework regions on the light chain and the heavy chain into four sub-regions (FR1, FR2, FR3 and FR4) on each chain, in which CDR1 is positioned between FR1 and FR2, CDR2 between FR2 and FR3, and CDR3 between FR3 and FR4. Without specifying the particular sub-regions as FR1, FR2, FR3 or FR4, a framework region, as referred by others, represents the combined FRs within the variable region of a single, naturally occurring immunoglobulin chain. As used herein, a FR represents one of the four sub-regions, and FRs represents two or more of the four sub-regions constituting a framework region. Human heavy chain and light chain acceptor sequences are known in the art. In one embodiment, the acceptor sequences known in the art may be used in the antibodies disclosed herein.

[00050] Human antibody: The term "human antibody", as used herein, is intended to include antibodies having variable and constant regions derived from human germline immunoglobulin sequences. The human antibodies of the disclosure may include amino acid residues not encoded by human germline immunoglobulin sequences (*e.g.*, mutations introduced by random or site-specific mutagenesis in vitro or by somatic mutation *in vivo*), for example in

the CDRs and in particular CDR3. However, the term "human antibody", as used herein, is not intended to include antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences.

[00051] **Humanized antibody:** The term "humanized antibody" refers to antibodies which comprise heavy and light chain variable region sequences from a non-human species (*e.g.,* a mouse) but in which at least a portion of the VH and/or (e.g., and) VL sequence has been altered to be more "human-like", *i.e.,* more similar to human germline variable sequences. One type of humanized antibody is a CDR-grafted antibody, in which human CDR sequences are introduced into non-human VH and VL sequences to replace the corresponding non-human CDR sequences. In one embodiment, humanized anti-TfR1 antibodies and antigen binding portions are provided. Such antibodies may be generated by obtaining murine anti-TfR1 monoclonal antibodies using traditional hybridoma technology followed by humanization using *in vitro* genetic engineering, such as those disclosed in Kasaian et al PCT publication No. WO 2005/123126 A2.

[00052] **Internalizing cell surface receptor:** As used herein, the term, "internalizing cell surface receptor" refers to a cell surface receptor that is internalized by cells, e.g., upon external stimulation, e.g., ligand binding to the receptor. In some embodiments, an internalizing cell surface receptor is internalized by endocytosis. In some embodiments, an internalizing cell surface receptor is internalized by clathrin-mediated endocytosis. However, in some embodiments, an internalizing cell surface receptor is internalized by a clathrin-independent pathway, such as, for example, phagocytosis, macropinocytosis, caveolae- and raft-mediated uptake or constitutive clathrin-independent endocytosis. In some embodiments, the internalizing cell surface receptor comprises an intracellular domain, a transmembrane domain, and/or (e.g., and) an extracellular domain, which may optionally further comprise a ligand-binding domain. In some embodiments, a cell surface receptor becomes internalized by a cell after ligand binding. In some embodiments, a ligand may be a muscle-targeting agent or a muscle-targeting antibody. In some embodiments, an internalizing cell surface receptor is a transferrin receptor.

[00053] **Isolated antibody:** An "isolated antibody", as used herein, is intended to refer to an antibody that is substantially free of other antibodies having different antigenic specificities (*e.g.*, an isolated antibody that specifically binds transferrin receptor is substantially free of antibodies that specifically bind antigens other than transferrin receptor). An isolated antibody that specifically binds transferrin receptor complex may, however, have cross-reactivity to other antigens, such as transferrin receptor molecules from other species. Moreover, an isolated antibody may be substantially free of other cellular material and/or (e.g., and) chemicals.

[00054] **Kabat numbering:** The terms "Kabat numbering", "Kabat definitions and "Kabat labeling" are used interchangeably herein. These terms, which are recognized in the art, refer to a system of numbering amino acid residues which are more variable (i.e. hypervariable) than other amino acid residues in the heavy and light chain variable regions of an antibody, or an antigen binding portion thereof (Kabat et al. (1971) Ann. NY Acad. Sci. 190:382-391 and, Kabat, E. A., *et al.* (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242). For the heavy chain variable region, the hypervariable region ranges from amino acid positions 31 to 35 for CDR1, amino acid positions 50 to 65 for CDR2, and amino acid positions 95 to 102 for CDR3. For the light chain variable region, the hypervariable region ranges from amino acid positions 24 to 34 for CDR1, amino acid positions 50 to 56 for CDR2, and amino acid positions 89 to 97 for CDR3.

[00055] **Molecular payload:** As used herein, the term "molecular payload" refers to a molecule or species that functions to modulate a biological outcome. In some embodiments, a molecular payload is linked to, or otherwise associated with a muscle-targeting agent. In some embodiments, the molecular payload is a small molecule, a protein, a peptide, a nucleic acid, or an oligonucleotide. In some embodiments, the molecular payload functions to modulate the transcription of a DNA sequence, to modulate the expression of a protein, or to modulate the activity of a protein. In some embodiments, the molecular payload is an oligonucleotide that comprises a strand having a region of complementarity to a target gene.

[00056] **Muscle-targeting agent:** As used herein, the term, "muscle-targeting agent," refers to a molecule that specifically binds to an antigen expressed on muscle cells. The antigen in or on muscle cells may be a membrane protein, for example an integral membrane protein or a peripheral membrane protein. Typically, a muscle-targeting agent specifically binds to an antigen on muscle cells that facilitates internalization of the muscle-targeting agent (and any associated molecular payload) into the muscle cells. In some embodiments, a muscle-targeting agent specifically binds to an internalizing, cell surface receptor on muscles and is capable of being internalized into muscle cells through receptor mediated internalization. In some embodiments, the muscle-targeting agent is a small molecule, a protein, a peptide, a nucleic acid (*e.g.*, an aptamer), or an antibody. In some embodiments, the muscle-targeting agent is linked to a molecular payload.

[00057] **Muscle-targeting antibody:** As used herein, the term, "muscle-targeting antibody," refers to a muscle-targeting agent that is an antibody that specifically binds to an antigen found in or on muscle cells. In some embodiments, a muscle-targeting antibody specifically binds to an antigen on muscle cells that facilitates internalization of the muscle-

targeting antibody (and any associated molecular payment) into the muscle cells. In some embodiments, the muscle-targeting antibody specifically binds to an internalizing, cell surface receptor present on muscle cells. In some embodiments, the muscle-targeting antibody is an antibody that specifically binds to a transferrin receptor.

[00058] **Oligonucleotide:** As used herein, the term "oligonucleotide" refers to an oligomeric nucleic acid compound of up to 200 nucleotides in length. Examples of oligonucleotides include, but are not limited to, RNAi oligonucleotides (e.g., siRNAs, shRNAs), microRNAs, gapmers, mixmers, phosphorodiamidate morpholinos, peptide nucleic acids, aptamers, guide nucleic acids (e.g., Cas9 guide RNAs), etc. Oligonucleotides may be single-stranded or double-stranded. In some embodiments, an oligonucleotide may comprise one or more modified nucleosides (e.g., 2′-O-methyl sugar modifications, purine or pyrimidine modifications). In some embodiments, an oligonucleotide may comprise one or more modified internucleoside linkages. In some embodiments, an oligonucleotide may comprise one or more phosphorothioate linkages, which may be in the Rp or Sp stereochemical conformation.

[00059] **Recombinant antibody:** The term "recombinant human antibody", as used herein, is intended to include all human antibodies that are prepared, expressed, created or isolated by recombinant means, such as antibodies expressed using a recombinant expression vector transfected into a host cell (described in more details in this disclosure), antibodies isolated from a recombinant, combinatorial human antibody library (Hoogenboom H. R., (1997) TIB Tech. 15:62-70; Azzazy H., and Highsmith W. E., (2002) Clin. Biochem. 35:425-445; Gavilondo J. V., and Larrick J. W. (2002) BioTechniques 29:128-145; Hoogenboom H., and Chames P. (2000) Immunology Today 21:371-378), antibodies isolated from an animal (*e.g.*, a mouse) that is transgenic for human immunoglobulin genes (see e.g., Taylor, L. D., et al. (1992) Nucl. Acids Res. 20:6287-6295; Kellermann S-A., and Green L. L. (2002) Current Opinion in Biotechnology 13:593-597; Little M. et al (2000) Immunology Today 21:364-370) or antibodies prepared, expressed, created or isolated by any other means that involves splicing of human immunoglobulin gene sequences to other DNA sequences. Such recombinant human antibodies have variable and constant regions derived from human germline immunoglobulin sequences. In certain embodiments, however, such recombinant human antibodies are subjected to in vitro mutagenesis (or, when an animal transgenic for human Ig sequences is used, *in vivo* somatic mutagenesis) and thus the amino acid sequences of the VH and VL regions of the recombinant antibodies are sequences that, while derived from and related to human germline VH and VL sequences, may not naturally exist within the human antibody germline repertoire in vivo. One embodiment of the disclosure provides fully human antibodies capable of binding human transferrin receptor which can be generated using techniques well known in the art, such as, but

not limited to, using human Ig phage libraries such as those disclosed in Jermutus et al., PCT publication No. WO 2005/007699 A2.

[00060] **Region of complementarity:** As used herein, the term "region of complementarity" refers to a nucleotide sequence, e.g., of an oligonucleotide, that is sufficiently complementary to a cognate nucleotide sequence, e.g., of a target nucleic acid, such that the two nucleotide sequences are capable of annealing to one another under physiological conditions (e.g., in a cell). In some embodiments, a region of complementarity is fully complementary to a cognate nucleotide sequence of target nucleic acid. However, in some embodiments, a region of complementarity is partially complementary to a cognate nucleotide sequence of target nucleic acid (e.g., at least 80%, 90%, 95% or 99% complementarity). In some embodiments, a region of complementarity contains 1, 2, 3, or 4 mismatches compared with a cognate nucleotide sequence of a target nucleic acid.

[00061] **Specifically binds:** As used herein, the term "specifically binds" refers to the ability of a molecule to bind to a binding partner with a degree of affinity or avidity that enables the molecule to be used to distinguish the binding partner from an appropriate control in a binding assay or other binding context. With respect to an antibody, the term, "specifically binds", refers to the ability of the antibody to bind to a specific antigen with a degree of affinity or avidity, compared with an appropriate reference antigen or antigens, that enables the antibody to be used to distinguish the specific antigen from others, e.g., to an extent that permits preferential targeting to certain cells, e.g., muscle cells, through binding to the antigen, as described herein. In some embodiments, an antibody specifically binds to a target if the antibody has a K_D for binding the target of at least about 10^{-4} M, 10^{-5} M, 10^{-6} M, 10^{-7} M, 10^{-8} M, 10^{-9} M, 10^{-10} M, 10^{-11} M, 10^{-12} M, 10^{-13} M, or less. In some embodiments, an antibody specifically binds to the transferrin receptor, e.g., an epitope of the apical domain of transferrin receptor.

[00062] **Splice acceptor site:** As used herein, the term "splice acceptor site" or "splice acceptor" refers to a nucleic acid sequence motif at the 3' end of an intron or across an intron/exon junction of a gene or pre-mRNA that is involved in splicing of pre-mRNA into mRNA (*i.e.*, removing introns from the pre-mRNA), and can be referred to as a splicing feature. A splice acceptor site includes a terminal AG sequence at the 3' end of an intron, which is typically preceded (5'-ward) by a region high in pyrimidines (C/U). Upstream from the splice acceptor site is the branch point. Formation of a lariat loop intermediate structure by a transesterification reaction between the branch point and the splice donor site releases a 3'-OH of the 5' exon, which subsequently reacts with the first nucleotide of the 3' exon, thereby joining the exons and releasing the intron lariat. The AG sequence at the 3' end of the intron in the

splice acceptor site is known to be critical for proper splicing, as changing one of these nucleotides results in inhibition of splicing. Rarely, alternative splice acceptor sites have an AC at the 3' end of the intron, instead of the more common AG. A common splice acceptor site motif has a sequence of or similar to [Y-rich region]-NCAGG or Y_xNYAGG, in which Y represents a pyrimidine, N represents any nucleotide, and x is a number from 4 to 20. The cut site follows the AG, which represent the 3'-terminal nucleotides of the excised intron.

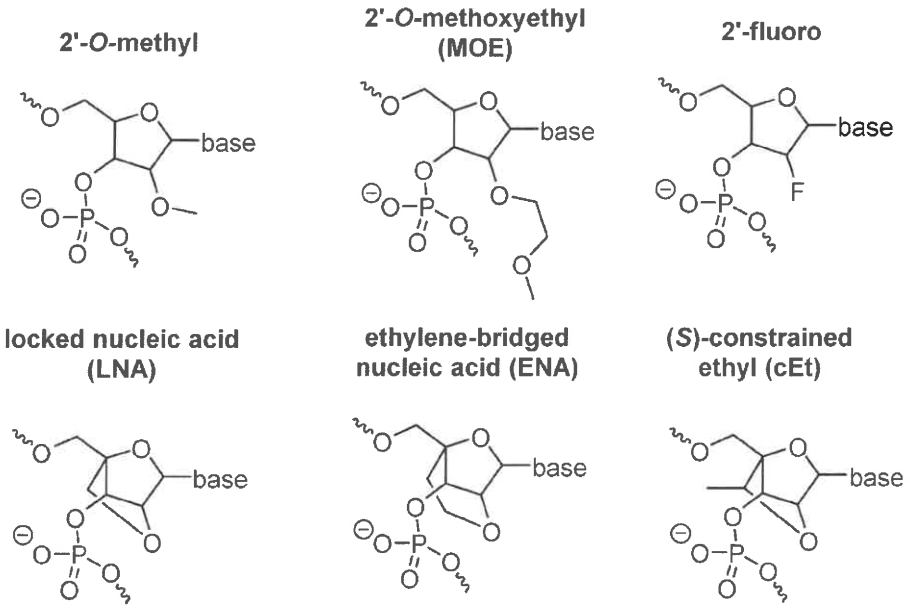
[00063] **Splice donor site:** As used herein, the term "splice donor site" or "splice donor" refers to a nucleic acid sequence motif at the 5' end of an intron or across an exon/intron junction of a gene or pre-mRNA that is involved in splicing of pre-mRNA into mRNA (*i.e.*, removing introns from the pre-mRNA), and can be referred to as a splicing feature. A splice donor site includes a terminal GU sequence at the 5' end of the intron, within a larger and fairly unconstrained sequence. During splicing, the 2'-OH of a nucleotide within the branch point initiates a transesterification reaction via a nucleophilic attack on the 5' G of the intron within the splice donor site. The G is thereby cleaved from the pre-mRNA and bonds instead to the branch point nucleotide, forming a loop lariat structure. The 3' nucleotide of the upstream exon subsequently binds the splice acceptor site, joining the exons and excising the intron. A typical splice donor site has a sequence of or similar to GGGURAGU or AGGURNG, in which R represents a purine and N represents any nucleotide. The cut site precedes the first GU (*i.e.*, GG/GURAGU or AG/GURNG), which represent the 5'-terminal nucleotides of the excised intron.

[00064] **Subject:** As used herein, the term "subject" refers to a mammal. In some embodiments, a subject is non-human primate, or rodent. In some embodiments, a subject is a human. In some embodiments, a subject is a patient, e.g., a human patient that has or is suspected of having a disease. In some embodiments, the subject is a human patient who has or is suspected of having a disease resulting from a mutated DMD gene sequence, e.g., a mutation in an exon of a DMD gene sequence. In some embodiments, a subject has a dystrophinopathy, e.g., Duchenne muscular dystrophy. In some embodiments, a subject is a patient that has a mutation of the DMD gene that is amenable to exon 55 skipping.

[00065] **Transferrin receptor:** As used herein, the term, "transferrin receptor" (also known as TFRC, CD71, p90, or TFR1) refers to an internalizing cell surface receptor that binds transferrin to facilitate iron uptake by endocytosis. In some embodiments, a transferrin receptor may be of human (NCBI Gene ID 7037), non-human primate (e.g., NCBI Gene ID 711568 or NCBI Gene ID 102136007), or rodent (e.g., NCBI Gene ID 22042) origin. In addition, multiple human transcript variants have been characterized that encoded different isoforms of the

receptor (e.g., as annotated under GenBank RefSeq Accession Numbers: NP_001121620.1, NP_003225.2, NP_001300894.1, and NP_001300895.1).

[00066] **2'-modified nucleoside**: As used herein, the terms "2'-modified nucleoside" and "2'-modified ribonucleoside" are used interchangeably and refer to a nucleoside having a sugar moiety modified at the 2' position. In some embodiments, the 2'-modified nucleoside is a 2'-4' bicyclic nucleoside, where the 2' and 4' positions of the sugar are bridged (e.g., via a methylene, an ethylene, or a (S)-constrained ethyl bridge). In some embodiments, the 2'-modified nucleoside is a non-bicyclic 2'-modified nucleoside, e.g., where the 2' position of the sugar moiety is substituted. Non-limiting examples of 2'-modified nucleosides include: 2'-deoxy, 2'-fluoro (2'-F), 2'-O-methyl (2'-O-Me), 2'-O-methoxyethyl (2'-MOE), 2'-O-aminopropyl (2'-O-AP), 2'-O-dimethylaminoethyl (2'-O-DMAOE), 2'-O-dimethylaminopropyl (2'-O-DMAP), 2'-O-dimethylaminoethyloxyethyl (2'-O-DMAEOE), 2'-O-N-methylacetamido (2'-O-NMA), locked nucleic acid (LNA, methylene-bridged nucleic acid), ethylene-bridged nucleic acid (ENA), and (S)-constrained ethyl-bridged nucleic acid (cEt). In some embodiments, the 2'-modified nucleosides described herein are high-affinity modified nucleosides and oligonucleotides comprising the 2'-modified nucleosides have increased affinity to a target sequences, relative to an unmodified oligonucleotide. Examples of structures of 2'-modified nucleosides are provided below:



These examples are shown with phosphate groups, but any internucleoside linkages are contemplated between 2'-modified nucleosides.

II. Complexes

[00067] Provided herein are complexes that comprise a targeting agent, e.g. an antibody, covalently linked to a molecular payload. In some embodiments, a complex comprises a muscle-targeting antibody covalently linked to an oligonucleotide. A complex may comprise an antibody that specifically binds a single antigenic site or that binds to at least two antigenic sites that may exist on the same or different antigens.

[00068] A complex may be used to modulate the activity or function of at least one gene, protein, and/or (e.g., and) nucleic acid. In some embodiments, the molecular payload present within a complex is responsible for the modulation of a gene, protein, and/or (e.g., and) nucleic acids. A molecular payload may be a small molecule, protein, nucleic acid, oligonucleotide, or any molecular entity capable of modulating the activity or function of a gene, protein, and/or (e.g., and) nucleic acid in a cell.

[00069] In some embodiments, a complex comprises a muscle-targeting agent, *e.g.*, an anti-transferrin receptor antibody, covalently linked to a molecular payload, *e.g.*, an antisense oligonucleotide that targets DMD to promote exon skipping, *e.g.*, in a transcript encoded from a mutated DMD allele. In some embodiments, the complex targets a DMD pre-mRNA to promote skipping of exon 55 in the DMD pre-mRNA.

A. Muscle-Targeting Agents

[00070] Some aspects of the disclosure provide muscle-targeting agents, *e.g.,* for delivering a molecular payload to a muscle cell. In some embodiments, such muscle-targeting agents are capable of binding to a muscle cell, *e.g.*, via specifically binding to an antigen on the muscle cell, and delivering an associated molecular payload to the muscle cell. In some embodiments, the molecular payload is bound (*e.g.,* covalently bound) to the muscle targeting agent and is internalized into the muscle cell upon binding of the muscle targeting agent to an antigen on the muscle cell, *e.g.,* via endocytosis. It should be appreciated that various types of muscle-targeting agents may be used in accordance with the disclosure, and that any muscle targets (*e.g.*, muscle surface proteins) can be targeted by any type of muscle-targeting agent described herein. For example, the muscle-targeting agent may comprise, or consist of, a small molecule, a nucleic acid (*e.g.,* DNA or RNA), a peptide (*e.g.,* an antibody), a lipid (*e.g.,* a microvesicle), or a sugar moiety (*e.g.,* a polysaccharide). Exemplary muscle-targeting agents are described in further detail herein, however, it should be appreciated that the exemplary muscle-targeting agents provided herein are not meant to be limiting.

[00071] Some aspects of the disclosure provide muscle-targeting agents that specifically bind to an antigen on muscle, such as skeletal muscle, smooth muscle, or cardiac muscle. In some embodiments, any of the muscle-targeting agents provided herein bind to (*e.g.,* specifically

bind to) an antigen on a skeletal muscle cell, a smooth muscle cell, and/or (e.g., and) a cardiac muscle cell.

[00072] By interacting with muscle-specific cell surface recognition elements (*e.g.,* cell membrane proteins), both tissue localization and selective uptake into muscle cells can be achieved. In some embodiments, molecules that are substrates for muscle uptake transporters are useful for delivering a molecular payload into muscle tissue. Binding to muscle surface recognition elements followed by endocytosis can allow even large molecules such as antibodies to enter muscle cells. As another example molecular payloads conjugated to transferrin or anti-TfR1 antibodies can be taken up by muscle cells via binding to transferrin receptor, which may then be endocytosed, *e.g.,* via clathrin-mediated endocytosis.

[00073] The use of muscle-targeting agents may be useful for concentrating a molecular payload (*e.g.,* oligonucleotide) in muscle while reducing toxicity associated with effects in other tissues. In some embodiments, the muscle-targeting agent concentrates a bound molecular payload in muscle cells as compared to another cell type within a subject. In some embodiments, the muscle-targeting agent concentrates a bound molecular payload in muscle cells (*e.g.*, skeletal, smooth, or cardiac muscle cells) in an amount that is at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, or 100 times greater than an amount in non-muscle cells (*e.g.,* liver, neuronal, blood, or fat cells). In some embodiments, a toxicity of the molecular payload in a subject is reduced by at least 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 90%, or 95% when it is delivered to the subject when bound to the muscle-targeting agent.

[00074] In some embodiments, to achieve muscle selectivity, a muscle recognition element (*e.g.,* a muscle cell antigen) may be required. As one example, a muscle-targeting agent may be a small molecule that is a substrate for a muscle-specific uptake transporter. As another example, a muscle-targeting agent may be an antibody that enters a muscle cell via transporter-mediated endocytosis. As another example, a muscle targeting agent may be a ligand that binds to cell surface receptor on a muscle cell. It should be appreciated that while transporter-based approaches provide a direct path for cellular entry, receptor-based targeting may involve stimulated endocytosis to reach the desired site of action.

i. Muscle-Targeting Antibodies

[00075] In some embodiments, the muscle-targeting agent is an antibody. Generally, the high specificity of antibodies for their target antigen provides the potential for selectively targeting muscle cells (*e.g.,* skeletal, smooth, and/or (e.g., and) cardiac muscle cells). This specificity may also limit off-target toxicity. Examples of antibodies that are capable of targeting a surface antigen of muscle cells have been reported and are within the scope of the

disclosure. For example, antibodies that target the surface of muscle cells are described in Arahata K., et al. "Immunostaining of skeletal and cardiac muscle surface membrane with antibody against Duchenne muscular dystrophy peptide" *Nature* 1988; 333: 861-3; Song K.S., et al. "Expression of caveolin-3 in skeletal, cardiac, and smooth muscle cells. Caveolin-3 is a component of the sarcolemma and co-fractionates with dystrophin and dystrophin-associated glycoproteins" *J Biol Chem* 1996; 271: 15160-5; and Weisbart R.H. et al., "Cell type specific targeted intracellular delivery into muscle of a monoclonal antibody that binds myosin IIb" *Mol Immunol.* 2003 Mar, 39(13):78309; the entire contents of each of which are incorporated herein by reference.

a. Anti-Transferrin Receptor (TfR) Antibodies

[00076] Some aspects of the disclosure are based on the recognition that agents binding to transferrin receptor, e.g., anti-transferrin-receptor antibodies, are capable of targeting muscle cell. Transferrin receptors are internalizing cell surface receptors that transport transferrin across the cellular membrane and participate in the regulation and homeostasis of intracellular iron levels. Some aspects of the disclosure provide transferrin receptor binding proteins, which are capable of binding to transferrin receptor. Accordingly, aspects of the disclosure provide binding proteins (*e.g.,* antibodies) that bind to transferrin receptor. In some embodiments, binding proteins that bind to transferrin receptor are internalized, along with any bound molecular payload, into a muscle cell. As used herein, an antibody that binds to a transferrin receptor may be referred to interchangeably as an, transferrin receptor antibody, an anti-transferrin receptor antibody, or an anti-TfR1 antibody. Antibodies that bind, e.g. specifically bind, to a transferrin receptor may be internalized into the cell, e.g. through receptor-mediated endocytosis, upon binding to a transferrin receptor.

[00077] It should be appreciated that anti-TfR1 antibodies may be produced, synthesized, and/or (e.g., and) derivatized using several known methodologies, e.g. library design using phage display. Exemplary methodologies have been characterized in the art and are incorporated by reference (Díez, P. et al. "High-throughput phage-display screening in array format", Enzyme and microbial technology, 2015, 79, 34-41.; Christoph M. H. and Stanley, J.R. "Antibody Phage Display: Technique and Applications" J Invest Dermatol. 2014, 134:2.; Engleman, Edgar (Ed.) "Human Hybridomas and Monoclonal Antibodies." 1985, Springer.). In other embodiments, an anti-TfR1 antibody has been previously characterized or disclosed. Antibodies that specifically bind to transferrin receptor are known in the art (see, e.g. US Patent. No. 4,364,934, filed 12/4/1979, "Monoclonal antibody to a human early thymocyte antigen and methods for preparing same"; US Patent No. 8,409,573, filed 6/14/2006, "Anti-CD71 monoclonal antibodies and uses thereof for treating malignant tumor cells"; US Patent No.

9,708,406, filed 5/20/2014, "Anti-transferrin receptor antibodies and methods of use"; US 9,611,323, filed 12/19/2014, "Low affinity blood brain barrier receptor antibodies and uses therefor"; WO 2015/098989, filed 12/24/2014, "Novel anti-Transferrin receptor antibody that passes through blood-brain barrier"; Schneider C. et al. "Structural features of the cell surface receptor for transferrin that is recognized by the monoclonal antibody OKT9." J Biol Chem. 1982, 257:14, 8516-8522.; Lee et al. "Targeting Rat Anti-Mouse Transferrin Receptor Monoclonal Antibodies through Blood-Brain Barrier in Mouse" 2000, J Pharmacol. Exp. Ther., 292: 1048-1052.).

[00078] In some embodiments, the anti-TfR1 antibody described herein binds to transferrin receptor with high specificity and affinity. In some embodiments, the anti-TfR1 antibody described herein specifically binds to any extracellular epitope of a transferrin receptor or an epitope that becomes exposed to an antibody. In some embodiments, anti-TfR1 antibodies provided herein bind specifically to transferrin receptor from human, non-human primates, mouse, rat, *etc*. In some embodiments, anti-TfR1 antibodies provided herein bind to human transferrin receptor. In some embodiments, the anti-TfR1 antibody described herein binds to an amino acid segment of a human or non-human primate transferrin receptor, as provided in SEQ ID NOs: 105-108. In some embodiments, the anti-TfR1 antibody described herein binds to an amino acid segment corresponding to amino acids 90-96 of a human transferrin receptor as set forth in SEQ ID NO: 105, which is not in the apical domain of the transferrin receptor.

[00079] In some embodiments, the anti-TfR1 antibodies described herein (e.g., Anti-TfR clone 8 in Table 2 below) bind an epitope in TfR1, wherein the epitope comprises residues in amino acids 214-241 and/or amino acids 354-381 of SEQ ID NO: 105. In some embodiments, the anti-TfR1 antibodies described herein bind an epitope comprising residues in amino acids 214-241 and amino acids 354-381 of SEQ ID NO: 105. In some embodiments, the anti-TfR1 antibodies described herein bind an epitope comprising one or more of residues Y222, T227, K231, H234, T367, S368, S370, T376, and S378 of human TfR1 as set forth in SEQ ID NO: 105. In some embodiments, the anti-TfR1 antibodies described herein bind an epitope comprising residues Y222, T227, K231, H234, T367, S368, S370, T376, and S378 of human TfR1 as set forth in SEQ ID NO: 105.

[00080] In some embodiments, the anti-TfR1 antibody described herein (e.g., 3M12 in Table 2 below and its variants) bind an epitope in TfR1, wherein the epitope comprises residues in amino acids 258-291 and/or amino acids 358-381 of SEQ ID NO: 105. In some embodiments, the anti-TfR1 antibodies (e.g., 3M12 in Table 2 below and its variants) described herein bind an epitope comprising residues in amino acids amino acids 258-291 and amino acids 358-381 of SEQ ID NO: 105. In some embodiments, the anti-TfR1 antibodies described herein

(e.g., 3M12 in Table 2 below and its variants) bind an epitope comprising one or more of residues K261, S273, Y282, T362, S368, S370, and K371 of human TfR1 as set forth in SEQ ID NO: 105. In some embodiments, the anti-TfR1 antibodies described herein (e.g., 3M12 in Table 2 below and its variants) bind an epitope comprising residues K261, S273, Y282, T362, S368, S370, and K371 of human TfR1 as set forth in SEQ ID NO: 105.

[00081] An example human transferrin receptor amino acid sequence, corresponding to NCBI sequence NP_003225.2 (transferrin receptor protein 1 isoform 1, homo sapiens) is as follows:

MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVT
KPKRCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPA
ARRLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREF
KLSKVWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLV
HANFGTKKDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNA
ELSFFGHAHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCP
SDWKTDSTCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAW
GPGAAKSGVGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGY
LSSLHLKAFTYINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWA
SKVEKLTLDNAAFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARA
AAEVAGQFVIKLTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARG
DFFRATSRLTTDFGNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSG
SHTLPALLENLKLRKQNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
(SEQ ID NO: 105).

[00082] An example non-human primate transferrin receptor amino acid sequence, corresponding to NCBI sequence NP_001244232.1(transferrin receptor protein 1, Macaca mulatta) is as follows:

MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLGVDEEENTDNNTKPNGT
KPKRCGGNICYGTIAVIIFFLIGFMIGYLGYCKGVEPKTECERLAGTESPAREEPEEDFPA
APRLYWDDLKRKLSEKLDTTDFTSTIKLLNENLYVPREAGSQKDENLALYIENQFREFK
LSKVWRDQHFVKIQVKDSAQNSVIIVDKNGGLVYLVENPGGYVAYSKAATVTGKLVH
ANFGTKKDFEDLDSPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVKAD
LSFFGHAHLGTGDPYTPGFPSFNHTQFPPSQSSGLPNIPVQTISRAAAEKLFGNMEGDCPS
DWKTDSTCKMVTSENKSVKLTVSNVLKETKILNIFGVIKGFVEPDHYVVVGAQRDAW
GPGAAKSSVGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGY
LSSLHLKAFTYINLDKAVLGTSNFKVSASPLLYTLIEKTMQDVKHPVTGRSLYQDSNWA
SKVEKLTLDNAAFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELVERIPELNKVAR

AAAEVAGQFVIKLTHDTELNLDYERYNSQLLLFLRDLNQYRADVKEMGLSLQWLYSA
RGDFFRATSRLTTDFRNAEKRDKFVMKKLNDRVMRVEYYFLSPYVSPKESPFRHVFWG
SGSHTLSALLESLKLRRQNNSAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
(SEQ ID NO: 106)

[00083] An example non-human primate transferrin receptor amino acid sequence, corresponding to NCBI sequence XP_005545315.1 (transferrin receptor protein 1, Macaca fascicularis) is as follows:

MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLGVDEEENTDNNTKANGT
KPKRCGGNICYGTIAVIIFFLIGFMIGYLGYCKGVEPKTECERLAGTESPAREEPEEDFPA
APRLYWDDLKRKLSEKLDTTDFTSTIKLLNENLYVPREAGSQKDENLALYIENQFREFK
LSKVWRDQHFVKIQVKDSAQNSVIIVDKNGGLVYLVENPGGYVAYSKAATVTGKLVH
ANFGTKKDFEDLDSPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVKAD
LSFFGHAHLGTGDPYTPGFPSFNHTQFPPSQSSGLPNIPVQTISRAAAEKLFGNMEGDCPS
DWKTDSTCKMVTSENKSVKLTVSNVLKETKILNIFGVIKGFVEPDHYVVVGAQRDAW
GPGAAKSSVGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGY
LSSLHLKAFTYINLDKAVLGTSNFKVSASPLLYTLIEKTMQDVKHPVTGRSLYQDSNWA
SKVEKLTLDNAAFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELVERIPELNKVAR
AAAEVAGQFVIKLTHDTELNLDYERYNSQLLLFLRDLNQYRADVKEMGLSLQWLYSA
RGDFFRATSRLTTDFRNAEKRDKFVMKKLNDRVMRVEYYFLSPYVSPKESPFRHVFWG
SGSHTLSALLESLKLRRQNNSAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
(SEQ ID NO: 107).

[00084] An example mouse transferrin receptor amino acid sequence, corresponding to NCBI sequence NP_001344227.1 (transferrin receptor protein 1, mus musculus) is as follows:

MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAADEEENADNNMKASV
RKPKRFNGRLCFAAIALVIFFLIGFMSGYLGYCKRVEQKEECVKLAETEETDKSETMETE
DVPTSSRLYWADLKTLLSEKLNSIEFADTIKQLSQNTYTPREAGSQKDESLAYYIENQFH
EFKFSKVWRDEHYVKIQVKSSIGQNMVTIVQSNGNLDPVESPEGYVAFSKPTEVSGKLV
HANFGTKKDFEELSYSVNGSLVIVRAGEITFAEKVANAQSFNAIGVLIYMDKNKFPVVE
ADLALFGHAHLGTGDPYTPGFPSFNHTQFPPSQSSGLPNIPVQTISRAAAEKLFGKMEGS
CPARWNIDSSCKLELSQNQNVKLIVKNVLKERRILNIFGVIKGYEEPDRYVVVGAQRDA
LGAGVAAKSSVGTGLLLKLAQVFSDMISKDGFRPSRSIIFASWTAGDFGAVGATEWLEG
YLSSLHLKAFTYINLDKVVLGTSNFKVSASPLLYTLMGKIMQDVKHPVDGKSLYRDSN
WISKVEKLSFDNAAYPFLAYSGIPAVSFCFCEDADYPYLGTRLDTYEALTQKVPQLNQM
VRTAAEVAGQLIIKLTHDVELNLDYEMYNSKLLSFMKDLNQFKTDIRDMGLSLQWLYS

ARGDYFRATSRLTTDFHNAEKTNRFVMREINDRIMKVEYHFLSPYVSPRESPFRHIFWG SGSHTLSALVENLKLRQKNITAFNETLFRNQLALATWTIQGVANALSGDIWNIDNEF (SEQ ID NO: 108)

[00085] In some embodiments, an anti-TfR1 antibody binds to an amino acid segment of the receptor as follows:

FVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKKDFE DLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHAHLG TGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDSTCR MVTSESKNVKLTVSNVLKE (SEQ ID NO: 109) and does not inhibit the binding interactions between transferrin receptors and transferrin and/or (e.g., and) human hemochromatosis protein (also known as HFE). In some embodiments, the anti-TfR1 antibody described herein does not bind an epitope in SEQ ID NO: 109.

[00086] Appropriate methodologies may be used to obtain and/or (e.g., and) produce antibodies, antibody fragments, or antigen-binding agents, e.g., through the use of recombinant DNA protocols. In some embodiments, an antibody may also be produced through the generation of hybridomas (see, e.g., Kohler, G and Milstein, C. "Continuous cultures of fused cells secreting antibody of predefined specificity" Nature, 1975, 256: 495-497). The antigen-of-interest may be used as the immunogen in any form or entity, e.g., recombinant or a naturally occurring form or entity. Hybridomas are screened using standard methods, e.g. ELISA screening, to find at least one hybridoma that produces an antibody that targets a particular antigen. Antibodies may also be produced through screening of protein expression libraries that express antibodies, e.g., phage display libraries. Phage display library design may also be used, in some embodiments, (see, e.g. U.S. Patent No 5,223,409, filed 3/1/1991, "Directed evolution of novel binding proteins"; WO 1992/18619, filed 4/10/1992, "Heterodimeric receptor libraries using phagemids"; WO 1991/17271, filed 5/1/1991, "Recombinant library screening methods"; WO 1992/20791, filed 5/15/1992, "Methods for producing members of specific binding pairs"; WO 1992/15679, filed 2/28/1992, and "Improved epitope displaying phage"). In some embodiments, an antigen-of-interest may be used to immunize a non-human animal, e.g., a rodent or a goat. In some embodiments, an antibody is then obtained from the non-human animal, and may be optionally modified using a number of methodologies, e.g., using recombinant DNA techniques. Additional examples of antibody production and methodologies are known in the art (see, e.g. Harlow et al. "Antibodies: A Laboratory Manual", Cold Spring Harbor Laboratory, 1988.).

[00087] In some embodiments, an antibody is modified, e.g., modified via glycosylation, phosphorylation, sumoylation, and/or (e.g., and) methylation. In some embodiments, an

antibody is a glycosylated antibody, which is conjugated to one or more sugar or carbohydrate molecules. In some embodiments, the one or more sugar or carbohydrate molecule are conjugated to the antibody via N-glycosylation, O-glycosylation, C-glycosylation, glypiation (GPI anchor attachment), and/or (e.g., and) phosphoglycosylation. In some embodiments, the one or more sugar or carbohydrate molecules are monosaccharides, disaccharides, oligosaccharides, or glycans. In some embodiments, the one or more sugar or carbohydrate molecule is a branched oligosaccharide or a branched glycan. In some embodiments, the one or more sugar or carbohydrate molecule includes a mannose unit, a glucose unit, an N-acetylglucosamine unit, an N-acetylgalactosamine unit, a galactose unit, a fucose unit, or a phospholipid unit. In some embodiments, there are about 1-10, about 1-5, about 5-10, about 1-4, about 1-3, or about 2 sugar molecules. In some embodiments, a glycosylated antibody is fully or partially glycosylated. In some embodiments, an antibody is glycosylated by chemical reactions or by enzymatic means. In some embodiments, an antibody is glycosylated in vitro or inside a cell, which may optionally be deficient in an enzyme in the N- or O- glycosylation pathway, e.g. a glycosyltransferase. In some embodiments, an antibody is functionalized with sugar or carbohydrate molecules as described in International Patent Application Publication WO2014065661, published on May 1, 2014, entitled, "*Modified antibody, antibody-conjugate and process for the preparation thereof*".

[00088] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a VL domain and/or (e.g., and) a VH domain of any one of the anti-TfR1 antibodies selected from any one of Tables 2-7, and comprises a constant region comprising the amino acid sequences of the constant regions of an IgG, IgE, IgM, IgD, IgA or IgY immunoglobulin molecule, any class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2), or any subclass (e.g., IgG2a and IgG2b) of immunoglobulin molecule. Non-limiting examples of human constant regions are described in the art, *e.g.*, see Kabat E A et al., (1991) supra.

[00089] In some embodiments, agents binding to transferrin receptor, e.g., anti-TfR1 antibodies, are capable of targeting muscle cell and/or (e.g., and) mediate the transportation of an agent across the blood brain barrier. Transferrin receptors are internalizing cell surface receptors that transport transferrin across the cellular membrane and participate in the regulation and homeostasis of intracellular iron levels. Some aspects of the disclosure provide transferrin receptor binding proteins, which are capable of binding to transferrin receptor. Antibodies that bind, e.g. specifically bind, to a transferrin receptor may be internalized into the cell, e.g. through receptor-mediated endocytosis, upon binding to a transferrin receptor.

[00090] Provided herein, in some aspects, are humanized antibodies that bind to transferrin receptor with high specificity and affinity. In some embodiments, the humanized

anti-TfR1 antibody described herein specifically binds to any extracellular epitope of a transferrin receptor or an epitope that becomes exposed to an antibody. In some embodiments, the humanized anti-TfR1 antibodies provided herein bind specifically to transferrin receptor from human, non-human primates, mouse, rat, *etc*. In some embodiments, the humanized anti-TfR1 antibodies provided herein bind to human transferrin receptor. In some embodiments, the humanized anti-TfR1 antibody described herein binds to an amino acid segment of a human or non-human primate transferrin receptor, as provided in SEQ ID NOs: 105-108. In some embodiments, the humanized anti-TfR1 antibody described herein binds to an amino acid segment corresponding to amino acids 90-96 of a human transferrin receptor as set forth in SEQ ID NO: 105, which is not in the apical domain of the transferrin receptor. In some embodiments, the humanized anti-TfR1 antibodies described herein binds to TfR1 but does not bind to TfR2.

[00091] In some embodiments, an anti-TFR1 antibody specifically binds a TfR1 (e.g., a human or non-human primate TfR1) with binding affinity (e.g., as indicated by Kd) of at least about 10^{-4} M, 10^{-5} M, 10^{-6} M, 10^{-7} M, 10^{-8} M, 10^{-9} M, 10^{-10} M, 10^{-11} M, 10^{-12} M, 10^{-13} M, or less. In some embodiments, the anti-TfR1 antibodies described herein bind to TfR1 with a KD of sub-nanomolar range. In some embodiments, the anti-TfR1 antibodies described herein selectively bind to transferrin receptor 1 (TfR1) but do not bind to transferrin receptor 2 (TfR2). In some embodiments, the anti-TfR1 antibodies described herein bind to human TfR1 and cyno TfR1 (e.g., with a Kd of 10^{-7} M, 10^{-8} M, 10^{-9} M, 10^{-10} M, 10^{-11} M, 10^{-12} M, 10^{-13} M, or less), but do not bind to a mouse TfR1. The affinity and binding kinetics of the anti-TfR1 antibody can be tested using any suitable method including but not limited to biosensor technology (e.g., OCTET or BIACORE). In some embodiments, binding of any one of the anti-TfR1 antibodies described herein does not complete with or inhibit transferrin binding to the TfR1. In some embodiments, binding of any one of the anti-TfR1 antibodies described herein does not complete with or inhibit HFE-beta-2-microglobulin binding to the TfR1.

[00092] Non-limiting examples of anti-TfR1 antibodies are provided in Table 2.

Table 2. Examples of Anti-TfR1 Antibodies

Ab	No. system	IMGT	Kabat	Chothia
3-A4	CDR-H1	GFNIKDDY (SEQ ID NO: 1)	DDYMY (SEQ ID NO: 7)	GFNIKDD (SEQ ID NO: 12)
	CDR-H2	IDPENGDT (SEQ ID NO: 2)	WIDPENGDTEYASKFQD (SEQ ID NO: 8)	ENG (SEQ ID NO: 13)
	CDR-H3	TLWLRRGLDY (SEQ ID NO: 3)	WLRRGLDY (SEQ ID NO: 9)	LRRGLD (SEQ ID NO: 14)
	CDR-L1	KSLLHSNGYTY (SEQ ID NO: 4)	RSSKSLLHSNGYTYLF (SEQ ID NO: 10)	SKSLLHSNGYTY (SEQ ID NO: 15)
	CDR-L2	RMS (SEQ ID NO: 5)	RMSNLAS (SEQ ID NO: 11)	RMS (SEQ ID NO: 5)

Ab	No. system	IMGT	Kabat	Chothia
	CDR-L3	MQHLEYPFT (SEQ ID NO: 6)	MQHLEYPFT (SEQ ID NO: 6)	HLEYPF (SEQ ID NO: 16)
	VH	EVQLQQSGAELVRPGASVKLSCTASGFNIKDDYMYWVKQRPEQGLEWIGWIDPENGDT EYASKFQDKATVTADTSSNTAYLQLSSLTSEDTAVYYCTLWLRRGLDYWGQGTSVTVS S (SEQ ID NO: 17)		
	VL	DIVMTQAAPSVPVTPGESVSISCRSSKSLLHSNGYTYLFWFLQRPGQSPQLLIYRMSNLA SGVPDRFSGSGSGTAFTLRISRVEAEDVGVYYCMQHLEYPFTFGGGTKLEIK (SEQ ID NO: 18)		
3-A4 N54T*	CDR-H1	GFNIKDDY (SEQ ID NO: 1)	DDYMY (SEQ ID NO: 7)	GFNIKDD (SEQ ID NO: 12)
	CDR-H2	IDPETGDT (SEQ ID NO: 19)	WIDPETGDTEYASKFQD (SEQ ID NO: 20)	ETG (SEQ ID NO: 21)
	CDR-H3	TLWLRRGLDY (SEQ ID NO: 3)	WLRRGLDY (SEQ ID NO: 9)	LRRGLD (SEQ ID NO: 14)
	CDR-L1	KSLLHSNGYTY (SEQ ID NO: 4)	RSSKSLLHSNGYTYLF (SEQ ID NO: 10)	SKSLLHSNGYTY (SEQ ID NO: 15)
	CDR-L2	RMS (SEQ ID NO: 5)	RMSNLAS (SEQ ID NO: 11)	RMS(SEQ ID NO: 5)
	CDR-L3	MQHLEYPFT (SEQ ID NO: 6)	MQHLEYPFT (SEQ ID NO: 6)	HLEYPF (SEQ ID NO: 16)
	VH	EVQLQQSGAELVRPGASVKLSCTASGFNIKDDYMYWVKQRPEQGLEWIGWIDPETGDT EYASKFQDKATVTADTSSNTAYLQLSSLTSEDTAVYYCTLWLRRGLDYWGQGTSVTVS S (SEQ ID NO: 22)		
	VL	DIVMTQAAPSVPVTPGESVSISCRSSKSLLHSNGYTYLFWFLQRPGQSPQLLIYRMSNLA SGVPDRFSGSGSGTAFTLRISRVEAEDVGVYYCMQHLEYPFTFGGGTKLEIK (SEQ ID NO: 18)		
3-A4 N54S*	CDR-H1	GFNIKDDY (SEQ ID NO: 1)	DDYMY (SEQ ID NO: 7)	GFNIKDD (SEQ ID NO: 12)
	CDR-H2	IDPESGDT (SEQ ID NO: 23)	WIDPESGDTEYASKFQD (SEQ ID NO: 24)	ESG (SEQ ID NO: 25)
	CDR-H3	TLWLRRGLDY (SEQ ID NO: 3)	WLRRGLDY (SEQ ID NO: 9)	LRRGLD (SEQ ID NO: 14)
	CDR-L1	KSLLHSNGYTY (SEQ ID NO: 4)	RSSKSLLHSNGYTYLF (SEQ ID NO: 10)	SKSLLHSNGYTY (SEQ ID NO: 15)
	CDR-L2	RMS (SEQ ID NO: 5)	RMSNLAS (SEQ ID NO: 11)	RMS (SEQ ID NO: 5)
	CDR-L3	MQHLEYPFT (SEQ ID NO: 6)	MQHLEYPFT (SEQ ID NO: 6)	HLEYPF (SEQ ID NO: 16)
	VH	EVQLQQSGAELVRPGASVKLSCTASGFNIKDDYMYWVKQRPEQGLEWIGWIDPESGDT EYASKFQDKATVTADTSSNTAYLQLSSLTSEDTAVYYCTLWLRRGLDYWGQGTSVTVS S (SEQ ID NO: 26)		
	VL	DIVMTQAAPSVPVTPGESVSISCRSSKSLLHSNGYTYLFWFLQRPGQSPQLLIYRMSNLA SGVPDRFSGSGSGTAFTLRISRVEAEDVGVYYCMQHLEYPFTFGGGTKLEIK (SEQ ID NO: 18)		
3-M12	CDR-H1	GYSITSGYY (SEQ ID NO: 27)	SGYYWN (SEQ ID NO: 33)	GYSITSGY (SEQ ID NO: 38)
	CDR-H2	ITFDGAN (SEQ ID NO: 28)	YITFDGANNYNPSLKN (SEQ ID NO: 34)	FDG (SEQ ID NO: 39)
	CDR-H3	TRSSYDYDVLDY (SEQ ID NO: 29)	SSYDYDVLDY (SEQ ID NO: 35)	SYDYDVLD (SEQ ID NO: 40)
	CDR-L1	QDISNF (SEQ ID NO: 30)	RASQDISNFLN (SEQ ID NO: 36)	SQDISNF (SEQ ID NO: 41)
	CDR-L2	YTS (SEQ ID NO: 31)	YTSRLHS (SEQ ID NO: 37)	YTS (SEQ ID NO: 31)
	CDR-L3	QQGHTLPYT (SEQ ID NO: 32)	QQGHTLPYT (SEQ ID NO: 32)	GHTLPY (SEQ ID NO: 42)
	VH	DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFPGNKLEWMGYITFDGAN NYNPSLKNRISITRDTSKNQFFLKLTSVTTEDTATYYCTRSSYDYDVLDYWGQGTTLTV SS (SEQ ID NO: 43)		

Ab	No. system	IMGT	Kabat	Chothia
	VL	DIQMTQTTSSLSASLGDRVTISCRASQDISNFLNWYQQRPDGTVKLLIYYTSRLHSGVPS RFSGSGSGTDFSLTVSNLEQEDIATYFCQQGHTLPYTFGGGTKLEIK (SEQ ID NO: 44)		
5-H12	CDR-H1	GYSFTDYC (SEQ ID NO: 45)	DYCIN (SEQ ID NO: 51)	GYSFTDY (SEQ ID NO: 56)
	CDR-H2	IYPGSGNT (SEQ ID NO: 46)	WIYPGSGNTRYSERFKG (SEQ ID NO: 52)	GSG (SEQ ID NO: 57)
	CDR-H3	AREDYYPYHGMDY (SEQ ID NO: 47)	EDYYPYHGMDY (SEQ ID NO: 53)	DYYPYHGMD (SEQ ID NO: 58)
	CDR-L1	ESVDGYDNSF (SEQ ID NO: 48)	RASESVDGYDNSFMH (SEQ ID NO: 54)	SESVDGYDNSF (SEQ ID NO: 59)
	CDR-L2	RAS (SEQ ID NO: 49)	RASNLES (SEQ ID NO: 55)	RAS (SEQ ID NO: 49)
	CDR-L3	QQSSEDPWT (SEQ ID NO: 50)	QQSSEDPWT (SEQ ID NO: 50)	SSEDPW (SEQ ID NO: 60)
	VH	QIQLQQSGPELVRPGASVKISCKASGYSFTDYCINWVNQRPGQGLEWIGWIYPGSGNTR YSERFKGKATLTVDTSSNTAYMQLSSLTSEDSAVYFCAREDYYPYHGMDYWGQGTSV TVSS (SEQ ID NO: 61)		
	VL	DIVLTQSPTSLAVSLGQRATISCRASESVDGYDNSFMHWYQQKPGQPPKLLIFRASNLES GIPARFSGSGSRTDFTLTINPVEAADVATYYCQQSSEDPWTFGGGTKLEIK (SEQ ID NO: 62)		
5-H12 C33Y*	CDR-H1	GYSFTDYY (SEQ ID NO: 63)	DYYIN (SEQ ID NO: 64)	GYSFTDY (SEQ ID NO: 56)
	CDR-H2	IYPGSGNT (SEQ ID NO: 46)	WIYPGSGNTRYSERFKG (SEQ ID NO: 52)	GSG (SEQ ID NO: 57)
	CDR-H3	AREDYYPYHGMDY (SEQ ID NO: 47)	EDYYPYHGMDY (SEQ ID NO: 53)	DYYPYHGMD (SEQ ID NO: 58)
	CDR-L1	ESVDGYDNSF (SEQ ID NO: 48)	RASESVDGYDNSFMH (SEQ ID NO: 54)	SESVDGYDNSF (SEQ ID NO: 59)
	CDR-L2	RAS (SEQ ID NO: 49)	RASNLES (SEQ ID NO: 55)	RAS (SEQ ID NO: 49)
	CDR-L3	QQSSEDPWT (SEQ ID NO: 50)	QQSSEDPWT (SEQ ID NO: 50)	SSEDPW (SEQ ID NO: 60)
	VH	QIQLQQSGPELVRPGASVKISCKASGYSFTDYYINWVNQRPGQGLEWIGWIYPGSGNTR YSERFKGKATLTVDTSSNTAYMQLSSLTSEDSAVYFCAREDYYPYHGMDYWGQGTSV TVSS (SEQ ID NO: 65)		
	VL	DIVLTQSPTSLAVSLGQRATISCRASESVDGYDNSFMHWYQQKPGQPPKLLIFRASNLES GIPARFSGSGSRTDFTLTINPVEAADVATYYCQQSSEDPWTFGGGTKLEIK (SEQ ID NO: 62)		
5-H12 C33D*	CDR-H1	GYSFTDYD (SEQ ID NO: 66)	DYDIN (SEQ ID NO: 67)	GYSFTDY (SEQ ID NO: 56)
	CDR-H2	IYPGSGNT (SEQ ID NO: 46)	WIYPGSGNTRYSERFKG (SEQ ID NO: 52)	GSG (SEQ ID NO: 57)
	CDR-H3	AREDYYPYHGMDY (SEQ ID NO: 47)	EDYYPYHGMDY (SEQ ID NO: 53)	DYYPYHGMD (SEQ ID NO: 58)
	CDR-L1	ESVDGYDNSF (SEQ ID NO: 48)	RASESVDGYDNSFMH (SEQ ID NO: 54)	SESVDGYDNSF (SEQ ID NO: 59)
	CDR-L2	RAS (SEQ ID NO: 49)	RASNLES (SEQ ID NO: 55)	RAS (SEQ ID NO: 49)
	CDR-L3	QQSSEDPWT (SEQ ID NO: 50)	QQSSEDPWT (SEQ ID NO: 50)	SSEDPW (SEQ ID NO: 60)
	VH	QIQLQQSGPELVRPGASVKISCKASGYSFTDYDINWVNQRPGQGLEWIGWIYPGSGNTRY SERFKGKATLTVDTSSNTAYMQLSSLTSEDSAVYFCAREDYYPYHGMDYWGQGTSVTV SS (SEQ ID NO: 68)		
	VL	DIVLTQSPTSLAVSLGQRATISCRASESVDGYDNSFMHWYQQKPGQPPKLLIFRASNLES GIPARFSGSGSRTDFTLTINPVEAADVATYYCQQSSEDPWTFGGGTKLEIK (SEQ ID NO: 62)		
	CDR-H1	GYSFTSYW (SEQ ID NO: 138)	SYWIG (SEQ ID NO: 144)	GYSFTSY (SEQ ID NO: 149)

Ab	No. system	IMGT	Kabat	Chothia
Anti-TfR clone 8	CDR-H2	IYPGDSDT (SEQ ID NO: 139)	IIYPGDSDTRYSPSFQGQ (SEQ ID NO: 145)	GDS (SEQ ID NO: 150)
	CDR-H3	ARFPYDSSGYYSFDY (SEQ ID NO: 140)	FPYDSSGYYSFDY (SEQ ID NO: 146)	PYDSSGYYSFD (SEQ ID NO: 151)
	CDR-L1	QSISSY (SEQ ID NO: 141)	RASQSISSYLN (SEQ ID NO: 147)	SQSISSY (SEQ ID NO: 152)
	CDR-L2	AAS (SEQ ID NO: 142)	AASSLQS (SEQ ID NO: 148)	AAS (SEQ ID NO: 142)
	CDR-L3	QQSYSTPLT (SEQ ID NO: 143)	QQSYSTPLT (SEQ ID NO: 143)	SYSTPL (SEQ ID NO: 153)

** mutation positions are according to Kabat numbering of the respective VH sequences containing the mutations*

[00093] In some embodiments, the anti-TfR1 antibody of the present disclosure is a humanized variant of any one of the anti-TfR1 antibodies provided in Table 2. In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a CDR-H1, a CDR-H2, a CDR-H3, a CDR-L1, a CDR-L2, and a CDR-L3 that are the same as the CDR-H1, CDR-H2, and CDR-H3 in any one of the anti-TfR1 antibodies provided in Table 2, and comprises a humanized heavy chain variable region and/or (e.g., and) a humanized light chain variable region.

[00094] Examples of amino acid sequences of anti-TfR1 antibodies described herein are provided in Table 3.

Table 3. Variable Regions of Anti-TfR1 Antibodies

Antibody	Variable Region Amino Acid Sequence**
3A4 VH3 (N54T*)/Vκ4	V_H: EVQLVQSGSELKKPGASVKVSCTASGFNIK**DDYMY**WVRQPPGKGLEWIG**WIDP ETGDTEYASKFQD**RVTVTADTSTNTAYMELSSLRSEDTAVYYCTL**WLRRGLD** **Y**WGQGTLVTVSS (SEQ ID NO: 69)
	V_L: DIVMTQSPLSLPVTPGEPASISC**RSSKSLLHSNGYTYLF**WFQQRPGQSPRLLIY**R MSNLAS**GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQHLEYPFT**FGGGTK VEIK (SEQ ID NO: 70)
3A4 VH3 (N54S*)/Vκ4	V_H: EVQLVQSGSELKKPGASVKVSCTASGFNIK**DDYMY**WVRQPPGKGLEWIG**WIDP ESGDTEYASKFQD**RVTVTADTSTNTAYMELSSLRSEDTAVYYCTL**WLRRGLD** **Y**WGQGTLVTVSS (SEQ ID NO: 71)
	V_L: DIVMTQSPLSLPVTPGEPASISC**RSSKSLLHSNGYTYLF**WFQQRPGQSPRLLIY**R MSNLAS**GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQHLEYPFT**FGGGTK VEIK (SEQ ID NO: 70)
3A4 VH3 /Vκ4	VH: EVQLVQSGSELKKPGASVKVSCTASGFNIK**DDYMY**WVRQPPGKGLEWIG**WIDP ENGDTEYASKFQD**RVTVTADTSTNTAYMELSSLRSEDTAVYYCTL**WLRRGLD** **Y**WGQGTLVTVSS (SEQ ID NO: 72)
	VL: DIVMTQSPLSLPVTPGEPASISC**RSSKSLLHSNGYTYLF**WFQQRPGQSPRLLIY**R MSNLAS**GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQHLEYPFT**FGGGTK VEIK (SEQ ID NO: 70)
3M12 VH3/Vκ2	VH: QVQLQESGPGLVKPSQTLSLTCSVTGYSIT**SGYYWN**WIRQPPGKGLEWMG**YITF DGANNYNPSLKN**RVSISRDTSKNQFSLKLSSVTAEDTATYYCTR**SSYDYDVLDY** WGQGTTVTVSS (SEQ ID NO: 73)

Antibody	Variable Region Amino Acid Sequence**
	VL: DIQMTQSPSSLSASVGDRVTITC**RASQDISNFLN**WYQQKPGQPVKLLIY**YTSRLH** **S**GVPSRFSGSGSGTDFTLTISSLQPEDFATYFC**QQGHTLPYT**FGQGTKLEIK (SEQ ID NO: 74)
3M12 VH3/Vκ3	VH: QVQLQESGPGLVKPSQTLSLTCSVTGYSIT**SGYYWN**WIRQPPGKGLEWMG**YITF** **DGANNYNPSLKN**RVSISRDTSKNQFSLKLSSVTAEDTATYYCTR**SSYDYDVLDY** WGQGTTVTVSS (SEQ ID NO: 73)
	VL: DIQMTQSPSSLSASVGDRVTITC**RASQDISNFLN**WYQQKPGQPVKLLIY**YTSRLH** **S**GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC**QQGHTLPYT**FGQGTKLEIK (SEQ ID NO: 75)
3M12 VH4/Vκ2	VH: QVQLQESGPGLVKPSQTLSLTCTVTGYSIT**SGYYWN**WIRQPPGKGLEWIG**YITFD** **GANNYNPSLKN**RVSISRDTSKNQFSLKLSSVTAEDTATYYCTR**SSYDYDVLDY**W GQGTTVTVSS (SEQ ID NO: 76)
	VL: DIQMTQSPSSLSASVGDRVTITC**RASQDISNFLN**WYQQKPGQPVKLLIY**YTSRLH** **S**GVPSRFSGSGSGTDFTLTISSLQPEDFATYFC**QQGHTLPYT**FGQGTKLEIK (SEQ ID NO: 74)
3M12 VH4/Vκ3	VH: QVQLQESGPGLVKPSQTLSLTCTVTGYSIT**SGYYWN**WIRQPPGKGLEWIG**YITFD** **GANNYNPSLKN**RVSISRDTSKNQFSLKLSSVTAEDTATYYCTR**SSYDYDVLDY**W GQGTTVTVSS (SEQ ID NO: 76)
	VL: DIQMTQSPSSLSASVGDRVTITC**RASQDISNFLN**WYQQKPGQPVKLLIY**YTSRLH** **S**GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC**QQGHTLPYT**FGQGTKLEIK (SEQ ID NO: 75)
5H12 VH5 (C33Y*)/Vκ3	VH: QVQLVQSGAEVKKPGASVKVSCKASGYSFT**DYYIN**WVRQAPGQGLEWMG**WIY** **PGSGNTRYSERFKG**RVTITRDTSASTAYMELSSLRSEDTAVYYCAR**EDYYPYH** **GMDY**WGQGTLVTVSS (SEQ ID NO: 77)
	VL: DIVLTQSPDSLAVSLGERATINC**RASESVDGYDNSFMH**WYQQKPGQPPKLLIF**R** **ASNLES**GVPDRFSGSGSRTDFTLTISSLQAEDVAVYYC**QQSSEDPWT**FGQGTKL EIK (SEQ ID NO: 78)
5H12 VH5 (C33D*)/Vκ4	VH: QVQLVQSGAEVKKPGASVKVSCKASGYSFT**DYDIN**WVRQAPGQGLEWMG**WIY** **PGSGNTRYSERFKG**RVTITRDTSASTAYMELSSLRSEDTAVYYCAR**EDYYPYH** **GMDY**WGQGTLVTVSS (SEQ ID NO: 79)
	VL: DIVMTQSPDSLAVSLGERATINC**RASESVDGYDNSFMH**WYQQKPGQPPKLLIF**R** **ASNLES**GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC**QQSSEDPWT**FGQGTKL EIK (SEQ ID NO: 80)
5H12 VH5 (C33Y*)/Vκ4	VH: QVQLVQSGAEVKKPGASVKVSCKASGYSFT**DYYIN**WVRQAPGQGLEWMG**WIY** **PGSGNTRYSERFKG**RVTITRDTSASTAYMELSSLRSEDTAVYYCAR**EDYYPYH** **GMDY**WGQGTLVTVSS (SEQ ID NO: 77)
	VL: DIVMTQSPDSLAVSLGERATINC**RASESVDGYDNSFMH**WYQQKPGQPPKLLIF**R** **ASNLES**GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC**QQSSEDPWT**FGQGTKL EIK (SEQ ID NO: 80)
Anti-TfR clone 8	VH: QVQLVQSGAEVKKPGESLKISCKGSGYSFT**SYWIG**WVRQMPGKGLEWMG**IIYP** **GDSDTRYSPSFQGQ**VTISADKSISTAYLQWSSLKASDTAMYYCAR**FPYDSSGYY** **SFDY**WGQGTLVTVSS (SEQ ID NO: 154)
	VL: DIQMTQSPSSLSASVGDRVTITC**RASQSISSYLN**WYQQKPGKAPKLLIY**AASSLQ** **S**GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC**QQSYSTPLT**FGGGTKVEIK (SEQ ID NO: 155)

** mutation positions are according to Kabat numbering of the respective VH sequences containing the mutations*

** *CDRs according to the Kabat numbering system are bolded*

[00095] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a VH comprising the CDR-H1, CDR-H2, and CDR-H3 of any one of the anti-TfR1 antibodies provided in Table 3 and comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) amino acid variations in the framework regions as compared with the respective VH provided in Table 3. Alternatively or in addition (e.g., in addition), the anti-TfR1 antibody of the present disclosure comprises a VL comprising the CDR-L1, CDR-L2, and CDR-L3 of any one of the anti-TfR1 antibodies provided in Table 3 and comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) amino acid variations in the framework regions as compared with the respective VL provided in Table 3. In some embodiments, the VH of the anti-TfR1 antibody is a humanized VH, and/or the VL of the anti-TfR1 antibody is a humanized VL.

[00096] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a VH comprising the CDR-H1, CDR-H2, and CDR-H3 of any one of the anti-TfR1 antibodies provided in Table 3 and comprising an amino acid sequence that is at least 70% (e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 99%) identical in the framework regions as compared with the respective VH provided in Table 3. Alternatively or in addition (e.g., in addition), the anti-TfR1 antibody of the present disclosure comprises a VL comprising the CDR-L1, CDR-L2, and CDR-L3 of any one of the anti-TfR1 antibodies provided in Table 3 and comprising an amino acid sequence that is at least 70% (e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 99%) identical in the framework regions as compared with the respective VL provided in Table 3. In some embodiments, the VH of the anti-TfR1 antibody is a humanized VH, and/or the VL of the anti-TfR1 antibody is a humanized VL.

[00097] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a VH comprising the amino acid sequence of SEQ ID NO: 69 and a VL comprising the amino acid sequence of SEQ ID NO: 70.

[00098] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a VH comprising the amino acid sequence of SEQ ID NO: 71 and a VL comprising the amino acid sequence of SEQ ID NO: 70.

[00099] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a VH comprising the amino acid sequence of SEQ ID NO: 72 and a VL comprising the amino acid sequence of SEQ ID NO: 70.

[000100] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a VH comprising the amino acid sequence of SEQ ID NO: 73 and a VL comprising the amino acid sequence of SEQ ID NO: 74.

[000101] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a VH comprising the amino acid sequence of SEQ ID NO: 73 and a VL comprising the amino acid sequence of SEQ ID NO: 75.

[000102] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a VH comprising the amino acid sequence of SEQ ID NO: 76 and a VL comprising the amino acid sequence of SEQ ID NO: 74.

[000103] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a VH comprising the amino acid sequence of SEQ ID NO: 76 and a VL comprising the amino acid sequence of SEQ ID NO: 75.

[000104] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a VH comprising the amino acid sequence of SEQ ID NO: 77 and a VL comprising the amino acid sequence of SEQ ID NO: 78.

[000105] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a VH comprising the amino acid sequence of SEQ ID NO: 79 and a VL comprising the amino acid sequence of SEQ ID NO: 80.

[000106] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a VH comprising the amino acid sequence of SEQ ID NO: 77 and a VL comprising the amino acid sequence of SEQ ID NO: 80.

[000107] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a VH comprising the amino acid sequence of SEQ ID NO: 154 and a VL comprising the amino acid sequence of SEQ ID NO: 155.

[000108] In some embodiments, the anti-TfR1 antibody described herein is a full-length IgG, which can include a heavy constant region and a light constant region from a human antibody. In some embodiments, the heavy chain of any of the anti-TfR1 antibodies as described herein may comprise a heavy chain constant region (CH) or a portion thereof (e.g., CH1, CH2, CH3, or a combination thereof). The heavy chain constant region can be of any suitable origin, e.g., human, mouse, rat, or rabbit. In one specific example, the heavy chain constant region is from a human IgG (a gamma heavy chain), e.g., IgG1, IgG2, or IgG4. An example of a human IgG1 constant region is given below:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE

QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 81)

[000109] In some embodiments, the heavy chain of any of the anti-TfR1 antibodies described herein comprises a mutant human IgG1 constant region. For example, the introduction of LALA mutations (a mutant derived from mAb b12 that has been mutated to replace the lower hinge residues Leu234 Leu235 with Ala234 and Ala235) in the CH2 domain of human IgG1 is known to reduce Fcγ receptor binding (Bruhns, P., et al . (2009) and Xu, D. et al. (2000)). The mutant human IgG1 constant region is provided below (mutations bonded and underlined):

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE**AA**
GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 82)

[000110] In some embodiments, the light chain of any of the anti-TfR1 antibodies described herein may further comprise a light chain constant region (CL), which can be any CL known in the art. In some examples, the CL is a kappa light chain. In other examples, the CL is a lambda light chain. In some embodiments, the CL is a kappa light chain, the sequence of which is provided below:

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ
DSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 83)

[000111] Other antibody heavy and light chain constant regions are well known in the art, e.g., those provided in the IMGT database (www.imgt.org) or at www.vbase2.org/vbstat.php, both of which are incorporated by reference herein.

[000112] In some embodiments, the anti-TfR1 antibody described herein comprises a heavy chain comprising any one of the VH as listed in Table 3 or any variants thereof and a heavy chain constant region that is at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identical to SEQ ID NO: 81 or SEQ ID NO: 82. In some embodiments, the anti-TfR1 antibody described herein comprises a heavy chain comprising any one of the VH as listed in Table 3 or any variants thereof and a heavy chain constant region that contains no more than 25 amino acid variations (e.g., no more than 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acid variation) as compared with SEQ ID NO: 81 or SEQ ID NO: 82. In some embodiments, the anti-TfR1 antibody described herein comprises a heavy

chain comprising any one of the VH as listed in Table 3 or any variants thereof and a heavy chain constant region as set forth in SEQ ID NO: 81. In some embodiments, the anti-TfR1 antibody described herein comprises heavy chain comprising any one of the VH as listed in Table 3 or any variants thereof and a heavy chain constant region as set forth in SEQ ID NO: 82.

[000113] In some embodiments, the anti-TfR1 antibody described herein comprises a light chain comprising any one of the VL as listed in Table 3 or any variants thereof and a light chain constant region that is at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identical to SEQ ID NO: 83. In some embodiments, the anti-TfR1 antibody described herein comprises a light chain comprising any one of the VL as listed in Table 3 or any variants thereof and a light chain constant region contains no more than 25 amino acid variations (e.g., no more than 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acid variation) as compared with SEQ ID NO: 83. In some embodiments, the anti-TfR1 antibody described herein comprises a light chain comprising any one of the VL as listed in Table 3 or any variants thereof and a light chain constant region set forth in SEQ ID NO: 83.

[000114] Examples of IgG heavy chain and light chain amino acid sequences of the anti-TfR1 antibodies described are provided in Table 4 below.

Table 4. Heavy chain and light chain sequences of examples of anti-TfR1 IgGs

Antibody	IgG Heavy Chain/Light Chain Sequences**
3A4 VH3 (N54T*)/Vκ4	Heavy Chain (with wild type human IgG1 constant region) EVQLVQSGSELKKPGASVKVSCTASGFNIK**DDYMY**WVRQPPGKGLEWIG**WIDPE** **TGDTEYASKFQD**RVTVTADTSTNTAYMELSSLRSEDTAVYYCTL**WLRRGLDY**W GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK (SEQ ID NO: 84)
	Light Chain (with kappa light chain constant region) DIVMTQSPLSLPVTPGEPASISC**RSSKSLLHSNGYTYLF**WFQQRPGQSPRLLIY**RMS** **NLAS**GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQHLEYPFT**FGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 85)
3A4 VH3 (N54S*)/Vκ4	Heavy Chain (with wild type human IgG1 constant region) EVQLVQSGSELKKPGASVKVSCTASGFNIK**DDYMY**WVRQPPGKGLEWIG**WIDPE** **SGDTEYASKFQD**RVTVTADTSTNTAYMELSSLRSEDTAVYYCTL**WLRRGLDY**W GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK (SEQ ID NO: 86)

Antibody	IgG Heavy Chain/Light Chain Sequences**
	Light Chain (with kappa light chain constant region) DIVMTQSPLSLPVTPGEPASISC**RSSKSLLHSNGYTYLF**WFQQRPGQSPRLLIY**RMS** **NLAS**GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQHLEYPFT**FGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 85)
3A4 VH3 /Vκ4	Heavy Chain (with wild type human IgG1 constant region) EVQLVQSGSELKKPGASVKVSCTASGFNIK**DDYMY**WVRQPPGKGLEWIG**WIDPE** **NGDTEYASKFQD**RVTVTADTSTNTAYMELSSLRSEDTAVYYCTL**WLRRGLDY**W GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK (SEQ ID NO: 87)
	Light Chain (with kappa light chain constant region) DIVMTQSPLSLPVTPGEPASISC**RSSKSLLHSNGYTYLF**WFQQRPGQSPRLLIY**RMS** **NLAS**GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQHLEYPFT**FGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 85)
3M12 VH3/Vκ2	Heavy Chain (with wild type human IgG1 constant region) QVQLQESGPGLVKPSQTLSLTCSVTGYSIT**SGYYWN**WIRQPPGKGLEWMG**YITFD** **GANNYNPSLKN**RVSISRDTSKNQFSLKLSSVTAEDTATYYCTR**SSYDYDVLDY**WG QGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK (SEQ ID NO: 88)
	Light Chain (with kappa light chain constant region) DIQMTQSPSSLSASVGDRVTITC**RASQDISNFLN**WYQQKPGQPVKLLIY**YTSRLHS** GVPSRFSGSGSGTDFTLTISSLQPEDFATYFC**QQGHTLPYT**FGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 89)
3M12 VH3/Vκ3	Heavy Chain (with wild type human IgG1 constant region) QVQLQESGPGLVKPSQTLSLTCSVTGYSIT**SGYYWN**WIRQPPGKGLEWMG**YITFD** **GANNYNPSLKN**RVSISRDTSKNQFSLKLSSVTAEDTATYYCTR**SSYDYDVLDY**WG QGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK (SEQ ID NO: 88)
	Light Chain (with kappa light chain constant region) DIQMTQSPSSLSASVGDRVTITC**RASQDISNFLN**WYQQKPGQPVKLLIY**YTSRLHS** GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC**QQGHTLPYT**FGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 90)

Antibody	IgG Heavy Chain/Light Chain Sequences**
3M12 VH4/Vκ2	Heavy Chain (with wild type human IgG1 constant region) QVQLQESGPGLVKPSQTLSLTCTVTGYSIT**SGYYWN**WIRQPPGKGLEWIG**YITFDG** **ANNYNPSLKN**RVSISRDTSKNQFSLKLSSVTAEDTATYYCTR**SSYDYDVLDY**WGQ GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK (SEQ ID NO: 91)
	Light Chain (with kappa light chain constant region) DIQMTQSPSSLSASVGDRVTITC**RASQDISNFLN**WYQQKPGQPVKLLIY**YTSRLHS** GVPSRFSGSGSGTDFTLTISSLQPEDFATYFC**QQGHTLPYT**FGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 89)
3M12 VH4/Vκ3	Heavy Chain (with wild type human IgG1 constant region) QVQLQESGPGLVKPSQTLSLTCTVTGYSIT**SGYYWN**WIRQPPGKGLEWIG**YITFDG** **ANNYNPSLKN**RVSISRDTSKNQFSLKLSSVTAEDTATYYCTR**SSYDYDVLDY**WGQ GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK (SEQ ID NO: 91)
	Light Chain (with kappa light chain constant region) DIQMTQSPSSLSASVGDRVTITC**RASQDISNFLN**WYQQKPGQPVKLLIY**YTSRLHS** GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC**QQGHTLPYT**FGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 90)
5H12 VH5 (C33Y*)/Vκ3	Heavy Chain (with wild type human IgG1 constant region) QVQLVQSGAEVKKPGASVKVSCKASGYSFT**DYYIN**WVRQAPGQGLEWMG**WIYP** **GSGNTRYSERFKG**RVTITRDTSASTAYMELSSLRSEDTAVYYCAR**EDYYPYHGM** **DY**WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK (SEQ ID NO: 92)
	Light Chain (with kappa light chain constant region) DIVLTQSPDSLAVSLGERATINC**RASESVDGYDNSFMH**WYQQKPGQPPKLLIF**RAS** **NLES**GVPDRFSGSGSRTDFTLTISSLQAEDVAVYYC**QQSSEDPWT**FGQGTKLEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 93)
5H12 VH5 (C33D*)/Vκ4	Heavy Chain (with wild type human IgG1 constant region) QVQLVQSGAEVKKPGASVKVSCKASGYSFT**DYDIN**WVRQAPGQGLEWMG**WIYP** **GSGNTRYSERFKG**RVTITRDTSASTAYMELSSLRSEDTAVYYCAR**EDYYPYHGM** **DY**WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK (SEQ ID NO: 94)

Antibody	IgG Heavy Chain/Light Chain Sequences**
5H12 VH5 (C33Y*)/Vκ4	Light Chain (with kappa light chain constant region) DIVMTQSPDSLAVSLGERATINC**RASESVDGYDNSFMH**WYQQKPGQPPKLLIF**RA SNLES**GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC**QQSSEDPWT**FGQGTKLEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 95)
	Heavy Chain (with wild type human IgG1 constant region) QVQLVQSGAEVKKPGASVKVSCKASGYSFT**DYYIN**WVRQAPGQGLEWMG**WIYP GSGNTRYSERFKG**RVTITRDTSASTAYMELSSLRSEDTAVYYCAR**EDYYPYHGM DY**WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK (SEQ ID NO: 92)
	Light Chain (with kappa light chain constant region) DIVMTQSPDSLAVSLGERATINC**RASESVDGYDNSFMH**WYQQKPGQPPKLLIF**RA SNLES**GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC**QQSSEDPWT**FGQGTKLEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 95)
Anti-TfR clone 8	VH: QVQLVQSGAEVKKPGESLKISCKGSGYSFT**SYWIG**WVRQMPGKGLEWMG**IIYPG DSDTRYSPSFQG**QVTISADKSISTAYLQWSSLKASDTAMYYCAR**FPYDSSGYYSF DY**WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK (SEQ ID NO: 156)
	VL: DIQMTQSPSSLSASVGDRVTITC**RASQSISSYLN**WYQQKPGKAPKLLIY**AASSLQS** GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC**QQSYSTPLT**FGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 157)

** mutation positions are according to Kabat numbering of the respective VH sequences containing the mutations*
*** CDRs according to the Kabat numbering system are bolded; VH/VL sequences underlined*

[000115] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain containing no more than 25 amino acid variations (e.g., no more than 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acid variation) as compared with the heavy chain as set forth in any one of SEQ ID NOs: 84, 86, 87, 88, 91, 92, 94, and 156. Alternatively or in addition (e.g., in addition), the anti-TfR1 antibody of the present disclosure comprises a light chain containing no more than 25 amino acid variations (e.g., no more than 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acid variation) as compared with the light chain as set forth in any one of SEQ ID NOs: 85, 89, 90, 93, 95, and 157.

[000116] In some embodiments, the anti-TfR1 antibody described herein comprises a heavy chain comprising an amino acid sequence that is at least 75% (e.g., 75%, 80%, 85%, 90%,

95%, 98%, or 99%) identical to any one of SEQ ID NOs: 84, 86, 87, 88, 91, 92, 94, and 156. Alternatively or in addition (e.g., in addition), the anti-TfR1 antibody described herein comprises a light chain comprising an amino acid sequence that is at least 75% (e.g., 75%, 80%, 85%, 90%, 95%, 98%, or 99%) identical to any one of SEQ ID NOs: 85, 89, 90, 93, 95, and 157. In some embodiments, the anti-TfR1 antibody described herein comprises a heavy chain comprising the amino acid sequence of any one of SEQ ID NOs: 84, 86, 87, 88, 91, 92, 94, and 156. Alternatively or in addition (e.g., in addition), the anti-TfR1 antibody described herein comprises a light chain comprising the amino acid sequence of any one of SEQ ID NOs: 85, 89, 90, 93, 95 and 157.

[000117] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 84 and a light chain comprising the amino acid sequence of SEQ ID NO: 85.

[000118] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 86 and a light chain comprising the amino acid sequence of SEQ ID NO: 85.

[000119] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 87 and a light chain comprising the amino acid sequence of SEQ ID NO: 85.

[000120] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 88 and a light chain comprising the amino acid sequence of SEQ ID NO: 89.

[000121] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 88 and a light chain comprising the amino acid sequence of SEQ ID NO: 90.

[000122] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 91 and a light chain comprising the amino acid sequence of SEQ ID NO: 89.

[000123] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 91 and a light chain comprising the amino acid sequence of SEQ ID NO: 90.

[000124] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 92 and a light chain comprising the amino acid sequence of SEQ ID NO: 93.

[000125] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 94 and a light chain comprising the amino acid sequence of SEQ ID NO: 95.

[000126] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 92 and a light chain comprising the amino acid sequence of SEQ ID NO: 95.

[000127] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 156 and a light chain comprising the amino acid sequence of SEQ ID NO: 157.

[000128] In some embodiments, the anti-TfR1 antibody is a Fab fragment, Fab' fragment, or $F(ab')_2$ fragment of an intact antibody (full-length antibody). Antigen binding fragment of an intact antibody (full-length antibody) can be prepared via routine methods (e.g., recombinantly or by digesting the heavy chain constant region of a full-length IgG using an enzyme such as papain). For example, $F(ab')_2$ fragments can be produced by pepsin or papain digestion of an antibody molecule, and Fab fragments that can be generated by reducing the disulfide bridges of $F(ab')_2$ fragments. In some embodiments, a heavy chain constant region in a Fab fragment of the anti-TfR1 antibody described herein comprises the amino acid sequence of: ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO: 96)

[000129] In some embodiments, the anti-TfR1 antibody described herein comprises a heavy chain comprising any one of the VH as listed in Table 3 or any variants thereof and a heavy chain constant region that is at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identical to SEQ ID NO: 96. In some embodiments, the anti-TfR1 antibody described herein comprises a heavy chain comprising any one of the VH as listed in Table 3 or any variants thereof and a heavy chain constant region that contains no more than 25 amino acid variations (e.g., no more than 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acid variation) as compared with SEQ ID NO: 96. In some embodiments, the anti-TfR1 antibody described herein comprises a heavy chain comprising any one of the VH as listed in Table 3 or any variants thereof and a heavy chain constant region as set forth in SEQ ID NO: 96.

[000130] In some embodiments, the anti-TfR1 antibody described herein comprises a light chain comprising any one of the VL as listed in Table 3 or any variants thereof and a light chain constant region that is at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identical to SEQ ID NO: 83. In some embodiments, the anti-TfR1 antibody described herein

comprises a light chain comprising any one of the VL as listed in Table 3 or any variants thereof and a light chain constant region contains no more than 25 amino acid variations (e.g., no more than 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acid variation) as compared with SEQ ID NO: 83. In some embodiments, the anti-TfR1 antibody described herein comprises a light chain comprising any one of the VL as listed in Table 3 or any variants thereof and a light chain constant region set forth in SEQ ID NO: 83.

[000131] Examples of Fab heavy chain and light chain amino acid sequences of the anti-TfR1 antibodies described are provided in Table 5 below.

Table 5. Heavy chain and light chain sequences of examples of anti-TfR1 Fabs

Antibody	Fab Heavy Chain/Light Chain Sequences**
3A4 VH3 (N54T*)/Vκ4	Heavy Chain (with partial human IgG1 constant region) EVQLVQSGSELKKPGASVKVSCTASGFNIK**DDYMY**WVRQPPGKGLEWIG**WIDPE** **TGDTEYASKFQD**RVTVTADTSTNTAYMELSSLRSEDTAVYYCTL**WLRRGLDY**W GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHT (SEQ ID NO: 97)
	Light Chain (with kappa light chain constant region) DIVMTQSPLSLPVTPGEPASISC**RSSKSLLHSNGYTYLF**WFQQRPGQSPRLLIY**RMS** **NLAS**GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQHLEYPFT**FGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 85)
3A4 VH3 (N54S*)/Vκ4	Heavy Chain (with partial human IgG1 constant region) EVQLVQSGSELKKPGASVKVSCTASGFNIK**DDYMY**WVRQPPGKGLEWIG**WIDPE** **SGDTEYASKFQD**RVTVTADTSTNTAYMELSSLRSEDTAVYYCTL**WLRRGLDY**W GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHT (SEQ ID NO: 98)
	Light Chain (with kappa light chain constant region) DIVMTQSPLSLPVTPGEPASISC**RSSKSLLHSNGYTYLF**WFQQRPGQSPRLLIY**RMS** **NLAS**GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQHLEYPFT**FGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 85)
3A4 VH3 /Vκ4	Heavy Chain (with partial human IgG1 constant region) EVQLVQSGSELKKPGASVKVSCTASGFNIK**DDYMY**WVRQPPGKGLEWIG**WIDPE** **NGDTEYASKFQD**RVTVTADTSTNTAYMELSSLRSEDTAVYYCTL**WLRRGLDY**W GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHT (SEQ ID NO: 99)
	Light Chain (with kappa light chain constant region) DIVMTQSPLSLPVTPGEPASISC**RSSKSLLHSNGYTYLF**WFQQRPGQSPRLLIY**RMS** **NLAS**GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQHLEYPFT**FGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 85)
3M12 VH3/Vκ2	Heavy Chain (with partial human IgG1 constant region) QVQLQESGPGLVKPSQTLSLTCSVTGYSIT**SGYYWN**WIRQPPGKGLEWMG**YITFD** **GANNYNPSLKN**RVSISRDTSKNQFSLKLSSVTAEDTATYYCTR**SSYDYDVLDY**WG QGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC DKTHT (SEQ ID NO: 100)

Antibody	Fab Heavy Chain/Light Chain Sequences**
	Light Chain (with kappa light chain constant region) DIQMTQSPSSLSASVGDRVTITC**RASQDISNFLN**WYQQKPGQPVKLLIY**YTSRLHS** GVPSRFSGSGSGTDFTLTISSLQPEDFATYFC**QQGHTLPYT**FGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 89)
3M12 VH3/Vκ3	Heavy Chain (with partial human IgG1 constant region) QVQLQESGPGLVKPSQTLSLTCSVTGYSIT**SGYYWN**WIRQPPGKGLEWMG**YITFD** **GANNYNPSLKN**RVSISRDTSKNQFSLKLSSVTAEDTATYYCTR**SSYDYDVLDY**WG QGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC DKTHT (SEQ ID NO: 100)
	Light Chain (with kappa light chain constant region) DIQMTQSPSSLSASVGDRVTITC**RASQDISNFLN**WYQQKPGQPVKLLIY**YTSRLHS** GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC**QQGHTLPYT**FGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 90)
3M12 VH4/Vκ2	Heavy Chain (with partial human IgG1 constant region) QVQLQESGPGLVKPSQTLSLTCTVTGYSIT**SGYYWN**WIRQPPGKGLEWIG**YITFDG** **ANNYNPSLKN**RVSISRDTSKNQFSLKLSSVTAEDTATYYCTR**SSYDYDVLDY**WGQ GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD KTHT (SEQ ID NO: 101)
	Light Chain (with kappa light chain constant region) DIQMTQSPSSLSASVGDRVTITC**RASQDISNFLN**WYQQKPGQPVKLLIY**YTSRLHS** GVPSRFSGSGSGTDFTLTISSLQPEDFATYFC**QQGHTLPYT**FGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 89)
3M12 VH4/Vκ3	Heavy Chain (with partial human IgG1 constant region) QVQLQESGPGLVKPSQTLSLTCTVTGYSIT**SGYYWN**WIRQPPGKGLEWIG**YITFDG** **ANNYNPSLKN**RVSISRDTSKNQFSLKLSSVTAEDTATYYCTR**SSYDYDVLDY**WGQ GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD KTHT (SEQ ID NO: 101)
	Light Chain (with kappa light chain constant region) DIQMTQSPSSLSASVGDRVTITC**RASQDISNFLN**WYQQKPGQPVKLLIY**YTSRLHS** GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC**QQGHTLPYT**FGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 90)
5H12 VH5 (C33Y*)/Vκ3	Heavy Chain (with partial human IgG1 constant region) QVQLVQSGAEVKKPGASVKVSCKASGYSFT**DYYIN**WVRQAPGQGLEWMG**WIYP** **GSGNTRYSERFKG**RVTITRDTSASTAYMELSSLRSEDTAVYYCAR**EDYYPYHGM** **DY**WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHT (SEQ ID NO: 102)
	Light Chain (with kappa light chain constant region) DIVLTQSPDSLAVSLGERATINC**RASESVDGYDNSFMH**WYQQKPGQPPKLLIF**RAS** **NLES**GVPDRFSGSGSRTDFTLTISSLQAEDVAVYYC**QQSSEDPWT**FGQGTKLEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 93)
5H12 VH5 (C33D*)/Vκ4	Heavy Chain (with partial human IgG1 constant region) QVQLVQSGAEVKKPGASVKVSCKASGYSFT**DYDIN**WVRQAPGQGLEWMG**WIYP** **GSGNTRYSERFKG**RVTITRDTSASTAYMELSSLRSEDTAVYYCAR**EDYYPYHGM** **DY**WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHT (SEQ ID NO: 103)

Antibody	Fab Heavy Chain/Light Chain Sequences**
5H12 VH5 (C33Y*)/Vκ4	Light Chain (with kappa light chain constant region) DIVMTQSPDSLAVSLGERATINC**RASESVDGYDNSFMH**WYQQKPGQPPKLLIF**RA** **SNLES**GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC**QQSSEDPWT**FGQGTKLEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 95)
	Heavy Chain (with partial human IgG1 constant region) QVQLVQSGAEVKKPGASVKVSCKASGYSFT**DYYIN**WVRQAPGQGLEWMG**WIYP** **GSGNTRYSERFKG**RVTITRDTSASTAYMELSSLRSEDTAVYYCAR**EDYYPYHGM** **DY**WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHT (SEQ ID NO: 102)
	Light Chain (with kappa light chain constant region) DIVMTQSPDSLAVSLGERATINC**RASESVDGYDNSFMH**WYQQKPGQPPKLLIF**RA** **SNLES**GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC**QQSSEDPWT**FGQGTKLEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 95)
Anti-TfR clone 8 Version 1	VH: QVQLVQSGAEVKKPGESLKISCKGSGYSFT**SYWIG**WVRQMPGKGLEWMG**IIYPG** **DSDTRYSPSFQGQ**VTISADKSISTAYLQWSSLKASDTAMYYCAR**FPYDSSGYYSF** **DY**WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCP (SEQ ID NO: 158)
	VL: DIQMTQSPSSLSASVGDRVTITC**RASQSISSYLN**WYQQKPGKAPKLLIY**AASSLQS** GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC**QQSYSTPLT**FGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 157)
Anti-TfR clone 8 Version 2	VH: QVQLVQSGAEVKKPGESLKISCKGSGYSFT**SYWIG**WVRQMPGKGLEWMG**IIYPG** **DSDTRYSPSFQGQ**VTISADKSISTAYLQWSSLKASDTAMYYCAR**FPYDSSGYYSF** **DY**WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHT (SEQ ID NO: 159)
	VL: DIQMTQSPSSLSASVGDRVTITC**RASQSISSYLN**WYQQKPGKAPKLLIY**AASSLQS** GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC**QQSYSTPLT**FGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 157)

** mutation positions are according to Kabat numbering of the respective VH sequences containing the mutations*
*** CDRs according to the Kabat numbering system are bolded; VH/VL sequences underlined*

[000132] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain containing no more than 25 amino acid variations (e.g., no more than 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acid variation) as compared with the heavy chain as set forth in any one of SEQ ID NOs: 97-103, 158 and 159. Alternatively or in addition (e.g., in addition), the anti-TfR1 antibody of the present disclosure comprises a light chain containing no more than 25 amino acid variations (e.g., no more than 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acid variation) as compared with the light chain as set forth in any one of SEQ ID NOs: 85, 89, 90, 93, 95, and 157.

[000133] In some embodiments, the anti-TfR1 antibody described herein comprises a heavy chain comprising an amino acid sequence that is at least 75% (e.g., 75%, 80%, 85%, 90%, 95%, 98%, or 99%) identical to any one of SEQ ID NOs: 97-103, 158 and 159. Alternatively or in addition (e.g., in addition), the anti-TfR1 antibody described herein comprises a light chain comprising an amino acid sequence that is at least 75% (e.g., 75%, 80%, 85%, 90%, 95%, 98%, or 99%) identical to any one of SEQ ID NOs: 85, 89, 90, 93, 95, and 157. In some embodiments, the anti-TfR1 antibody described herein comprises a heavy chain comprising the amino acid sequence of any one of SEQ ID NOs: 97-103, 158 and 159. Alternatively or in addition (e.g., in addition), the anti-TfR1 antibody described herein comprises a light chain comprising the amino acid sequence of any one of SEQ ID NOs: 85, 89, 90, 93, 95, and 157.

[000134] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 97 and a light chain comprising the amino acid sequence of SEQ ID NO: 85.

[000135] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 98 and a light chain comprising the amino acid sequence of SEQ ID NO: 85.

[000136] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 99 and a light chain comprising the amino acid sequence of SEQ ID NO: 85.

[000137] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 100 and a light chain comprising the amino acid sequence of SEQ ID NO: 89.

[000138] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 100 and a light chain comprising the amino acid sequence of SEQ ID NO: 90.

[000139] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 101 and a light chain comprising the amino acid sequence of SEQ ID NO: 89.

[000140] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 101 and a light chain comprising the amino acid sequence of SEQ ID NO: 90.

[000141] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 102 and a light chain comprising the amino acid sequence of SEQ ID NO: 93.

[000142] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 103 and a light chain comprising the amino acid sequence of SEQ ID NO: 95.

[000143] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 102 and a light chain comprising the amino acid sequence of SEQ ID NO: 95.

[000144] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 158 and a light chain comprising the amino acid sequence of SEQ ID NO: 157.

[000145] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 159 and a light chain comprising the amino acid sequence of SEQ ID NO: 157.

Other known anti-TfR1 antibodies

[000146] Any other appropriate anti-TfR1 antibodies known in the art may be used as the muscle-targeting agent in the complexes disclosed herein. Examples of known anti-TfR1 antibodies, including associated references and binding epitopes, are listed in Table 6. In some embodiments, the anti-TfR1 antibody comprises the complementarity determining regions (CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3) of any of the anti-TfR1 antibodies provided herein, e.g., anti-TfR1 antibodies listed in Table 6.

Table 6 – List of anti-TfR1 antibody clones, including associated references and binding epitope information.

Antibody Clone Name	**Reference(s)**	**Epitope / Notes**
OKT9	US Patent. No. 4,364,934, filed 12/4/1979, entitled "MONOCLONAL ANTIBODY TO A HUMAN EARLY THYMOCYTE ANTIGEN AND METHODS FOR PREPARING SAME" Schneider C. et al. "Structural features of the cell surface receptor for transferrin that is recognized by the monoclonal antibody OKT9." J Biol Chem. 1982, 257:14, 8516-8522.	Apical domain of TfR1 (residues 305-366 of human TfR1 sequence XM_052730.3, available in GenBank)
(From JCR) Clone M11 Clone M23 Clone M27 Clone B84	• WO 2015/098989, filed 12/24/2014, "Novel anti-Transferrin receptor antibody that passes through blood-brain barrier" • US Patent No. 9,994,641, filed 12/24/2014, "Novel anti-Transferrin receptor antibody that passes through blood-brain barrier"	Apical domain (residues 230-244 and 326-347 of TfR1) and protease-like domain (residues 461-473)

Antibody Clone Name	Reference(s)	Epitope / Notes
(From Genentech) 7A4, 8A2, 15D2, 10D11, 7B10, 15G11, 16G5, 13C3, 16G4, 16F6, 7G7, 4C2, 1B12, and 13D4	• WO 2016/081643, filed 5/26/2016, entitled "ANTI-TRANSFERRIN RECEPTOR ANTIBODIES AND METHODS OF USE" • US Patent No. 9,708,406, filed 5/20/2014, "Anti-transferrin receptor antibodies and methods of use"	Apical domain and non-apical regions
(From Armagen) 8D3	• Lee et al. "Targeting Rat Anti-Mouse Transferrin Receptor Monoclonal Antibodies through Blood-Brain Barrier in Mouse" 2000, J Pharmacol. Exp. Ther., 292: 1048-1052. • US Patent App. 2010/077498, filed 9/11/2008, entitled "COMPOSITIONS AND METHODS FOR BLOOD-BRAIN BARRIER DELIVERY IN THE MOUSE"	
OX26	• Haobam, B. et al. 2014. Rab17-mediated recycling endosomes contribute to autophagosome formation in response to Group A Streptococcus invasion. Cellular microbiology. 16: 1806-21.	
DF1513	• Ortiz-Zapater E et al. Trafficking of the human transferrin receptor in plant cells: effects of tyrphostin A23 and brefeldin A. Plant J 48:757-70 (2006).	
1A1B2, 66IG10, MEM-189, JF0956, 29806, 1A1B2, TFRC/1818, 1E6, 66Ig10, TFRC/1059, Q1/71, 23D10, 13E4, TFRC/1149, ER-MP21, YTA74.4, BU54, 2B6, RI7 217	• Commercially available anti-transferrin receptor antibodies.	Novus Biologicals 8100 Southpark Way, A-8 Littleton CO 80120
(From INSERM) BA120g	• US Patent App. 2011/0311544A1, filed 6/15/2005, entitled "ANTI-CD71 MONOCLONAL ANTIBODIES AND USES THEREOF FOR TREATING MALIGNANT TUMOR CELLS"	Does not compete with OKT9
LUCA31	• US Patent No. 7,572,895, filed 6/7/2004, entitled "TRANSFERRIN RECEPTOR ANTIBODIES"	"LUCA31 epitope"

Antibody Clone Name	Reference(s)	Epitope / Notes
(Salk Institute) B3/25 T58/30	• Trowbridge, I.S. et al. "Anti-transferrin receptor monoclonal antibody and toxin–antibody conjugates affect growth of human tumour cells." Nature, 1981, volume 294, pages 171–173	
R17 217.1.3, 5E9C11, OKT9 (BE0023 clone)	• Commercially available anti-transferrin receptor antibodies.	BioXcell 10 Technology Dr., Suite 2B West Lebanon, NH 03784-1671 USA
BK19.9, B3/25, T56/14 and T58/1	• Gatter, K.C. et al. "Transferrin receptors in human tissues: their distribution and possible clinical relevance." J Clin Pathol. 1983 May;36(5):539-45.	

Anti-TfR1 antibody
CDRH1 (SEQ ID NO: 2179)
CDRH2 (SEQ ID NO: 2180)
CDRH3 (SEQ ID NO: 2181)
CDRL1 (SEQ ID NO: 2182)
CDRL2 (SEQ ID NO: 2183)
CDRL3 (SEQ ID NO: 2184)
VH (SEQ ID NO: 2185)
VL (SEQ ID NO: 2186)

Additional Anti-TfR1 antibody SEQ ID NOs

	VH/VL	CDR1	CDR2	CDR3
VH1	2194	2187	2188	2181
VH2	2195	2187	2189	2181
VH3	2196	2187	2190	2181
VH4	2197	2187	2189	2181
VL1	2198	2182	2183	115
VL2	2199	2182	2183	115
VL3	2200	2182	2191	2184
VL4	2201	2192	2193	2184

[000147] In some embodiments, anti-TfR1 antibodies of the present disclosure include one or more of the CDR-H (*e.g.,* CDR-H1, CDR-H2, and CDR-H3) amino acid sequences from any one of the anti-TfR1 antibodies selected from Table 6. In some embodiments, anti-TfR1 antibodies include the CDR-L1, CDR-L2, and CDR-L3 as provided for any one of the anti-TfR1 antibodies selected from Table 6. In some embodiments, anti-TfR1 antibodies include the CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 as provided for any one of the anti-TfR1 antibodies selected from Table 6.

[000148] In some embodiments, anti-TfR1 antibodies of the disclosure include any antibody that includes a heavy chain variable domain and/or (e.g., and) a light chain variable domain of any anti-TfR1 antibody, such as any one of the anti-TfR1 antibodies selected from Table 6. In some embodiments, anti-TfR1 antibodies of the disclosure include any antibody that includes the heavy chain variable and light chain variable pairs of any anti-TfR1 antibody, such as any one of the anti-TfR1 antibodies selected from Table 6.

[000149] Aspects of the disclosure provide anti-TfR1 antibodies having a heavy chain variable (VH) and/or (e.g., and) a light chain variable (VL) domain amino acid sequence homologous to any of those described herein. In some embodiments, the anti-TfR1 antibody

comprises a heavy chain variable sequence or a light chain variable sequence that is at least 75% (*e.g.*, 80%, 85%, 90%, 95%, 98%, or 99%) identical to the heavy chain variable sequence and/ or any light chain variable sequence of any anti-TfR1 antibody, such as any one of the anti-TfR1 antibodies selected from Table 6. In some embodiments, the homologous heavy chain variable and/or (e.g., and) a light chain variable amino acid sequences do not vary within any of the CDR sequences provided herein. For example, in some embodiments, the degree of sequence variation (*e.g.*, 75%, 80%, 85%, 90%, 95%, 98%, or 99%) may occur within a heavy chain variable and/or (e.g., and) a light chain variable sequence excluding any of the CDR sequences provided herein. In some embodiments, any of the anti-TfR1 antibodies provided herein comprise a heavy chain variable sequence and a light chain variable sequence that comprises a framework sequence that is at least 75%, 80%, 85%, 90%, 95%, 98%, or 99% identical to the framework sequence of any anti-TfR1 antibody, such as any one of the anti-TfR1 antibodies selected from Table 6.

[000150] An example of a transferrin receptor antibody that may be used in accordance with the present disclosure is described in International Application Publication WO 2016/081643, incorporated herein by reference. The amino acid sequences of this antibody are provided in Table 7.

Table 7. Heavy chain and light chain CDRs of an example of a known anti-TfR1 antibody

Sequence Type	Kabat	Chothia	Contact
CDR-H1	SYWMH (SEQ ID NO: 110)	GYTFTSY (SEQ ID NO: 116)	TSYWMH (SEQ ID NO: 118)
CDR-H2	EINPTNGRTNYIE KFKS (SEQ ID NO: 111)	NPTNGR (SEQ ID NO: 117)	WIGEINPTNGRTN (SEQ ID NO: 119)
CDR-H3	GTRAYHY (SEQ ID NO: 112)	GTRAYHY (SEQ ID NO: 112)	ARGTRA (SEQ ID NO: 120)
CDR-L1	RASDNLYSNLA (SEQ ID NO: 113)	RASDNLYSNLA (SEQ ID NO: 113)	YSNLAWY (SEQ ID NO: 121)
CDR-L2	DATNLAD (SEQ ID NO: 114)	DATNLAD (SEQ ID NO: 114)	LLVYDATNLA (SEQ ID NO: 122)
CDR-L3	QHFWGTPLT (SEQ ID NO: 115)	QHFWGTPLT (SEQ ID NO: 115)	QHFWGTPL (SEQ ID NO: 123)
Murine VH	QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGEINP TNGRTNYIEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARGTRAYHYW GQGTSVTVSS (SEQ ID NO: 124)		
Murine VL	DIQMTQSPASLSVSVGETVTITCRASDNLYSNLAWYQQKQGKSPQLLVYDATNL ADGVPSRFSGSGSGTQYSLKINSLQSEDFGTYYCQHFWGTPLTFGAGTKLELK (SEQ ID NO: 125)		
Humanized VH	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQAPGQRLEWIGEIN PTNGRTNYIEKFKSRATLTVDKSASTAYMELSSLRSEDTAVYYCARGTRAYHY WGQGTMVTVSS (SEQ ID NO: 128)		
Humanized VL	DIQMTQSPSSLSASVGDRVTITCRASDNLYSNLAWYQQKPGKSPKLLVYDATNL ADGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQHFWGTPLTFGQGTKVEIK (SEQ ID NO: 129)		

Sequence Type	Kabat	Chothia	Contact
HC of chimeric full-length IgG1	QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGEINP TNGRTNYIEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARGTRAYHYW GQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK (SEQ ID NO: 132)		
LC of chimeric full-length IgG1	DIQMTQSPASLSVSVGETVTITCRASDNLYSNLAWYQQKQGKSPQLLVYDATNL ADGVPSRFSGSGSGTQYSLKINSLQSEDFGTYYCQHFWGTPLTFGAGTKLELKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 133)		
HC of fully human full-length IgG1	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQAPGQRLEWIGEIN PTNGRTNYIEKFKSRATLTVDKSASTAYMELSSLRSEDTAVYYCARGTRAYHY WGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK (SEQ ID NO: 134)		
LC of fully human full-length IgG1	DIQMTQSPSSLSASVGDRVTITCRASDNLYSNLAWYQQKPGKSPKLLVYDATNL ADGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQHFWGTPLTFGQGTKVEIKRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV TEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 135)		
HC of chimeric Fab	QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGEINP TNGRTNYIEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARGTRAYHYW GQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCP (SEQ ID NO: 136)		
HC of fully human Fab	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQAPGQRLEWIGEIN PTNGRTNYIEKFKSRATLTVDKSASTAYMELSSLRSEDTAVYYCARGTRAYHY WGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCP (SEQ ID NO: 137)		

[000151] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a CDR-H1, a CDR-H2, and a CDR-H3 that are the same as the CDR-H1, CDR-H2, and CDR-H3 shown in Table 7. Alternatively or in addition (e.g., in addition), the anti-TfR1 antibody of the present disclosure comprises a CDR-L1, a CDR-L2, and a CDR-L3 that are the same as the CDR-L1, CDR-L2, and CDR-L3 shown in Table 7.

[000152] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a CDR-L3, which contains no more than 3 amino acid variations (e.g., no more than 3, 2, or 1 amino acid variation) as compared with the CDR-L3 as shown in Table 7. In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a CDR-L3 containing one amino acid variation as compared with the CDR-L3 as shown in Table 7. In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a CDR-L3 of QHFAGTPLT (SEQ ID NO: 126) (according to the Kabat and Chothia definition system) or QHFAGTPL (SEQ ID NO: 127) (according to the Contact definition system). In some

embodiments, the anti-TfR1 antibody of the present disclosure comprises a CDR-H1, a CDR-H2, a CDR-H3, a CDR-L1 and a CDR-L2 that are the same as the CDR-H1, CDR-H2, and CDR-H3 shown in Table 7, and comprises a CDR-L3 of QHFAGTPLT (SEQ ID NO: 126) (according to the Kabat and Chothia definition system) or QHFAGTPL (SEQ ID NO: 127) (according to the Contact definition system).

[000153] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises heavy chain CDRs that collectively are at least 80% (e.g., 80%, 85%, 90%, 95%, or 98%) identical to the heavy chain CDRs as shown in Table 7. Alternatively or in addition (e.g., in addition), the anti-TfR1 antibody of the present disclosure comprises light chain CDRs that collectively are at least 80% (e.g., 80%, 85%, 90%, 95%, or 98%) identical to the light chain CDRs as shown in Table 7.

[000154] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a VH comprising the amino acid sequence of SEQ ID NO: 124. Alternatively or in addition (e.g., in addition), the anti-TfR1 antibody of the present disclosure comprises a VL comprising the amino acid sequence of SEQ ID NO: 125.

[000155] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a VH comprising the amino acid sequence of SEQ ID NO: 128. Alternatively or in addition (e.g., in addition), the anti-TfR1 antibody of the present disclosure comprises a VL comprising the amino acid sequence of SEQ ID NO: 129.

[000156] In some embodiments, the anti-TfR1 antibody of the present disclosure comprises a VH containing no more than 25 amino acid variations (e.g., no more than 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acid variation) as compared with the VH as set forth in SEQ ID NO: 128. Alternatively or in addition (e.g., in addition), the anti-TfR1 antibody of the present disclosure comprises a VL containing no more than 15 amino acid variations (e.g., no more than 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acid variation) as compared with the VL as set forth in SEQ ID NO: 129.

[000157] In some embodiments, the anti-TfR1 antibody of the present disclosure is a full-length IgG1 antibody, which can include a heavy constant region and a light constant region from a human antibody. In some embodiments, the heavy chain of any of the anti-TfR1 antibodies as described herein may comprises a heavy chain constant region (CH) or a portion thereof (e.g., CH1, CH2, CH3, or a combination thereof). The heavy chain constant region can of any suitable origin, e.g., human, mouse, rat, or rabbit. In one specific example, the heavy chain constant region is from a human IgG (a gamma heavy chain), e.g., IgG1, IgG2, or IgG4. An example of human IgG1 constant region is given below:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 81)

[000158] In some embodiments, the light chain of any of the anti-TfR1 antibodies described herein may further comprise a light chain constant region (CL), which can be any CL known in the art. In some examples, the CL is a kappa light chain. In other examples, the CL is a lambda light chain. In some embodiments, the CL is a kappa light chain, the sequence of which is provided below:

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ
DSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 83)

[000159] In some embodiments, the anti-TfR1 antibody described herein is a chimeric antibody that comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 132. Alternatively or in addition (e.g., in addition), the anti-TfR1 antibody described herein comprises a light chain comprising the amino acid sequence of SEQ ID NO: 133.

[000160] In some embodiments, the anti-TfR1 antibody described herein is a fully human antibody that comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 134. Alternatively or in addition (e.g., in addition), the anti-TfR1 antibody described herein comprises a light chain comprising the amino acid sequence of SEQ ID NO: 135.

[000161] In some embodiments, the anti-TfR1 antibody is an antigen binding fragment (Fab) of an intact antibody (full-length antibody). In some embodiments, the anti-TfR1 Fab described herein comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 136. Alternatively or in addition (e.g., in addition), the anti-TfR1 Fab described herein comprises a light chain comprising the amino acid sequence of SEQ ID NO: 133. In some embodiments, the anti-TfR1 Fab described herein comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 137. Alternatively or in addition (e.g., in addition), the anti-TfR1 Fab described herein comprises a light chain comprising the amino acid sequence of SEQ ID NO: 135.

[000162] The anti-TfR1 antibodies described herein can be in any antibody form, including, but not limited to, intact (i.e., full-length) antibodies, antigen-binding fragments thereof (such as Fab, Fab', F(ab')2, Fv), single chain antibodies, bi-specific antibodies, or nanobodies. In some embodiments, the anti-TfR1 antibody described herein is an scFv. In some embodiments, the anti-TfR1 antibody described herein is an scFv-Fab (e.g., scFv fused to

a portion of a constant region). In some embodiments, the anti-TfR1 antibody described herein is an scFv fused to a constant region (e.g., human IgG1 constant region as set forth in SEQ ID NO: 81).

[000163] In some embodiments, conservative mutations can be introduced into antibody sequences (e.g., CDRs or framework sequences) at positions where the residues are not likely to be involved in interacting with a target antigen (e.g., transferrin receptor), for example, as determined based on a crystal structure. In some embodiments, one, two or more mutations (*e.g.,* amino acid substitutions) are introduced into the Fc region of an anti-TfR1 antibody described herein (*e.g.,* in a CH2 domain (residues 231-340 of human IgG1) and/or (e.g., and) CH3 domain (residues 341-447 of human IgG1) and/or (e.g., and) the hinge region, with numbering according to the Kabat numbering system (*e.g.,* the EU index in Kabat)) to alter one or more functional properties of the antibody, such as serum half-life, complement fixation, Fc receptor binding and/or (e.g., and) antigen-dependent cellular cytotoxicity.

[000164] In some embodiments, one, two or more mutations (*e.g.,* amino acid substitutions) are introduced into the hinge region of the Fc region (CH1 domain) such that the number of cysteine residues in the hinge region are altered (*e.g.,* increased or decreased) as described in, e.g., U.S. Pat. No. 5,677,425. The number of cysteine residues in the hinge region of the CH1 domain can be altered to, *e.g.,* facilitate assembly of the light and heavy chains, or to alter (*e.g.,* increase or decrease) the stability of the antibody or to facilitate linker conjugation.

[000165] In some embodiments, one, two or more mutations (*e.g.,* amino acid substitutions) are introduced into the Fc region of a muscle-targeting antibody described herein (e.g., in a CH2 domain (residues 231-340 of human IgG1) and/or (e.g., and) CH3 domain (residues 341-447 of human IgG1) and/or (e.g., and) the hinge region, with numbering according to the Kabat numbering system (*e.g.,* the EU index in Kabat)) to increase or decrease the affinity of the antibody for an Fc receptor (*e.g.*, an activated Fc receptor) on the surface of an effector cell. Mutations in the Fc region of an antibody that decrease or increase the affinity of an antibody for an Fc receptor and techniques for introducing such mutations into the Fc receptor or fragment thereof are known to one of skill in the art. Examples of mutations in the Fc receptor of an antibody that can be made to alter the affinity of the antibody for an Fc receptor are described in, e.g., Smith P et al., (2012) PNAS 109: 6181-6186, U.S. Pat. No. 6,737,056, and International Publication Nos. WO 02/060919; WO 98/23289; and WO 97/34631, which are incorporated herein by reference.

[000166] In some embodiments, one, two or more amino acid mutations (*i.e.,* substitutions, insertions or deletions) are introduced into an IgG constant domain, or FcRn-binding fragment thereof (preferably an Fc or hinge-Fc domain fragment) to alter (*e.g.,* decrease or increase) half-

life of the antibody *in vivo*. See, e.g., International Publication Nos. WO 02/060919; WO 98/23289; and WO 97/34631; and U.S. Pat. Nos. 5,869,046, 6,121,022, 6,277,375 and 6,165,745 for examples of mutations that will alter (*e.g.*, decrease or increase) the half-life of an antibody *in vivo*.

[000167] In some embodiments, one, two or more amino acid mutations (*i.e.*, substitutions, insertions or deletions) are introduced into an IgG constant domain, or FcRn-binding fragment thereof (preferably an Fc or hinge-Fc domain fragment) to decrease the half-life of the anti-TfR1 antibody *in vivo*. In some embodiments, one, two or more amino acid mutations (*i.e.*, substitutions, insertions or deletions) are introduced into an IgG constant domain, or FcRn-binding fragment thereof (preferably an Fc or hinge-Fc domain fragment) to increase the half-life of the antibody *in vivo*. In some embodiments, the antibodies can have one or more amino acid mutations (*e.g.*, substitutions) in the second constant (CH2) domain (residues 231-340 of human IgG1) and/or (e.g., and) the third constant (CH3) domain (residues 341-447 of human IgG1), with numbering according to the EU index in Kabat (Kabat E A et al., (1991) supra). In some embodiments, the constant region of the IgG1 of an antibody described herein comprises a methionine (M) to tyrosine (Y) substitution in position 252, a serine (S) to threonine (T) substitution in position 254, and a threonine (T) to glutamic acid (E) substitution in position 256, numbered according to the EU index as in Kabat. See U.S. Pat. No. 7,658,921, which is incorporated herein by reference. This type of mutant IgG, referred to as "YTE mutant" has been shown to display fourfold increased half-life as compared to wild-type versions of the same antibody (see Dall'Acqua W F et al., (2006) J Biol Chem 281: 23514-24). In some embodiments, an antibody comprises an IgG constant domain comprising one, two, three or more amino acid substitutions of amino acid residues at positions 251-257, 285-290, 308-314, 385-389, and 428-436, numbered according to the EU index as in Kabat.

[000168] In some embodiments, one, two or more amino acid substitutions are introduced into an IgG constant domain Fc region to alter the effector function(s) of the anti-TfR1 antibody. The effector ligand to which affinity is altered can be, for example, an Fc receptor or the C1 component of complement. This approach is described in further detail in U.S. Pat. Nos. 5,624,821 and 5,648,260. In some embodiments, the deletion or inactivation (through point mutations or other means) of a constant region domain can reduce Fc receptor binding of the circulating antibody thereby increasing tumor localization. See, e.g., U.S. Pat. Nos. 5,585,097 and 8,591,886 for a description of mutations that delete or inactivate the constant domain and thereby increase tumor localization. In some embodiments, one or more amino acid substitutions may be introduced into the Fc region of an antibody described herein to remove potential

glycosylation sites on Fc region, which may reduce Fc receptor binding (see, *e.g.,* Shields R L et al., (2001) J Biol Chem 276: 6591-604).

[000169] In some embodiments, one or more amino in the constant region of an anti-TfR1 antibody described herein can be replaced with a different amino acid residue such that the antibody has altered C1q binding and/or (e.g., and) reduced or abolished complement dependent cytotoxicity (CDC). This approach is described in further detail in U.S. Pat. No. 6,194,551 (Idusogie et al). In some embodiments, one or more amino acid residues in the N-terminal region of the CH2 domain of an antibody described herein are altered to thereby alter the ability of the antibody to fix complement. This approach is described further in International Publication No. WO 94/29351. In some embodiments, the Fc region of an antibody described herein is modified to increase the ability of the antibody to mediate antibody dependent cellular cytotoxicity (ADCC) and/or (e.g., and) to increase the affinity of the antibody for an Fcγ receptor. This approach is described further in International Publication No. WO 00/42072.

[000170] In some embodiments, the heavy and/or (e.g., and) light chain variable domain(s) sequence(s) of the antibodies provided herein can be used to generate, for example, CDR-grafted, chimeric, humanized, or composite human antibodies or antigen-binding fragments, as described elsewhere herein. As understood by one of ordinary skill in the art, any variant, CDR-grafted, chimeric, humanized, or composite antibodies derived from any of the antibodies provided herein may be useful in the compositions and methods described herein and will maintain the ability to specifically bind transferrin receptor, such that the variant, CDR-grafted, chimeric, humanized, or composite antibody has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% or more binding to transferrin receptor relative to the original antibody from which it is derived.

[000171] In some embodiments, the antibodies provided herein comprise mutations that confer desirable properties to the antibodies. For example, to avoid potential complications due to Fab-arm exchange, which is known to occur with native IgG4 mAbs, the antibodies provided herein may comprise a stabilizing 'Adair' mutation (Angal S., et al., "A single amino acid substitution abolishes the heterogeneity of chimeric mouse/human (IgG4) antibody," Mol Immunol 30, 105-108; 1993), where serine 228 (EU numbering; residue 241 Kabat numbering) is converted to proline resulting in an IgG1-like hinge sequence. Accordingly, any of the antibodies may include a stabilizing 'Adair' mutation.

[000172] In some embodiments, an antibody is modified, e.g., modified via glycosylation, phosphorylation, sumoylation, and/or (e.g., and) methylation. In some embodiments, an antibody is a glycosylated antibody, which is conjugated to one or more sugar or carbohydrate molecules. In some embodiments, the one or more sugar or carbohydrate molecule are

conjugated to the antibody via N-glycosylation, O-glycosylation, C-glycosylation, glypiation (GPI anchor attachment), and/or (e.g., and) phosphoglycosylation. In some embodiments, the one or more sugar or carbohydrate molecules are monosaccharides, disaccharides, oligosaccharides, or glycans. In some embodiments, the one or more sugar or carbohydrate molecule is a branched oligosaccharide or a branched glycan. In some embodiments, the one or more sugar or carbohydrate molecule includes a mannose unit, a glucose unit, an N-acetylglucosamine unit, an N-acetylgalactosamine unit, a galactose unit, a fucose unit, or a phospholipid unit. In some embodiments, there are about 1-10, about 1-5, about 5-10, about 1-4, about 1-3, or about 2 sugar molecules. In some embodiments, a glycosylated antibody is fully or partially glycosylated. In some embodiments, an antibody is glycosylated by chemical reactions or by enzymatic means. In some embodiments, an antibody is glycosylated in vitro or inside a cell, which may optionally be deficient in an enzyme in the N- or O- glycosylation pathway, e.g. a glycosyltransferase. In some embodiments, an antibody is functionalized with sugar or carbohydrate molecules as described in International Patent Application Publication WO2014065661, published on May 1, 2014, entitled, "*Modified antibody, antibody-conjugate and process for the preparation thereof*".

[000173] In some embodiments, any one of the anti-TfR1 antibodies described herein may comprise a signal peptide in the heavy and/or (e.g., and) light chain sequence (e.g., a N-terminal signal peptide). In some embodiments, the anti-TfR1 antibody described herein comprises any one of the VH and VL sequences, any one of the IgG heavy chain and light chain sequences, or any one of the F(ab') heavy chain and light chain sequences described herein, and further comprises a signal peptide (e.g., a N-terminal signal peptide). In some embodiments, the signal peptide comprises the amino acid sequence of MGWSCIILFLVATATGVHS (SEQ ID NO: 104).

[000174] In some embodiments, an antibody provided herein may have one or more post-translational modifications. In some embodiments, N-terminal cyclization, also called pyroglutamate formation (pyro-Glu), may occur in the antibody at N-terminal Glutamate (Glu) and/or Glutamine (Gln) residues during production. As such, it should be appreciated that an antibody specified as having a sequence comprising an N-terminal glutamate or glutamine residue encompasses antibodies that have undergone pyroglutamate formation resulting from a post-translational modification. In some embodiments, pyroglutamate formation occurs in a heavy chain sequence. In some embodiments, pyroglutamate formation occurs in a light chain sequence.

b. Other Muscle-Targeting Antibodies

[000175] In some embodiments, the muscle-targeting antibody is an antibody that specifically binds hemojuvelin, caveolin-3, Duchenne muscular dystrophy peptide, myosin IIb or CD63. In some embodiments, the muscle-targeting antibody is an antibody that specifically binds a myogenic precursor protein. Exemplary myogenic precursor proteins include, without limitation, ABCG2, M-Cadherin/Cadherin-15, Caveolin-1, CD34, FoxK1, Integrin alpha 7, Integrin alpha 7 beta 1, MYF-5, MyoD, Myogenin, NCAM-1/CD56, Pax3, Pax7, and Pax9. In some embodiments, the muscle-targeting antibody is an antibody that specifically binds a skeletal muscle protein. Exemplary skeletal muscle proteins include, without limitation, alpha-Sarcoglycan, beta-Sarcoglycan, Calpain Inhibitors, Creatine Kinase MM/CKMM, eIF5A, Enolase 2/Neuron-specific Enolase, epsilon-Sarcoglycan, FABP3/H-FABP, GDF-8/Myostatin, GDF-11/GDF-8, Integrin alpha 7, Integrin alpha 7 beta 1, Integrin beta 1/CD29, MCAM/CD146, MyoD, Myogenin, Myosin Light Chain Kinase Inhibitors, NCAM-1/CD56, and Troponin I. In some embodiments, the muscle-targeting antibody is an antibody that specifically binds a smooth muscle protein. Exemplary smooth muscle proteins include, without limitation, alpha-Smooth Muscle Actin, VE-Cadherin, Caldesmon/CALD1, Calponin 1, Desmin, Histamine H2 R, Motilin R/GPR38, Transgelin/TAGLN, and Vimentin. However, it should be appreciated that antibodies to additional targets are within the scope of this disclosure and the exemplary lists of targets provided herein are not meant to be limiting.

c. Antibody Features/Alterations

[000176] In some embodiments, conservative mutations can be introduced into antibody sequences (e.g., CDRs or framework sequences) at positions where the residues are not likely to be involved in interacting with a target antigen (e.g., transferrin receptor), for example, as determined based on a crystal structure. In some embodiments, one, two or more mutations (*e.g.,* amino acid substitutions) are introduced into the Fc region of a muscle-targeting antibody described herein (*e.g.,* in a CH2 domain (residues 231-340 of human IgG1) and/or (e.g., and) CH3 domain (residues 341-447 of human IgG1) and/or (e.g., and) the hinge region, with numbering according to the Kabat numbering system (*e.g.,* the EU index in Kabat)) to alter one or more functional properties of the antibody, such as serum half-life, complement fixation, Fc receptor binding and/or (e.g., and) antigen-dependent cellular cytotoxicity.

[000177] In some embodiments, one, two or more mutations (*e.g.,* amino acid substitutions) are introduced into the hinge region of the Fc region (CH1 domain) such that the number of cysteine residues in the hinge region are altered (*e.g.,* increased or decreased) as described in, e.g., U.S. Pat. No. 5,677,425. The number of cysteine residues in the hinge region of the CH1 domain can be altered to, *e.g.,* facilitate assembly of the light and heavy chains, or to alter (*e.g.,* increase or decrease) the stability of the antibody or to facilitate linker conjugation.

[000178] In some embodiments, one, two or more mutations (*e.g.,* amino acid substitutions) are introduced into the Fc region of a muscle-targeting antibody described herein (e.g., in a CH2 domain (residues 231-340 of human IgG1) and/or (e.g., and) CH3 domain (residues 341-447 of human IgG1) and/or (e.g., and) the hinge region, with numbering according to the Kabat numbering system (*e.g.,* the EU index in Kabat)) to increase or decrease the affinity of the antibody for an Fc receptor (*e.g.,* an activated Fc receptor) on the surface of an effector cell. Mutations in the Fc region of an antibody that decrease or increase the affinity of an antibody for an Fc receptor and techniques for introducing such mutations into the Fc receptor or fragment thereof are known to one of skill in the art. Examples of mutations in the Fc receptor of an antibody that can be made to alter the affinity of the antibody for an Fc receptor are described in, e.g., Smith P et al., (2012) PNAS 109: 6181-6186, U.S. Pat. No. 6,737,056, and International Publication Nos. WO 02/060919; WO 98/23289; and WO 97/34631, which are incorporated herein by reference.

[000179] In some embodiments, one, two or more amino acid mutations (*i.e.,* substitutions, insertions or deletions) are introduced into an IgG constant domain, or FcRn-binding fragment thereof (preferably an Fc or hinge-Fc domain fragment) to alter (*e.g.,* decrease or increase) half-life of the antibody *in vivo*. See, e.g., International Publication Nos. WO 02/060919; WO 98/23289; and WO 97/34631; and U.S. Pat. Nos. 5,869,046, 6,121,022, 6,277,375 and 6,165,745 for examples of mutations that will alter (*e.g.,* decrease or increase) the half-life of an antibody *in vivo*.

[000180] In some embodiments, one, two or more amino acid mutations (*i.e.,* substitutions, insertions or deletions) are introduced into an IgG constant domain, or FcRn-binding fragment thereof (preferably an Fc or hinge-Fc domain fragment) to decrease the half-life of the anti-transferrin receptor antibody *in vivo*. In some embodiments, one, two or more amino acid mutations (*i.e.,* substitutions, insertions or deletions) are introduced into an IgG constant domain, or FcRn-binding fragment thereof (preferably an Fc or hinge-Fc domain fragment) to increase the half-life of the antibody *in vivo*. In some embodiments, the antibodies can have one or more amino acid mutations (*e.g.,* substitutions) in the second constant (CH2) domain (residues 231-340 of human IgG1) and/or (e.g., and) the third constant (CH3) domain (residues 341-447 of human IgG1), with numbering according to the EU index in Kabat (Kabat E A et al., (1991) supra). In some embodiments, the constant region of the IgG1 of an antibody described herein comprises a methionine (M) to tyrosine (Y) substitution in position 252, a serine (S) to threonine (T) substitution in position 254, and a threonine (T) to glutamic acid (E) substitution in position 256, numbered according to the EU index as in Kabat. See U.S. Pat. No. 7,658,921, which is incorporated herein by reference. This type of mutant IgG, referred to as "YTE mutant"

has been shown to display fourfold increased half-life as compared to wild-type versions of the same antibody (see Dall'Acqua W F et al., (2006) J Biol Chem 281: 23514-24). In some embodiments, an antibody comprises an IgG constant domain comprising one, two, three or more amino acid substitutions of amino acid residues at positions 251-257, 285-290, 308-314, 385-389, and 428-436, numbered according to the EU index as in Kabat.

[000181] In some embodiments, one, two or more amino acid substitutions are introduced into an IgG constant domain Fc region to alter the effector function(s) of the anti-transferrin receptor antibody. The effector ligand to which affinity is altered can be, for example, an Fc receptor or the C1 component of complement. This approach is described in further detail in U.S. Pat. Nos. 5,624,821 and 5,648,260. In some embodiments, the deletion or inactivation (through point mutations or other means) of a constant region domain can reduce Fc receptor binding of the circulating antibody thereby increasing tumor localization. See, e.g., U.S. Pat. Nos. 5,585,097 and 8,591,886 for a description of mutations that delete or inactivate the constant domain and thereby increase tumor localization. In some embodiments, one or more amino acid substitutions may be introduced into the Fc region of an antibody described herein to remove potential glycosylation sites on Fc region, which may reduce Fc receptor binding (see, *e.g.*, Shields R L et al., (2001) J Biol Chem 276: 6591-604).

[000182] In some embodiments, one or more amino in the constant region of a muscle-targeting antibody described herein can be replaced with a different amino acid residue such that the antibody has altered C1q binding and/or (e.g., and) reduced or abolished complement dependent cytotoxicity (CDC). This approach is described in further detail in U.S. Pat. No. 6,194,551 (Idusogie et al). In some embodiments, one or more amino acid residues in the N-terminal region of the CH2 domain of an antibody described herein are altered to thereby alter the ability of the antibody to fix complement. This approach is described further in International Publication No. WO 94/29351. In some embodiments, the Fc region of an antibody described herein is modified to increase the ability of the antibody to mediate antibody dependent cellular cytotoxicity (ADCC) and/or (e.g., and) to increase the affinity of the antibody for an Fcγ receptor. This approach is described further in International Publication No. WO 00/42072.

[000183] In some embodiments, the heavy and/or (e.g., and) light chain variable domain(s) sequence(s) of the antibodies provided herein can be used to generate, for example, CDR-grafted, chimeric, humanized, or composite human antibodies or antigen-binding fragments, as described elsewhere herein. As understood by one of ordinary skill in the art, any variant, CDR-grafted, chimeric, humanized, or composite antibodies derived from any of the antibodies provided herein may be useful in the compositions and methods described herein and will maintain the ability to specifically bind transferrin receptor, such that the variant, CDR-grafted,

chimeric, humanized, or composite antibody has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% or more binding to transferrin receptor relative to the original antibody from which it is derived.

[000184] In some embodiments, the antibodies provided herein comprise mutations that confer desirable properties to the antibodies. For example, to avoid potential complications due to Fab-arm exchange, which is known to occur with native IgG4 mAbs, the antibodies provided herein may comprise a stabilizing 'Adair' mutation (Angal S., et al., "A single amino acid substitution abolishes the heterogeneity of chimeric mouse/human (IgG4) antibody," Mol Immunol 30, 105-108; 1993), where serine 228 (EU numbering; residue 241 Kabat numbering) is converted to proline resulting in an IgG1-like hinge sequence. Accordingly, any of the antibodies may include a stabilizing 'Adair' mutation.

[000185] As provided herein, antibodies of this disclosure may optionally comprise constant regions or parts thereof. For example, a VL domain may be attached at its C-terminal end to a light chain constant domain like Cκ or Cλ. Similarly, a VH domain or portion thereof may be attached to all or part of a heavy chain like IgA, IgD, IgE, IgG, and IgM, and any isotype subclass. Antibodies may include suitable constant regions (see, for example, Kabat et al., Sequences of Proteins of Immunological Interest, No. 91-3242, National Institutes of Health Publications, Bethesda, Md. (1991)). Therefore, antibodies within the scope of this may disclosure include VH and VL domains, or an antigen binding portion thereof, combined with any suitable constant regions.

ii. Muscle-Targeting Peptides

[000186] Some aspects of the disclosure provide muscle-targeting peptides as muscle-targeting agents. Short peptide sequences (e.g., peptide sequences of 5-20 amino acids in length) that bind to specific cell types have been described. For example, cell-targeting peptides have been described in Vines e., et al., A. "Cell-penetrating and cell-targeting peptides in drug delivery" *Biochim Biophys Acta* 2008, 1786: 126-38; Jarver P., et al., "In vivo biodistribution and efficacy of peptide mediated delivery" *Trends Pharmacol Sci* 2010; 31: 528-35; Samoylova T.I., et al., "Elucidation of muscle-binding peptides by phage display screening" *Muscle Nerve* 1999; 22: 460-6; U.S. Patent No. 6,329,501, issued on December 11, 2001, entitled "METHODS AND COMPOSITIONS FOR TARGETING COMPOUNDS TO MUSCLE"; and Samoylov A.M., et al., "Recognition of cell-specific binding of phage display derived peptides using an acoustic wave sensor." *Biomol Eng* 2002; 18: 269-72; the entire contents of each of which are incorporated herein by reference. By designing peptides to interact with specific cell surface antigens (*e.g.*, receptors), selectivity for a desired tissue, e.g., muscle, can be achieved. Skeletal muscle-targeting has been investigated and a range of molecular payloads are able to be

delivered. These approaches may have high selectivity for muscle tissue without many of the practical disadvantages of a large antibody or viral particle. Accordingly, in some embodiments, the muscle-targeting agent is a muscle-targeting peptide that is from 4 to 50 amino acids in length. In some embodiments, the muscle-targeting peptide is 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 amino acids in length. Muscle-targeting peptides can be generated using any of several methods, such as phage display.

[000187] In some embodiments, a muscle-targeting peptide may bind to an internalizing cell surface receptor that is overexpressed or relatively highly expressed in muscle cells, e.g. a transferrin receptor, compared with certain other cells. In some embodiments, a muscle-targeting peptide may target, e.g., bind to, a transferrin receptor. In some embodiments, a peptide that targets a transferrin receptor may comprise a segment of a naturally occurring ligand, e.g., transferrin. In some embodiments, a peptide that targets a transferrin receptor is as described in US Patent No. 6,743,893, filed 11/30/2000, "RECEPTOR-MEDIATED UPTAKE OF PEPTIDES THAT BIND THE HUMAN TRANSFERRIN RECEPTOR". In some embodiments, a peptide that targets a transferrin receptor is as described in Kawamoto, M. et al, "A novel transferrin receptor-targeted hybrid peptide disintegrates cancer cell membrane to induce rapid killing of cancer cells." BMC Cancer. 2011 Aug 18;11:359. In some embodiments, a peptide that targets a transferrin receptor is as described in US Patent No. 8,399,653, filed 5/20/2011, "TRANSFERRIN/TRANSFERRIN RECEPTOR-MEDIATED SIRNA DELIVERY".

[000188] As discussed above, examples of muscle targeting peptides have been reported. For example, muscle-specific peptides were identified using phage display library presenting surface heptapeptides. As one example a peptide having the amino acid sequence ASSLNIA (SEQ ID NO: 2170) bound to C2C12 murine myotubes *in vitro*, and bound to mouse muscle tissue *in vivo*. Accordingly, in some embodiments, the muscle-targeting agent comprises the amino acid sequence ASSLNIA (SEQ ID NO: 2170). This peptide displayed improved specificity for binding to heart and skeletal muscle tissue after intravenous injection in mice with reduced binding to liver, kidney, and brain. Additional muscle-specific peptides have been identified using phage display. For example, a 12 amino acid peptide was identified by phage display library for muscle targeting in the context of treatment for Duchenne muscular dystrophy. See, Yoshida D., et al., "Targeting of salicylate to skin and muscle following topical injections in rats." *Int J Pharm* 2002; 231: 177-84; the entire contents of which are hereby incorporated by reference. Here, a 12 amino acid peptide having the sequence

SKTFNTHPQSTP (SEQ ID NO: 2171) was identified and this muscle-targeting peptide showed improved binding to C2C12 cells relative to the ASSLNIA (SEQ ID NO: 2170) peptide.

[000189] An additional method for identifying peptides selective for muscle (*e.g.*, skeletal muscle) over other cell types includes *in vitro* selection, which has been described in Ghosh D., et al., "Selection of muscle-binding peptides from context-specific peptide-presenting phage libraries for adenoviral vector targeting" *J Virol* 2005; 79: 13667-72; the entire contents of which are incorporated herein by reference. By pre-incubating a random 12-mer peptide phage display library with a mixture of non-muscle cell types, non-specific cell binders were selected out. Following rounds of selection the 12 amino acid peptide TARGEHKEEELI (SEQ ID NO: 2172) appeared most frequently. Accordingly, in some embodiments, the muscle-targeting agent comprises the amino acid sequence TARGEHKEEELI (SEQ ID NO: 2172).

[000190] A muscle-targeting agent may an amino acid-containing molecule or peptide. A muscle-targeting peptide may correspond to a sequence of a protein that preferentially binds to a protein receptor found in muscle cells. In some embodiments, a muscle-targeting peptide contains a high propensity of hydrophobic amino acids, e.g. valine, such that the peptide preferentially targets muscle cells. In some embodiments, a muscle-targeting peptide has not been previously characterized or disclosed. These peptides may be conceived of, produced, synthesized, and/or (e.g., and) derivatized using any of several methodologies, e.g. phage displayed peptide libraries, one-bead one-compound peptide libraries, or positional scanning synthetic peptide combinatorial libraries. Exemplary methodologies have been characterized in the art and are incorporated by reference (Gray, B.P. and Brown, K.C. "Combinatorial Peptide Libraries: Mining for Cell-Binding Peptides" Chem Rev. 2014, 114:2, 1020–1081.; Samoylova, T.I. and Smith, B.F. "Elucidation of muscle-binding peptides by phage display screening." Muscle Nerve, 1999, 22:4. 460-6.). In some embodiments, a muscle-targeting peptide has been previously disclosed (see, e.g. Writer M.J. et al. "Targeted gene delivery to human airway epithelial cells with synthetic vectors incorporating novel targeting peptides selected by phage display." J. Drug Targeting. 2004;12:185; Cai, D. "BDNF-mediated enhancement of inflammation and injury in the aging heart." Physiol Genomics. 2006, 24:3, 191-7.; Zhang, L. "Molecular profiling of heart endothelial cells." Circulation, 2005, 112:11, 1601-11.; McGuire, M.J. et al. "In vitro selection of a peptide with high selectivity for cardiomyocytes in vivo." J Mol Biol. 2004, 342:1, 171-82.). Exemplary muscle-targeting peptides comprise an amino acid sequence of the following group: CQAQGQLVC (SEQ ID NO: 2173), CSERSMNFC (SEQ ID NO: 2174), CPKTRRVPC (SEQ ID NO: 2175), WLSEAGPVVTVRALRGTGSW (SEQ ID NO: 2176), ASSLNIA (SEQ ID NO: 2170), CMQHSMRVC (SEQ ID NO: 2177), and DDTRHWG (SEQ ID NO: 2178). In some embodiments, a muscle-targeting peptide may

comprise about 2-25 amino acids, about 2-20 amino acids, about 2-15 amino acids, about 2-10 amino acids, or about 2-5 amino acids. Muscle-targeting peptides may comprise naturally-occurring amino acids, e.g. cysteine, alanine, or non-naturally-occurring or modified amino acids. Non-naturally occurring amino acids include β-amino acids, homo-amino acids, proline derivatives, 3-substituted alanine derivatives, linear core amino acids, N-methyl amino acids, and others known in the art. In some embodiments, a muscle-targeting peptide may be linear; in other embodiments, a muscle-targeting peptide may be cyclic, e.g. bicyclic (see, e.g. Silvana, M.G. et al. Mol. Therapy, 2018, 26:1, 132–147.).

iii. Muscle-Targeting Receptor Ligands

[000191] A muscle-targeting agent may be a ligand, e.g. a ligand that binds to a receptor protein. A muscle-targeting ligand may be a protein, e.g. transferrin, which binds to an internalizing cell surface receptor expressed by a muscle cell. Accordingly, in some embodiments, the muscle-targeting agent is transferrin, or a derivative thereof that binds to a transferrin receptor. A muscle-targeting ligand may alternatively be a small molecule, e.g. a lipophilic small molecule that preferentially targets muscle cells relative to other cell types. Exemplary lipophilic small molecules that may target muscle cells include compounds comprising cholesterol, cholesteryl, stearic acid, palmitic acid, oleic acid, oleyl, linolene, linoleic acid, myristic acid, sterols, dihydrotestosterone, testosterone derivatives, glycerine, alkyl chains, trityl groups, and alkoxy acids.

iv. Muscle-Targeting Aptamers

[000192] A muscle-targeting agent may be an aptamer, e.g. an RNA aptamer, which preferentially targets muscle cells relative to other cell types. In some embodiments, a muscle-targeting aptamer has not been previously characterized or disclosed. These aptamers may be conceived of, produced, synthesized, and/or (e.g., and) derivatized using any of several methodologies, e.g. Systematic Evolution of Ligands by Exponential Enrichment. Exemplary methodologies have been characterized in the art and are incorporated by reference (Yan, A.C. and Levy, M. "Aptamers and aptamer targeted delivery" RNA biology, 2009, 6:3, 316-20.; Germer, K. et al. "RNA aptamers and their therapeutic and diagnostic applications." Int. J. Biochem. Mol. Biol. 2013; 4: 27–40.). In some embodiments, a muscle-targeting aptamer has been previously disclosed (see, e.g. Phillippou, S. et al. "Selection and Identification of Skeletal-Muscle-Targeted RNA Aptamers." Mol Ther Nucleic Acids. 2018, 10:199-214.; Thiel, W.H. et al. "Smooth Muscle Cell-targeted RNA Aptamer Inhibits Neointimal Formation." Mol Ther. 2016, 24:4, 779-87.). Exemplary muscle-targeting aptamers include the A01B RNA aptamer and RNA Apt 14. In some embodiments, an aptamer is a nucleic acid-based aptamer, an

oligonucleotide aptamer or a peptide aptamer. In some embodiments, an aptamer may be about 5-15 kDa, about 5-10 kDa, about 10-15 kDa, about 1-5 Da, about 1-3 kDa, or smaller.

v. Other Muscle-Targeting Agents

[000193] One strategy for targeting a muscle cell (e.g., a skeletal muscle cell) is to use a substrate of a muscle transporter protein, such as a transporter protein expressed on the sarcolemma. In some embodiments, the muscle-targeting agent is a substrate of an influx transporter that is specific to muscle tissue. In some embodiments, the influx transporter is specific to skeletal muscle tissue. Two main classes of transporters are expressed on the skeletal muscle sarcolemma, (1) the adenosine triphosphate (ATP) binding cassette (ABC) superfamily, which facilitate efflux from skeletal muscle tissue and (2) the solute carrier (SLC) superfamily, which can facilitate the influx of substrates into skeletal muscle. In some embodiments, the muscle-targeting agent is a substrate that binds to an ABC superfamily or an SLC superfamily of transporters. In some embodiments, the substrate that binds to the ABC or SLC superfamily of transporters is a naturally-occurring substrate. In some embodiments, the substrate that binds to the ABC or SLC superfamily of transporters is a non-naturally occurring substrate, for example, a synthetic derivative thereof that binds to the ABC or SLC superfamily of transporters.

[000194] In some embodiments, the muscle-targeting agent is any muscle targeting agent described herein (e.g., antibodies, nucleic acids, small molecules, peptides, aptamers, lipids, sugar moieties) that target SLC superfamily of transporters. In some embodiments, the muscle-targeting agent is a substrate of an SLC superfamily of transporters. SLC transporters are either equilibrative or use proton or sodium ion gradients created across the membrane to drive transport of substrates. Exemplary SLC transporters that have high skeletal muscle expression include, without limitation, the SATT transporter (ASCT1; SLC1A4), GLUT4 transporter (SLC2A4), GLUT7 transporter (GLUT7; SLC2A7), ATRC2 transporter (CAT-2; SLC7A2), LAT3 transporter (KIAA0245; SLC7A6), PHT1 transporter (PTR4; SLC15A4), OATP-J transporter (OATP5A1; SLC21A15), OCT3 transporter (EMT; SLC22A3), OCTN2 transporter (FLJ46769; SLC22A5), ENT transporters (ENT1; SLC29A1 and ENT2; SLC29A2), PAT2 transporter (SLC36A2), and SAT2 transporter (KIAA1382; SLC38A2). These transporters can facilitate the influx of substrates into skeletal muscle, providing opportunities for muscle targeting.

[000195] In some embodiments, the muscle-targeting agent is a substrate of an equilibrative nucleoside transporter 2 (ENT2) transporter. Relative to other transporters, ENT2 has one of the highest mRNA expressions in skeletal muscle. While human ENT2 (hENT2) is expressed in most body organs such as brain, heart, placenta, thymus, pancreas, prostate, and kidney, it is especially abundant in skeletal muscle. Human ENT2 facilitates the uptake of its

substrates depending on their concentration gradient. ENT2 plays a role in maintaining nucleoside homeostasis by transporting a wide range of purine and pyrimidine nucleobases. The hENT2 transporter has a low affinity for all nucleosides (adenosine, guanosine, uridine, thymidine, and cytidine) except for inosine. Accordingly, in some embodiments, the muscle-targeting agent is an ENT2 substrate. Exemplary ENT2 substrates include, without limitation, inosine, 2′,3′-dideoxyinosine, and calofarabine. In some embodiments, any of the muscle-targeting agents provided herein are associated with a molecular payload (e.g., oligonucleotide payload). In some embodiments, the muscle-targeting agent is covalently linked to the molecular payload. In some embodiments, the muscle-targeting agent is non-covalently linked to the molecular payload.

[000196] In some embodiments, the muscle-targeting agent is a substrate of an organic cation/carnitine transporter (OCTN2), which is a sodium ion-dependent, high affinity carnitine transporter. In some embodiments, the muscle-targeting agent is carnitine, mildronate, acetylcarnitine, or any derivative thereof that binds to OCTN2. In some embodiments, the carnitine, mildronate, acetylcarnitine, or derivative thereof is covalently linked to the molecular payload (e.g., oligonucleotide payload).

[000197] A muscle-targeting agent may be a protein that is protein that exists in at least one soluble form that targets muscle cells. In some embodiments, a muscle-targeting protein may be hemojuvelin (also known as repulsive guidance molecule C or hemochromatosis type 2 protein), a protein involved in iron overload and homeostasis. In some embodiments, hemojuvelin may be full length or a fragment, or a mutant with at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98% or at least 99% sequence identity to a functional hemojuvelin protein. In some embodiments, a hemojuvelin mutant may be a soluble fragment, may lack a N-terminal signaling, and/or (e.g., and) lack a C-terminal anchoring domain. In some embodiments, hemojuvelin may be annotated under GenBank RefSeq Accession Numbers NM_001316767.1, NM_145277.4, NM_202004.3, NM_213652.3, or NM_213653.3. It should be appreciated that a hemojuvelin may be of human, non-human primate, or rodent origin.

B. Molecular Payloads

[000198] Some aspects of the disclosure provide molecular payloads, e.g., for modulating a biological outcome, e.g., the transcription of a DNA sequence, the splicing and processing of an RNA sequence, the expression of a protein, or the activity of a protein. In some embodiments, a molecular payload is linked to, or otherwise associated with a muscle-targeting agent. In some embodiments, such molecular payloads are capable of targeting to a muscle cell, e.g., via specifically binding to a nucleic acid or protein in the muscle cell following delivery to the

muscle cell by an associated muscle-targeting agent. It should be appreciated that various types of molecular payloads may be used in accordance with the disclosure. For example, the molecular payload may comprise, or consist of, an oligonucleotide (e.g., antisense oligonucleotide), a peptide (e.g., a peptide that binds a nucleic acid or protein associated with disease in a muscle cell), a protein (e.g., a protein that binds a nucleic acid or protein associated with disease in a muscle cell), or a small molecule (e.g., a small molecule that modulates the function of a nucleic acid or protein associated with disease in a muscle cell). In some embodiments, the molecular payload is an oligonucleotide that comprises a strand having a region of complementarity to a mutated DMD allele. Exemplary molecular payloads are described in further detail herein, however, it should be appreciated that the exemplary molecular payloads provided herein are not meant to be limiting.

i. Oligonucleotides

[000199] Aspects of the disclosure relate to oligonucleotides configured to modulate (e.g., increase) expression of dystrophin, e.g., from a DMD allele. In some embodiments, oligonucleotides provided herein are configured to alter splicing of DMD pre-mRNA to promote expression of dystrophin protein (e.g., a functional truncated dystrophin protein). In some embodiments, oligonucleotides provided herein are configured to promote skipping of one or more exons in DMD, e.g., in a mutated DMD allele, in order to restore the reading frame. In some embodiments, the oligonucleotides allow for functional dystrophin protein expression (e.g., as described in Watanabe N, Nagata T, Satou Y, et al. NS-065/NCNP-01: an antisense oligonucleotide for potential treatment of exon 53 skipping in Duchenne muscular dystrophy. Mol Ther Nucleic Acids. 2018;13:442-449). In some embodiments, oligonucleotides provided are configured to promote skipping of exon 55 to produce a shorter but functional version of dystrophin (e.g., containing an in-frame deletion). In some embodiments, oligonucleotides are provided that promote exon 55 skipping (e.g., which may be relevant in a substantial number of patients, including, for example, patients amenable to exon 55 skipping, such as those having deletions in DMD exons 3-54, 4-54, 5-54, 6-54, 9-54, 10-54, 11-54, 13-54, 14-54, 15-54, 16-54, 17-54, 19-54, 21-54, 23-54, 24-54, 25-54, 26-54, 27-54, 28-54, 29-54, 30-54, 31-54, 32-54, 33-54, 34-54, 35-54, 36-54, 37-54, 38-54, 39-54, 40-54, 41-54, 42-54, 43-54, 45-54, 47-54, 48-54, 49-54, 50-54, 52-54, 54, 56, 56-62, 56-65, 56-68, 56-70, 56-71, 56-72, 56-73, or 56-74).

[000200] Table 8 provides non-limiting examples of sequences of oligonucleotides that are useful for targeting DMD, *e.g.,* for exon skipping, and for target sequences within DMD. In some embodiments, an oligonucleotide may comprise any antisense sequence provided in Table 8 or a sequence complementary to a target sequence provided in Table 8.

Table 8. Oligonucleotide sequences for targeting DMD.

SEQ ID NO	Target sequence† (5' to 3')	SEQ ID NO	Antisense Sequence† (5' to 3')	SEQ ID NO	Antisense Sequence† (5' to 3')	Target Site
160	GGAAGAAACUCAU AGAUUACUGCA	780	UGCAGUAAUCUAU GAGUUUCUUCC	1400	TGCAGTAATCTAT GAGTTTCTTCC	Exon 55
161	GAAACAACUGCCA AUGUCCUAC	781	GUAGGACAUUGGC AGUUGUUUC	1401	GTAGGACATTGGC AGTTGTTTC	Exon 55
162	GAAACAACUGCCA AUGUCCUACA	782	UGUAGGACAUUGG CAGUUGUUUC	1402	TGTAGGACATTGG CAGTTGTTTC	Exon 55
163	GAAACAACUGCCA AUGUCCUACAG	783	CUGUAGGACAUUG GCAGUUGUUUC	1403	CTGTAGGACATTG GCAGTTGTTTC	Exon 55
164	GAAACAACUGCCA AUGUCCUACAGG	784	CCUGUAGGACAUU GGCAGUUGUUUC	1404	CCTGTAGGACATT GGCAGTTGTTTC	Exon 55
165	AAACAACUGCCAA UGUCCUACAGG	785	CCUGUAGGACAUU GGCAGUUGUUU	1405	CCTGTAGGACATT GGCAGTTGTTT	Exon 55
166	AAACAACUGCCAA UGUCCUACAGGA	786	UCCUGUAGGACAU UGGCAGUUGUUU	1406	TCCTGTAGGACAT TGGCAGTTGTTT	Exon 55
167	AACAACUGCCAAU GUCCUACAG	787	CUGUAGGACAUUG GCAGUUGUU	1407	CTGTAGGACATTG GCAGTTGTT	Exon 55
168	AACAACUGCCAAU GUCCUACAGG	788	CCUGUAGGACAUU GGCAGUUGUU	1408	CCTGTAGGACATT GGCAGTTGTT	Exon 55
169	AACAACUGCCAAU GUCCUACAGGA	789	UCCUGUAGGACAU UGGCAGUUGUU	1409	TCCTGTAGGACAT TGGCAGTTGTT	Exon 55
170	ACAACUGCCAAUG UCCUACA	790	UGUAGGACAUUGG CAGUUGU	1410	TGTAGGACATTGG CAGTTGT	Exon 55
171	ACAACUGCCAAUG UCCUACAG	791	CUGUAGGACAUUG GCAGUUGU	1411	CTGTAGGACATTG GCAGTTGT	Exon 55
172	ACAACUGCCAAUG UCCUACAGG	792	CCUGUAGGACAUU GGCAGUUGU	1412	CCTGTAGGACATT GGCAGTTGT	Exon 55
173	ACAACUGCCAAUG UCCUACAGGA	793	UCCUGUAGGACAU UGGCAGUUGU	1413	TCCTGTAGGACAT TGGCAGTTGT	Exon 55
174	CAACUGCCAAUGU CCUACAGG	794	CCUGUAGGACAUU GGCAGUUG	1414	CCTGTAGGACATT GGCAGTTG	Exon 55
175	CAACUGCCAAUGU CCUACAGGA	795	UCCUGUAGGACAU UGGCAGUUG	1415	TCCTGTAGGACAT TGGCAGTTG	Exon 55
176	AACUGCCAAUGUC CUACAGGA	796	UCCUGUAGGACAU UGGCAGUU	1416	TCCTGTAGGACAT TGGCAGTT	Exon 55
177	ACUGCCAAUGUCC UACAGGA	797	UCCUGUAGGACAU UGGCAGU	1417	TCCTGTAGGACAT TGGCAGT	Exon 55
178	AGAAACUCAUAGA UUACUGCAACA	798	UGUUGCAGUAAUC UAUGAGUUUCU	1418	TGTTGCAGTAATC TATGAGTTTCT	Exon 55
179	AGAAACUCAUAGA UUACUGCAACAG	799	CUGUUGCAGUAAU CUAUGAGUUUCU	1419	CTGTTGCAGTAAT CTATGAGTTTCT	Exon 55
180	GAAACUCAUAGAU UACUGCAACAG	800	CUGUUGCAGUAAU CUAUGAGUUUC	1420	CTGTTGCAGTAAT CTATGAGTTTC	Exon 55
181	GAUGAUACCAGAA AAGUCCACAU	801	AUGUGGACUUUUC UGGUAUCAUC	1421	ATGTGGACTTTTC TGGTATCATC	Exon 54
182	GAUGAUACCAGAA AAGUCCACAUGA	802	UCAUGUGGACUUU UCUGGUAUCAUC	1422	TCATGTGGACTTT TCTGGTATCATC	Exon 54
183	AUGAUACCAGAAA AGUCCACAUGA	803	UCAUGUGGACUUU UCUGGUAUCAU	1423	TCATGTGGACTTT TCTGGTATCAT	Exon 54
184	AUGAUACCAGAAA AGUCCACAUGAU	804	AUCAUGUGGACUU UUCUGGUAUCAU	1424	ATCATGTGGACTT TTCTGGTATCAT	Exon 54
185	UGAUACCAGAAAA GUCCACAUGA	805	UCAUGUGGACUUU UCUGGUAUCA	1425	TCATGTGGACTTT TCTGGTATCA	Exon 54
186	UGAUACCAGAAAA GUCCACAUGAU	806	AUCAUGUGGACUU UUCUGGUAUCA	1426	ATCATGTGGACTT TTCTGGTATCA	Exon 54
187	GAUACCAGAAAAG UCCACAUGA	807	UCAUGUGGACUUU UCUGGUAUC	1427	TCATGTGGACTTT TCTGGTATC	Exon 54

188	GAUACCAGAAAAG UCCACAUGAU	808	AUCAUGUGGACUU UUCUGGUAUC	1428	ATCATGTGGACTT TTCTGGTATC	Exon 54
189	GAUACCAGAAAAG UCCACAUGAUAA	809	UUAUCAUGUGGAC UUUUCUGGUAUC	1429	TTATCATGTGGAC TTTTCTGGTATC	Exon 54
190	AUACCAGAAAAGU CCACAUGA	810	UCAUGUGGACUUU UCUGGUAU	1430	TCATGTGGACTTT TCTGGTAT	Exon 54
191	AUACCAGAAAAGU CCACAUGAU	811	AUCAUGUGGACUU UUCUGGUAU	1431	ATCATGTGGACTT TTCTGGTAT	Exon 54
192	AUACCAGAAAAGU CCACAUGAUAAC	812	GUUAUCAUGUGGA CUUUUCUGGUAU	1432	GTTATCATGTGGA CTTTTCTGGTAT	Exon 54
193	UACCAGAAAAGUC CACAUGA	813	UCAUGUGGACUUU UCUGGUA	1433	TCATGTGGACTTT TCTGGTA	Exon 54
194	UACCAGAAAAGUC CACAUGAU	814	AUCAUGUGGACUU UUCUGGUA	1434	ATCATGTGGACTT TTCTGGTA	Exon 54
195	UACCAGAAAAGUC CACAUGAUAA	815	UUAUCAUGUGGAC UUUUCUGGUA	1435	TTATCATGTGGAC TTTTCTGGTA	Exon 54
196	UACCAGAAAAGUC CACAUGAUAAC	816	GUUAUCAUGUGGA CUUUUCUGGUA	1436	GTTATCATGTGGA CTTTTCTGGTA	Exon 54
197	UACCAGAAAAGUC CACAUGAUAACA	817	UGUUAUCAUGUGG ACUUUUCUGGUA	1437	TGTTATCATGTGG ACTTTTCTGGTA	Exon 54
198	ACCAGAAAAGUCC ACAUGAU	818	AUCAUGUGGACUU UUCUGGU	1438	ATCATGTGGACTT TTCTGGT	Exon 54
199	ACCAGAAAAGUCC ACAUGAUAA	819	UUAUCAUGUGGAC UUUUCUGGU	1439	TTATCATGTGGAC TTTTCTGGT	Exon 54
200	ACCAGAAAAGUCC ACAUGAUAAC	820	GUUAUCAUGUGGA CUUUUCUGGU	1440	GTTATCATGTGGA CTTTTCTGGT	Exon 54
201	ACCAGAAAAGUCC ACAUGAUAACA	821	UGUUAUCAUGUGG ACUUUUCUGGU	1441	TGTTATCATGTGG ACTTTTCTGGT	Exon 54
202	ACCAGAAAAGUCC ACAUGAUAACAG	822	CUGUUAUCAUGUG GACUUUUCUGGU	1442	CTGTTATCATGTG GACTTTTCTGGT	Exon 54
203	CCAGAAAAGUCCA CAUGAUAA	823	UUAUCAUGUGGAC UUUUCUGG	1443	TTATCATGTGGAC TTTTCTGG	Exon 54
204	CCAGAAAAGUCCA CAUGAUAAC	824	GUUAUCAUGUGGA CUUUUCUGG	1444	GTTATCATGTGGA CTTTTCTGG	Exon 54
205	CCAGAAAAGUCCA CAUGAUAACA	825	UGUUAUCAUGUGG ACUUUUCUGG	1445	TGTTATCATGTGG ACTTTTCTGG	Exon 54
206	CCAGAAAAGUCCA CAUGAUAACAG	826	CUGUUAUCAUGUG GACUUUUCUGG	1446	CTGTTATCATGTG GACTTTTCTGG	Exon 54
207	CCAGAAAAGUCCA CAUGAUAACAGA	827	UCUGUUAUCAUGU GGACUUUUCUGG	1447	TCTGTTATCATGT GGACTTTTCTGG	Exon 54
208	CAGAAAAGUCCAC AUGAUAAC	828	GUUAUCAUGUGGA CUUUUCUG	1448	GTTATCATGTGGA CTTTTCTG	Exon 54
209	CAGAAAAGUCCAC AUGAUAACA	829	UGUUAUCAUGUGG ACUUUUCUG	1449	TGTTATCATGTGG ACTTTTCTG	Exon 54
210	CAGAAAAGUCCAC AUGAUAACAG	830	CUGUUAUCAUGUG GACUUUUCUG	1450	CTGTTATCATGTG GACTTTTCTG	Exon 54
211	CAGAAAAGUCCAC AUGAUAACAGA	831	UCUGUUAUCAUGU GGACUUUUCUG	1451	TCTGTTATCATGT GGACTTTTCTG	Exon 54
212	CAGAAAAGUCCAC AUGAUAACAGAG	832	CUCUGUUAUCAUG UGGACUUUUCUG	1452	CTCTGTTATCATG TGGACTTTTCTG	Exon 54
213	AGAAAAGUCCACA UGAUAACAGA	833	UCUGUUAUCAUGU GGACUUUUCU	1453	TCTGTTATCATGT GGACTTTTCT	Exon 54
214	AGAAAAGUCCACA UGAUAACAGAG	834	CUCUGUUAUCAUG UGGACUUUUCU	1454	CTCTGTTATCATG TGGACTTTTCT	Exon 54
215	AGAAAAGUCCACA UGAUAACAGAGA	835	UCUCUGUUAUCAU GUGGACUUUUCU	1455	TCTCTGTTATCAT GTGGACTTTTCT	Exon 54
216	GAAAAGUCCACAU GAUAACAG	836	CUGUUAUCAUGUG GACUUUUC	1456	CTGTTATCATGTG GACTTTTC	Exon 54
217	GAAAAGUCCACAU GAUAACAGA	837	UCUGUUAUCAUGU GGACUUUUC	1457	TCTGTTATCATGT GGACTTTTC	Exon 54
218	GAAAAGUCCACAU GAUAACAGAG	838	CUCUGUUAUCAUG UGGACUUUUC	1458	CTCTGTTATCATG TGGACTTTTC	Exon 54

219	GAAAAGUCCACAU GAUAACAGAGA	839	UCUCUGUUAUCAU GUGGACUUUUC	1459	TCTCTGTTATCAT GTGGACTTTTC	Exon 54
220	GAAAAGUCCACAU GAUAACAGAGAA	840	UUCUCUGUUAUCA UGUGGACUUUUC	1460	TTCTCTGTTATCA TGTGGACTTTTC	Exon 54
221	AAAAGUCCACAUG AUAACAGAG	841	CUCUGUUAUCAUG UGGACUUUU	1461	CTCTGTTATCATG TGGACTTTT	Exon 54
222	AAAAGUCCACAUG AUAACAGAGA	842	UCUCUGUUAUCAU GUGGACUUUU	1462	TCTCTGTTATCAT GTGGACTTTT	Exon 54
223	AAAAGUCCACAUG AUAACAGAGAA	843	UUCUCUGUUAUCA UGUGGACUUUU	1463	TTCTCTGTTATCA TGTGGACTTTT	Exon 54
224	AAAAGUCCACAUG AUAACAGAGAAU	844	AUUCUCUGUUAUC AUGUGGACUUUU	1464	ATTCTCTGTTATC ATGTGGACTTTT	Exon 54
225	AAAGUCCACAUGA UAACAGAG	845	CUCUGUUAUCAUG UGGACUUU	1465	CTCTGTTATCATG TGGACTTT	Exon 54
226	AAAGUCCACAUGA UAACAGAGA	846	UCUCUGUUAUCAU GUGGACUUU	1466	TCTCTGTTATCAT GTGGACTTT	Exon 54
227	AAAGUCCACAUGA UAACAGAGAA	847	UUCUCUGUUAUCA UGUGGACUUU	1467	TTCTCTGTTATCA TGTGGACTTT	Exon 54
228	AAAGUCCACAUGA UAACAGAGAAU	848	AUUCUCUGUUAUC AUGUGGACUUU	1468	ATTCTCTGTTATC ATGTGGACTTT	Exon 54
229	AAAGUCCACAUGA UAACAGAGAAUA	849	UAUUCUCUGUUAU CAUGUGGACUUU	1469	TATTCTCTGTTAT CATGTGGACTTT	Exon 54
230	AAGUCCACAUGAU AACAGAG	850	CUCUGUUAUCAUG UGGACUU	1470	CTCTGTTATCATG TGGACTT	Exon 54
231	AAGUCCACAUGAU AACAGAGA	851	UCUCUGUUAUCAU GUGGACUU	1471	TCTCTGTTATCAT GTGGACTT	Exon 54
232	AAGUCCACAUGAU AACAGAGAA	852	UUCUCUGUUAUCA UGUGGACUU	1472	TTCTCTGTTATCA TGTGGACTT	Exon 54
233	AAGUCCACAUGAU AACAGAGAAU	853	AUUCUCUGUUAUC AUGUGGACUU	1473	ATTCTCTGTTATC ATGTGGACTT	Exon 54
234	AAGUCCACAUGAU AACAGAGAAUA	854	UAUUCUCUGUUAU CAUGUGGACUU	1474	TATTCTCTGTTAT CATGTGGACTT	Exon 54
235	AAGUCCACAUGAU AACAGAGAAUAU	855	AUAUUCUCUGUUA UCAUGUGGACUU	1475	ATATTCTCTGTTA TCATGTGGACTT	Exon 54
236	AGUCCACAUGAUA ACAGAGAA	856	UUCUCUGUUAUCA UGUGGACU	1476	TTCTCTGTTATCA TGTGGACT	Exon 54
237	AGUCCACAUGAUA ACAGAGAAU	857	AUUCUCUGUUAUC AUGUGGACU	1477	ATTCTCTGTTATC ATGTGGACT	Exon 54
238	AGUCCACAUGAUA ACAGAGAAUA	858	UAUUCUCUGUUAU CAUGUGGACU	1478	TATTCTCTGTTAT CATGTGGACT	Exon 54
239	AGUCCACAUGAUA ACAGAGAAUAU	859	AUAUUCUCUGUUA UCAUGUGGACU	1479	ATATTCTCTGTTA TCATGTGGACT	Exon 54
240	AGUCCACAUGAUA ACAGAGAAUAUC	860	GAUAUUCUCUGUU AUCAUGUGGACU	1480	GATATTCTCTGTT ATCATGTGGACT	Exon 54
241	GUCCACAUGAUAA CAGAGAAUAUC	861	GAUAUUCUCUGUU AUCAUGUGGAC	1481	GATATTCTCTGTT ATCATGTGGAC	Exon 54
242	GUCCACAUGAUAA CAGAGAAUAUCA	862	UGAUAUUCUCUGU UAUCAUGUGGAC	1482	TGATATTCTCTGT TATCATGTGGAC	Exon 54
243	GGAAGAAACUCAU AGAUUACUGCAA	863	UUGCAGUAAUCUA UGAGUUUCUUCC	1483	TTGCAGTAATCTA TGAGTTTCTTCC	Exon 55
244	GCUGAAACAACUG CCAAUGUCCUA	864	UAGGACAUUGGCA GUUGUUUCAGC	1484	TAGGACATTGGCA GTTGTTTCAGC	Exon 55
245	GCUGAAACAACUG CCAAUGUCCUAC	865	GUAGGACAUUGGC AGUUGUUUCAGC	1485	GTAGGACATTGGC AGTTGTTTCAGC	Exon 55
246	UGAAACAACUGCC AAUGUCCUAC	866	GUAGGACAUUGGC AGUUGUUUCA	1486	GTAGGACATTGGC AGTTGTTTCA	Exon 55
247	UGAAACAACUGCC AAUGUCCUACA	867	UGUAGGACAUUGG CAGUUGUUUCA	1487	TGTAGGACATTGG CAGTTGTTTCA	Exon 55
248	UGAAACAACUGCC AAUGUCCUACAG	868	CUGUAGGACAUUG GCAGUUGUUUCA	1488	CTGTAGGACATTG GCAGTTGTTTCA	Exon 55
249	AACAACUGCCAAU GUCCUACAGGAU	869	AUCCUGUAGGACA UUGGCAGUUGUU	1489	ATCCTGTAGGACA TTGGCAGTTGTT	Exon 55

250	ACAACUGCCAAUG UCCUACAGGAU	870	AUCCUGUAGGACA UUGGCAGUUGU	1490	ATCCTGTAGGACA TTGGCAGTTGT	Exon 55
251	CAACUGCCAAUGU CCUACAGGAU	871	AUCCUGUAGGACA UUGGCAGUUG	1491	ATCCTGTAGGACA TTGGCAGTTG	Exon 55
252	AACUGCCAAUGUC CUACAGGAU	872	AUCCUGUAGGACA UUGGCAGUU	1492	ATCCTGTAGGACA TTGGCAGTT	Exon 55
253	AACUGCCAAUGUC CUACAGGAUGCU	873	AGCAUCCUGUAGG ACAUUGGCAGUU	1493	AGCATCCTGTAGG ACATTGGCAGTT	Exon 55
254	ACUGCCAAUGUCC UACAGGAU	874	AUCCUGUAGGACA UUGGCAGU	1494	ATCCTGTAGGACA TTGGCAGT	Exon 55
255	ACUGCCAAUGUCC UACAGGAUGCU	875	AGCAUCCUGUAGG ACAUUGGCAGU	1495	AGCATCCTGTAGG ACATTGGCAGT	Exon 55
256	CUGCCAAUGUCCU ACAGGAUGCU	876	AGCAUCCUGUAGG ACAUUGGCAG	1496	AGCATCCTGTAGG ACATTGGCAG	Exon 55
257	UGCCAAUGUCCUA CAGGAUGCU	877	AGCAUCCUGUAGG ACAUUGGCA	1497	AGCATCCTGTAGG ACATTGGCA	Exon 55
258	GCCAAUGUCCUAC AGGAUGCU	878	AGCAUCCUGUAGG ACAUUGGC	1498	AGCATCCTGTAGG ACATTGGC	Exon 55
259	AGAUGAUACCAGA AAAGUCC	879	GGACUUUUCUGGU AUCAUCU	1499	GGACTTTTCTGGT ATCATCT	Exon 54
260	AGAUGAUACCAGA AAAGUCCACA	880	UGUGGACUUUUCU GGUAUCAUCU	1500	TGTGGACTTTTCT GGTATCATCT	Exon 54
261	AGAUGAUACCAGA AAAGUCCACAU	881	AUGUGGACUUUUC UGGUAUCAUCU	1501	ATGTGGACTTTTC TGGTATCATCT	Exon 54
262	CUGAAACAACUGC CAAUGUCCUAC	882	GUAGGACAUUGGC AGUUGUUUCAG	1502	GTAGGACATTGGC AGTTGTTTCAG	Exon 55
263	CUGAAACAACUGC CAAUGUCCUACA	883	UGUAGGACAUUGG CAGUUGUUUCAG	1503	TGTAGGACATTGG CAGTTGTTTCAG	Exon 55
264	ACAACUGCCAAUG UCCUACAGGAUG	884	CAUCCUGUAGGAC AUUGGCAGUUGU	1504	CATCCTGTAGGAC ATTGGCAGTTGT	Exon 55
265	CAACUGCCAAUGU CCUACAGGAUG	885	CAUCCUGUAGGAC AUUGGCAGUUG	1505	CATCCTGTAGGAC ATTGGCAGTTG	Exon 55
266	AACUGCCAAUGUC CUACAGGAUG	886	CAUCCUGUAGGAC AUUGGCAGUU	1506	CATCCTGTAGGAC ATTGGCAGTT	Exon 55
267	ACUGCCAAUGUCC UACAGGAUG	887	CAUCCUGUAGGAC AUUGGCAGU	1507	CATCCTGTAGGAC ATTGGCAGT	Exon 55
268	ACUGCCAAUGUCC UACAGGAUGCUA	888	UAGCAUCCUGUAG GACAUUGGCAGU	1508	TAGCATCCTGTAG GACATTGGCAGT	Exon 55
269	CUGCCAAUGUCCU ACAGGAUG	889	CAUCCUGUAGGAC AUUGGCAG	1509	CATCCTGTAGGAC ATTGGCAG	Exon 55
270	CUGCCAAUGUCCU ACAGGAUGCUA	890	UAGCAUCCUGUAG GACAUUGGCAG	1510	TAGCATCCTGTAG GACATTGGCAG	Exon 55
271	UGCCAAUGUCCUA CAGGAUGCUA	891	UAGCAUCCUGUAG GACAUUGGCA	1511	TAGCATCCTGTAG GACATTGGCA	Exon 55
272	UGCCAAUGUCCUA CAGGAUGCUACC	892	GGUAGCAUCCUGU AGGACAUUGGCA	1512	GGTAGCATCCTGT AGGACATTGGCA	Exon 55
273	GCCAAUGUCCUAC AGGAUGCUA	893	UAGCAUCCUGUAG GACAUUGGC	1513	TAGCATCCTGTAG GACATTGGC	Exon 55
274	GCCAAUGUCCUAC AGGAUGCUACC	894	GGUAGCAUCCUGU AGGACAUUGGC	1514	GGTAGCATCCTGT AGGACATTGGC	Exon 55
275	CCAAGGGAGUAAA AGAGCUGA	895	UCAGCUCUUUUAC UCCCUUGG	1515	TCAGCTCTTTTAC TCCCTTGG	Exon 55
276	CCAAGGGAGUAAA AGAGCUGAU	896	AUCAGCUCUUUUA CUCCCUUGG	1516	ATCAGCTCTTTTA CTCCCTTGG	Exon 55
277	CCAAGGGAGUAAA AGAGCUGAUG	897	CAUCAGCUCUUUU ACUCCCUUGG	1517	CATCAGCTCTTTT ACTCCCTTGG	Exon 55
278	CCAAGGGAGUAAA AGAGCUGAUGA	898	UCAUCAGCUCUUU UACUCCCUUGG	1518	TCATCAGCTCTTT TACTCCCTTGG	Exon 55
279	CAAGGGAGUAAAA GAGCUGAUGA	899	UCAUCAGCUCUUU UACUCCCUUG	1519	TCATCAGCTCTTT TACTCCCTTG	Exon 55
280	CAAGGGAGUAAAA GAGCUGAUGAA	900	UUCAUCAGCUCUU UUACUCCCUUG	1520	TTCATCAGCTCTT TTACTCCCTTG	Exon 55

281	AGGGAGUAAAAGA GCUGAUGAAA	901	UUUCAUCAGCUCU UUUACUCCCU	1521	TTTCATCAGCTCT TTTACTCCCT	Exon 55
282	CUGAUGAAACAAU GGCAAGUAAGUC	902	GACUUACUUGCCA UUGUUUCAUCAG	1522	GACTTACTTGCCA TTGTTTCATCAG	Exon 55/intron 55 junction
283	UGAUGAAACAAUG GCAAGUAAGUC	903	GACUUACUUGCCA UUGUUUCAUCA	1523	GACTTACTTGCCA TTGTTTCATCA	Exon 55/intron 55 junction
284	GAUGAAACAAUGG CAAGUAAGUC	904	GACUUACUUGCCA UUGUUUCAUC	1524	GACTTACTTGCCA TTGTTTCATC	Exon 55/intron 55 junction
285	CCUGGAAGGUUCC GAUGAUGC	905	GCAUCAUCGGAAC CUUCCAGG	1525	GCATCATCGGAAC CTTCCAGG	Exon 56
286	CCUGGAAGGUUCC GAUGAUGCA	906	UGCAUCAUCGGAA CCUUCCAGG	1526	TGCATCATCGGAA CCTTCCAGG	Exon 56
287	CAGAUGAUACCAG AAAAGUCCACA	907	UGUGGACUUUUCU GGUAUCAUCUG	1527	TGTGGACTTTTCT GGTATCATCTG	Exon 54
288	CAGAUGAUACCAG AAAAGUCCACAU	908	AUGUGGACUUUUC UGGUAUCAUCUG	1528	ATGTGGACTTTTC TGGTATCATCTG	Exon 54
289	CUGCCAAUGUCCU ACAGGAUGCUAC	909	GUAGCAUCCUGUA GGACAUUGGCAG	1529	GTAGCATCCTGTA GGACATTGGCAG	Exon 55
290	UGCCAAUGUCCUA CAGGAUGCUAC	910	GUAGCAUCCUGUA GGACAUUGGCA	1530	GTAGCATCCTGTA GGACATTGGCA	Exon 55
291	GCCAAUGUCCUAC AGGAUGCUAC	911	GUAGCAUCCUGUA GGACAUUGGC	1531	GTAGCATCCTGTA GGACATTGGC	Exon 55
292	CCAAUGUCCUACA GGAUGCUAC	912	GUAGCAUCCUGUA GGACAUUGG	1532	GTAGCATCCTGTA GGACATTGG	Exon 55
293	AGGGAGUAAAAGA GCUGAUGAAAC	913	GUUUCAUCAGCUC UUUUACUCCCU	1533	GTTTCATCAGCTC TTTTACTCCCT	Exon 55
294	UGAUGAAACAAUG GCAAGUAAGUCA	914	UGACUUACUUGCC AUUGUUUCAUCA	1534	TGACTTACTTGCC ATTGTTTCATCA	Exon 55/intron 55 junction
295	GAUGAAACAAUGG CAAGUAAGUCA	915	UGACUUACUUGCC AUUGUUUCAUC	1535	TGACTTACTTGCC ATTGTTTCATC	Exon 55/intron 55 junction
296	CCUGGAAGGUUCC GAUGAUGCAG	916	CUGCAUCAUCGGA ACCUUCCAGG	1536	CTGCATCATCGGA ACCTTCCAGG	Exon 56
297	GGAAGGUUCCGAU GAUGCAG	917	CUGCAUCAUCGGA ACCUUCC	1537	CTGCATCATCGGA ACCTTCC	Exon 56
298	GAUCCAAUUGAAC AAUUCUCAGCA	918	UGCUGAGAAUUGU UCAAUUGGAUC	1538	TGCTGAGAATTGT TCAATTGGATC	Intron 55
299	AGGUUCCGAUGAU GCAGUCCUGU	919	ACAGGACUGCAUC AUCGGAACCU	1539	ACAGGACTGCATC ATCGGAACCT	Exon 56
300	GGUUCCGAUGAUG CAGUCCUGU	920	ACAGGACUGCAUC AUCGGAACC	1540	ACAGGACTGCATC ATCGGAACC	Exon 56
301	CCUGGAAGGUUCC GAUGAUGCAGU	921	ACUGCAUCAUCGG AACCUUCCAGG	1541	ACTGCATCATCGG AACCTTCCAGG	Exon 56
302	CUGGAAGGUUCCG AUGAUGCAGU	922	ACUGCAUCAUCGG AACCUUCCAG	1542	ACTGCATCATCGG AACCTTCCAG	Exon 56
303	GGAAGGUUCCGAU GAUGCAGU	923	ACUGCAUCAUCGG AACCUUCC	1543	ACTGCATCATCGG AACCTTCC	Exon 56
304	GAAGGUUCCGAUG AUGCAGUCCUGU	924	ACAGGACUGCAUC AUCGGAACCUUC	1544	ACAGGACTGCATC ATCGGAACCTTC	Exon 56
305	GGUUCCGAUGAUG CAGUCCUGUUAC	925	GUAACAGGACUGC AUCAUCGGAACC	1545	GTAACAGGACTGC ATCATCGGAACC	Exon 56
306	GUUCCGAUGAUGC AGUCCUGUUAC	926	GUAACAGGACUGC AUCAUCGGAAC	1546	GTAACAGGACTGC ATCATCGGAAC	Exon 56
307	GUGGAUCCAAUUG AACAAUUCUC	927	GAGAAUUGUUCAA UUGGAUCCAC	1547	GAGAATTGTTCAA TTGGATCCAC	Intron 55
308	GGAUCCAAUUGAA CAAUUCUCAGCA	928	UGCUGAGAAUUGU UCAAUUGGAUCC	1548	TGCTGAGAATTGT TCAATTGGATCC	Intron 55
309	GAUCCAAUUGAAC AAUUCUCAGCAU	929	AUGCUGAGAAUUG UUCAAUUGGAUC	1549	ATGCTGAGAATTG TTCAATTGGATC	Intron 55
310	AAGGUUCCGAUGA UGCAGUCCUGU	930	ACAGGACUGCAUC AUCGGAACCUU	1550	ACAGGACTGCATC ATCGGAACCTT	Exon 56
311	AGGUUCCGAUGAU GCAGUCC	931	GGACUGCAUCAUC GGAACCU	1551	GGACTGCATCATC GGAACCT	Exon 56

312	GUGGAUCCAAUUG AACAAUUCUCA	932	UGAGAAUUGUUCA AUUGGAUCCAC	1552	TGAGAATTGTTCA ATTGGATCCAC	Intron 55
313	AGGUUCCGAUGAU GCAGUCCUGUUA	933	UAACAGGACUGCA UCAUCGGAACCU	1553	TAACAGGACTGCA TCATCGGAACCT	Exon 56
314	GGUUCCGAUGAUG CAGUCCUGUUA	934	UAACAGGACUGCA UCAUCGGAACC	1554	TAACAGGACTGCA TCATCGGAACC	Exon 56
315	CUGGAAGGUUCCG AUGAUGCAGUCC	935	GGACUGCAUCAUC GGAACCUUCCAG	1555	GGACTGCATCATC GGAACCTTCCAG	Exon 56
316	UGGAAGGUUCCGA UGAUGCAGUCC	936	GGACUGCAUCAUC GGAACCUUCCA	1556	GGACTGCATCATC GGAACCTTCCA	Exon 56
317	GGAAGGUUCCGAU GAUGCAGUCC	937	GGACUGCAUCAUC GGAACCUUCC	1557	GGACTGCATCATC GGAACCTTCC	Exon 56
318	UGUGGAUCCAAUU GAACAAUUCUC	938	GAGAAUUGUUCAA UUGGAUCCACA	1558	GAGAATTGTTCAA TTGGATCCACA	Intron 55
319	UUGUGGAUCCAAU UGAACAAUUCUC	939	GAGAAUUGUUCAA UUGGAUCCACAA	1559	GAGAATTGTTCAA TTGGATCCACAA	Intron 55
320	UGUGGAUCCAAUU GAACAAUUCUCA	940	UGAGAAUUGUUCA AUUGGAUCCACA	1560	TGAGAATTGTTCA ATTGGATCCACA	Intron 55
321	GUUCCGAUGAUGC AGUCCUGU	941	ACAGGACUGCAUC AUCGGAAC	1561	ACAGGACTGCATC ATCGGAAC	Exon 56
322	UCCGAUGAUGCAG UCCUGUUA	942	UAACAGGACUGCA UCAUCGGA	1562	TAACAGGACTGCA TCATCGGA	Exon 56
323	UCCGAUGAUGCAG UCCUGUUAC	943	GUAACAGGACUGC AUCAUCGGA	1563	GTAACAGGACTGC ATCATCGGA	Exon 56
324	GUUCCGAUGAUGC AGUCCUGUUA	944	UAACAGGACUGCA UCAUCGGAAC	1564	TAACAGGACTGCA TCATCGGAAC	Exon 56
325	UUCCGAUGAUGCA GUCCUGUUAC	945	GUAACAGGACUGC AUCAUCGGAA	1565	GTAACAGGACTGC ATCATCGGAA	Exon 56
326	CUCCAAAUUCACA UUCAUCGCUUG	946	CAAGCGAUGAAUG UGAAUUUGGAG	1566	CAAGCGATGAATG TGAATTTGGAG	Intron 55
327	GAAGGUUCCGAUG AUGCAGUCC	947	GGACUGCAUCAUC GGAACCUUC	1567	GGACTGCATCATC GGAACCTTC	Exon 56
328	AAGGUUCCGAUGA UGCAGUCC	948	GGACUGCAUCAUC GGAACCUU	1568	GGACTGCATCATC GGAACCTT	Exon 56
329	GGAGCUUGGGAGG GUUCAAGACGA	949	UCGUCUUGAACCC UCCCAAGCUCC	1569	TCGTCTTGAACCC TCCCAAGCTCC	Intron 54
330	GGAGCUUGGGAGG GUUCAAGACGAU	950	AUCGUCUUGAACC CUCCCAAGCUCC	1570	ATCGTCTTGAACC CTCCCAAGCTCC	Intron 54
331	UGGCUGUAAUAAU GGGGUGGUG	951	CACCACCCCAUUA UUACAGCCA	1571	CACCACCCCATTA TTACAGCCA	Intron 54
332	UGGCUGUAAUAAU GGGGUGGUGA	952	UCACCACCCCAUU AUUACAGCCA	1572	TCACCACCCCATT ATTACAGCCA	Intron 54
333	GGCUGUAAUAAUG GGGUGGUGA	953	UCACCACCCCAUU AUUACAGCC	1573	TCACCACCCCATT ATTACAGCC	Intron 54
334	GGGGUGGUGAAAC UGGAUGG	954	CCAUCCAGUUUCA CCACCCC	1574	CCATCCAGTTTCA CCACCCC	Intron 54
335	UUGGCUGUAAUAA UGGGGUGGUGA	955	UCACCACCCCAUU AUUACAGCCAA	1575	TCACCACCCCATT ATTACAGCCAA	Intron 54
336	GGGGUGGUGAAAC UGGAUGGA	956	UCCAUCCAGUUUC ACCACCCC	1576	TCCATCCAGTTTC ACCACCCC	Intron 54
337	GCUGUAAUAAUGG GGUGGUGA	957	UCACCACCCCAUU AUUACAGC	1577	TCACCACCCCATT ATTACAGC	Intron 54
338	UGGGGUGGUGAAA CUGGAUGG	958	CCAUCCAGUUUCA CCACCCCA	1578	CCATCCAGTTTCA CCACCCCA	Intron 54
339	UGGCUGUAAUAAU GGGGUGGUGAAA	959	UUUCACCACCCCA UUAUUACAGCCA	1579	TTTCACCACCCCA TTATTACAGCCA	Intron 54
340	GGCUGUAAUAAUG GGGUGGUGAAA	960	UUUCACCACCCCA UUAUUACAGCC	1580	TTTCACCACCCCA TTATTACAGCC	Intron 54
341	UGGGGUGGUGAAA CUGGAUG	961	CAUCCAGUUUCAC CACCCCA	1581	CATCCAGTTTCAC CACCCCA	Intron 54
342	UGGGGUGGUGAAA CUGGAUGGA	962	UCCAUCCAGUUUC ACCACCCCA	1582	TCCATCCAGTTTC ACCACCCCA	Intron 54

343	AUGGCAAGUAAGU CAGGCAUUUCC	963	GGAAAUGCCUGAC UUACUUGCCAU	1583	GGAAATGCCTGAC TTACTTGCCAT	Exon 55/intron 55 junction
344	GCUGUAAUAAUGG GGUGGUGAAACU	964	AGUUUCACCACCC CAUUAUUACAGC	1584	AGTTTCACCACCC CATTATTACAGC	Intron 54
345	AUGGGGUGGUGAA ACUGGAUG	965	CAUCCAGUUUCAC CACCCCAU	1585	CATCCAGTTTCAC CACCCCAT	Intron 54
346	AUGGGGUGGUGAA ACUGGAUGG	966	CCAUCCAGUUUCA CCACCCCAU	1586	CCATCCAGTTTCA CCACCCCAT	Intron 54
347	GCAAGUAAGUCAG GCAUUUCCGC	967	GCGGAAAUGCCUG ACUUACUUGC	1587	GCGGAAATGCCTG ACTTACTTGC	Exon 55/intron 55 junction
348	GGCUGUAAUAAUG GGGUGGUGAAAC	968	GUUUCACCACCCC AUUAUUACAGCC	1588	GTTTCACCACCCC ATTATTACAGCC	Intron 54
349	AAUGGGGUGGUGA AACUGGAUG	969	CAUCCAGUUUCAC CACCCCAUU	1589	CATCCAGTTTCAC CACCCCATT	Intron 54
350	AUGGGGUGGUGAA ACUGGAUGGA	970	UCCAUCCAGUUUC ACCACCCCAU	1590	TCCATCCAGTTTC ACCACCCCAT	Intron 54
351	UGGCAAGUAAGUC AGGCAUUUCCGC	971	GCGGAAAUGCCUG ACUUACUUGCCA	1591	GCGGAAATGCCTG ACTTACTTGCCA	Exon 55/intron 55 junction
352	GCUGUAAUAAUGG GGUGGUGAAA	972	UUUCACCACCCCA UUAUUACAGC	1592	TTTCACCACCCCA TTATTACAGC	Intron 54
353	UAAUGGGGUGGUG AAACUGGAUG	973	CAUCCAGUUUCAC CACCCCAUUA	1593	CATCCAGTTTCAC CACCCCATTA	Intron 54
354	UAAUGGGGUGGUG AAACUGGAUGG	974	CCAUCCAGUUUCA CCACCCCAUUA	1594	CCATCCAGTTTCA CCACCCCATTA	Intron 54
355	AAUGGGGUGGUGA AACUGGAUGG	975	CCAUCCAGUUUCA CCACCCCAUU	1595	CCATCCAGTTTCA CCACCCCATT	Intron 54
356	AUGGCAAGUAAGU CAGGCAUUUC	976	GAAAUGCCUGACU UACUUGCCAU	1596	GAAATGCCTGACT TACTTGCCAT	Exon 55/intron 55 junction
357	GGCAAGUAAGUCA GGCAUUUCCGC	977	GCGGAAAUGCCUG ACUUACUUGCC	1597	GCGGAAATGCCTG ACTTACTTGCC	Exon 55/intron 55 junction
358	GGCAAGUAAGUCA GGCAUUUCCGCU	978	AGCGGAAAUGCCU GACUUACUUGCC	1598	AGCGGAAATGCCT GACTTACTTGCC	Exon 55/intron 55 junction
359	AAUGGGGUGGUGA AACUGGAUGGA	979	UCCAUCCAGUUUC ACCACCCCAUU	1599	TCCATCCAGTTTC ACCACCCCATT	Intron 54
360	GGGUGGUGAAACU GGAUGGA	980	UCCAUCCAGUUUC ACCACCC	1600	TCCATCCAGTTTC ACCACCC	Intron 54
361	AUAAUGGGGUGGU GAAACUGGAUG	981	CAUCCAGUUUCAC CACCCCAUUAU	1601	CATCCAGTTTCAC CACCCCATTAT	Intron 54
362	AUAAUGGGGUGGU GAAACUGGAUGG	982	CCAUCCAGUUUCA CCACCCCAUUAU	1602	CCATCCAGTTTCA CCACCCCATTAT	Intron 54
363	UAAUGGGGUGGUG AAACUGGAUGGA	983	UCCAUCCAGUUUC ACCACCCCAUUA	1603	TCCATCCAGTTTC ACCACCCCATTA	Intron 54
364	AAUGGCAAGUAAG UCAGGCAUUUC	984	GAAAUGCCUGACU UACUUGCCAUU	1604	GAAATGCCTGACT TACTTGCCATT	Exon 55/intron 55 junction
365	AAUAAUGGGGUGG UGAAACUGGAUG	985	CAUCCAGUUUCAC CACCCCAUUAUU	1605	CATCCAGTTTCAC CACCCCATTATT	Intron 54
366	AAUGGCAAGUAAG UCAGGCAUUUCC	986	GGAAAUGCCUGAC UUACUUGCCAUU	1606	GGAAATGCCTGAC TTACTTGCCATT	Exon 55/intron 55 junction
367	UGGCAAGUAAGUC AGGCAUUUCC	987	GGAAAUGCCUGAC UUACUUGCCA	1607	GGAAATGCCTGAC TTACTTGCCA	Exon 55/intron 55 junction
368	CCGAUGAUGCAGU CCUGUUAC	988	GUAACAGGACUGC AUCAUCGG	1608	GTAACAGGACTGC ATCATCGG	Exon 56
369	UCCAAAUUCACAU UCAUCGCUUGU	989	ACAAGCGAUGAAU GUGAAUUUGGA	1609	ACAAGCGATGAAT GTGAATTTGGA	Intron 55
370	GUAAUAAUGGGGU GGUGAAAC	990	GUUUCACCACCCC AUUAUUAC	1610	GTTTCACCACCCC ATTATTAC	Intron 54
371	GCUGUAAUAAUGG GGUGGUGAAAC	991	GUUUCACCACCCC AUUAUUACAGC	1611	GTTTCACCACCCC ATTATTACAGC	Intron 54
372	GCUUUGGAAGAAA CUCAUAGAUUAC	992	GUAAUCUAUGAGU UUCUUCCAAAGC	1612	GTAATCTATGAGT TTCTTCCAAAGC	Exon 55
373	UUGGAAGAAACUC AUAGAUUACUGC	993	GCAGUAAUCUAUG AGUUUCUUCCAA	1613	GCAGTAATCTATG AGTTTCTTCCAA	Exon 55

374	UGGAAGAAACUCA UAGAUUACUGC	994	GCAGUAAUCUAUG AGUUUCUUCCA	1614	GCAGTAATCTATG AGTTTCTTCCA	Exon 55
375	UGGAAGAAACUCA UAGAUUACUGCA	995	UGCAGUAAUCUAU GAGUUUCUUCCA	1615	TGCAGTAATCTAT GAGTTTCTTCCA	Exon 55
376	GGAAGAAACUCAU AGAUUACUGC	996	GCAGUAAUCUAUG AGUUUCUUCC	1616	GCAGTAATCTATG AGTTTCTTCC	Exon 55
377	GAAGAAACUCAUA GAUUACUGCA	997	UGCAGUAAUCUAU GAGUUUCUUC	1617	TGCAGTAATCTAT GAGTTTCTTC	Exon 55
378	AAACAACUGCCAA UGUCCUACA	998	UGUAGGACAUUGG CAGUUGUUU	1618	TGTAGGACATTGG CAGTTGTTT	Exon 55
379	AAACAACUGCCAA UGUCCUACAG	999	CUGUAGGACAUUG GCAGUUGUUU	1619	CTGTAGGACATTG GCAGTTGTTT	Exon 55
380	AACAACUGCCAAU GUCCUAC	1000	GUAGGACAUUGGC AGUUGUU	1620	GTAGGACATTGGC AGTTGTT	Exon 55
381	AACAACUGCCAAU GUCCUACA	1001	UGUAGGACAUUGG CAGUUGUU	1621	TGTAGGACATTGG CAGTTGTT	Exon 55
382	CAACUGCCAAUGU CCUACAG	1002	CUGUAGGACAUUG GCAGUUG	1622	CTGTAGGACATTG GCAGTTG	Exon 55
383	AACUGCCAAUGUC CUACAGG	1003	CCUGUAGGACAUU GGCAGUU	1623	CCTGTAGGACATT GGCAGTT	Exon 55
384	GAUGAAAACAGCC AAAAAAUCC	1004	GGAUUUUUUGGCU GUUUUCAUC	1624	GGATTTTTTGGCT GTTTTCATC	Exon 56
385	GAUGAAAACAGCC AAAAAAUCCU	1005	AGGAUUUUUUGGC UGUUUUCAUC	1625	AGGATTTTTTGGC TGTTTTCATC	Exon 56
386	GAUGAAAACAGCC AAAAAAUCCUG	1006	CAGGAUUUUUUGG CUGUUUUCAUC	1626	CAGGATTTTTTGG CTGTTTTCATC	Exon 56
387	GAUGAAAACAGCC AAAAAAUCCUGA	1007	UCAGGAUUUUUUG GCUGUUUUCAUC	1627	TCAGGATTTTTTG GCTGTTTTCATC	Exon 56
388	AUGAAAACAGCCA AAAAAUCCUGAG	1008	CUCAGGAUUUUUU GGCUGUUUUCAU	1628	CTCAGGATTTTTT GGCTGTTTTCAT	Exon 56
389	UGAAAACAGCCAA AAAAUCCUGAG	1009	CUCAGGAUUUUUU GGCUGUUUUCA	1629	CTCAGGATTTTTT GGCTGTTTTCA	Exon 56
390	UGAAAACAGCCAA AAAAUCCUGAGA	1010	UCUCAGGAUUUUU UGGCUGUUUUCA	1630	TCTCAGGATTTTT TGGCTGTTTTCA	Exon 56
391	GAAAACAGCCAAA AAAUCCUGAGA	1011	UCUCAGGAUUUUU UGGCUGUUUUC	1631	TCTCAGGATTTTT TGGCTGTTTTC	Exon 56
392	GAAAACAGCCAAA AAAUCCUGAGAU	1012	AUCUCAGGAUUUU UUGGCUGUUUUC	1632	ATCTCAGGATTTT TTGGCTGTTTTC	Exon 56
393	AAACAGCCAAAAA AUCCUGAGAUC	1013	GAUCUCAGGAUUU UUUGGCUGUUU	1633	GATCTCAGGATTT TTTGGCTGTTT	Exon 56
394	AAACAGCCAAAAA AUCCUGAGAUCC	1014	GGAUCUCAGGAUU UUUUGGCUGUUU	1634	GGATCTCAGGATT TTTTGGCTGTTT	Exon 56
395	AACAGCCAAAAAA UCCUGAGAUCC	1015	GGAUCUCAGGAUU UUUUGGCUGUU	1635	GGATCTCAGGATT TTTTGGCTGTT	Exon 56
396	AACAGCCAAAAAA UCCUGAGAUCCC	1016	GGGAUCUCAGGAU UUUUUGGCUGUU	1636	GGGATCTCAGGAT TTTTTGGCTGTT	Exon 56
397	CCUGAGAUCCCUG GAAGGUUC	1017	GAACCUUCCAGGG AUCUCAGG	1637	GAACCTTCCAGGG ATCTCAGG	Exon 56
398	GAAGAAACUCAUA GAUUACUGCAAC	1018	GUUGCAGUAAUCU AUGAGUUUCUUC	1638	GTTGCAGTAATCT ATGAGTTTCTTC	Exon 55
399	AAGAAACUCAUAG AUUACUGCAAC	1019	GUUGCAGUAAUCU AUGAGUUUCUU	1639	GTTGCAGTAATCT ATGAGTTTCTT	Exon 55
400	AAGAAACUCAUAG AUUACUGCAACA	1020	UGUUGCAGUAAUC UAUGAGUUUCUU	1640	TGTTGCAGTAATC TATGAGTTTCTT	Exon 55
401	AGAAACUCAUAGA UUACUGCAAC	1021	GUUGCAGUAAUCU AUGAGUUUCU	1641	GTTGCAGTAATCT ATGAGTTTCT	Exon 55
402	GAAACUCAUAGAU UACUGCAAC	1022	GUUGCAGUAAUCU AUGAGUUUC	1642	GTTGCAGTAATCT ATGAGTTTC	Exon 55
403	GAAACUCAUAGAU UACUGCAACA	1023	UGUUGCAGUAAUC UAUGAGUUUC	1643	TGTTGCAGTAATC TATGAGTTTC	Exon 55
404	AAACUCAUAGAUU ACUGCAACAG	1024	CUGUUGCAGUAAU CUAUGAGUUU	1644	CTGTTGCAGTAAT CTATGAGTTT	Exon 55

405	AACUCAUAGAUUA CUGCAAC	1025	GUUGCAGUAAUCU AUGAGUU	1645	GTTGCAGTAATCT ATGAGTT	Exon 55
406	AACUCAUAGAUUA CUGCAACA	1026	UGUUGCAGUAAUC UAUGAGUU	1646	TGTTGCAGTAATC TATGAGTT	Exon 55
407	AACUCAUAGAUUA CUGCAACAG	1027	CUGUUGCAGUAAU CUAUGAGUU	1647	CTGTTGCAGTAAT CTATGAGTT	Exon 55
408	ACUCAUAGAUUAC UGCAACA	1028	UGUUGCAGUAAUC UAUGAGU	1648	TGTTGCAGTAATC TATGAGT	Exon 55
409	ACUCAUAGAUUAC UGCAACAG	1029	CUGUUGCAGUAAU CUAUGAGU	1649	CTGTTGCAGTAAT CTATGAGT	Exon 55
410	GAUGAUACCAGAA AAGUCCA	1030	UGGACUUUUCUGG UAUCAUC	1650	TGGACTTTTCTGG TATCATC	Exon 54
411	GAUGAUACCAGAA AAGUCCAC	1031	GUGGACUUUUCUG GUAUCAUC	1651	GTGGACTTTTCTG GTATCATC	Exon 54
412	GAUGAUACCAGAA AAGUCCACA	1032	UGUGGACUUUUCU GGUAUCAUC	1652	TGTGGACTTTTCT GGTATCATC	Exon 54
413	GAUGAUACCAGAA AAGUCCACAUG	1033	CAUGUGGACUUUU CUGGUAUCAUC	1653	CATGTGGACTTTT CTGGTATCATC	Exon 54
414	AUGAUACCAGAAA AGUCCACAU	1034	AUGUGGACUUUUC UGGUAUCAU	1654	ATGTGGACTTTTC TGGTATCAT	Exon 54
415	AUGAUACCAGAAA AGUCCACAUG	1035	CAUGUGGACUUUU CUGGUAUCAU	1655	CATGTGGACTTTT CTGGTATCAT	Exon 54
416	UGAUACCAGAAAA GUCCACA	1036	UGUGGACUUUUCU GGUAUCA	1656	TGTGGACTTTTCT GGTATCA	Exon 54
417	UGAUACCAGAAAA GUCCACAU	1037	AUGUGGACUUUUC UGGUAUCA	1657	ATGTGGACTTTTC TGGTATCA	Exon 54
418	UGAUACCAGAAAA GUCCACAUG	1038	CAUGUGGACUUUU CUGGUAUCA	1658	CATGTGGACTTTT CTGGTATCA	Exon 54
419	UGAUACCAGAAAA GUCCACAUGAUA	1039	UAUCAUGUGGACU UUUCUGGUAUCA	1659	TATCATGTGGACT TTTCTGGTATCA	Exon 54
420	GAUACCAGAAAAG UCCACAU	1040	AUGUGGACUUUUC UGGUAUC	1660	ATGTGGACTTTTC TGGTATC	Exon 54
421	GAUACCAGAAAAG UCCACAUG	1041	CAUGUGGACUUUU CUGGUAUC	1661	CATGTGGACTTTT CTGGTATC	Exon 54
422	GAUACCAGAAAAG UCCACAUGAUA	1042	UAUCAUGUGGACU UUUCUGGUAUC	1662	TATCATGTGGACT TTTCTGGTATC	Exon 54
423	AUACCAGAAAAGU CCACAUG	1043	CAUGUGGACUUUU CUGGUAU	1663	CATGTGGACTTTT CTGGTAT	Exon 54
424	AUACCAGAAAAGU CCACAUGAUA	1044	UAUCAUGUGGACU UUUCUGGUAU	1664	TATCATGTGGACT TTTCTGGTAT	Exon 54
425	AUACCAGAAAAGU CCACAUGAUAA	1045	UUAUCAUGUGGAC UUUUCUGGUAU	1665	TTATCATGTGGAC TTTTCTGGTAT	Exon 54
426	UACCAGAAAAGUC CACAUGAUA	1046	UAUCAUGUGGACU UUUCUGGUA	1666	TATCATGTGGACT TTTCTGGTA	Exon 54
427	ACCAGAAAAGUCC ACAUGAUA	1047	UAUCAUGUGGACU UUUCUGGU	1667	TATCATGTGGACT TTTCTGGT	Exon 54
428	CCAGAAAAGUCCA CAUGAUA	1048	UAUCAUGUGGACU UUUCUGG	1668	TATCATGTGGACT TTTCTGG	Exon 54
429	CAGAAAAGUCCAC AUGAUAA	1049	UUAUCAUGUGGAC UUUUCUG	1669	TTATCATGTGGAC TTTTCTG	Exon 54
430	AGAAAAGUCCACA UGAUAAC	1050	GUUAUCAUGUGGA CUUUUCU	1670	GTTATCATGTGGA CTTTTCT	Exon 54
431	AGAAAAGUCCACA UGAUAACA	1051	UGUUAUCAUGUGG ACUUUUCU	1671	TGTTATCATGTGG ACTTTTCT	Exon 54
432	AGAAAAGUCCACA UGAUAACAG	1052	CUGUUAUCAUGUG GACUUUUCU	1672	CTGTTATCATGTG GACTTTTCT	Exon 54
433	GAAAAGUCCACAU GAUAACA	1053	UGUUAUCAUGUGG ACUUUUC	1673	TGTTATCATGTGG ACTTTTC	Exon 54
434	AAAAGUCCACAUG AUAACAGA	1054	UCUGUUAUCAUGU GGACUUUU	1674	TCTGTTATCATGT GGACTTTT	Exon 54
435	AAAGUCCACAUGA UAACAGA	1055	UCUGUUAUCAUGU GGACUUU	1675	TCTGTTATCATGT GGACTTT	Exon 54

436	AGUCCACAUGAUA ACAGAGA	1056	UCUCUGUUAUCAU GUGGACU	1676	TCTCTGTTATCAT GTGGACT	Exon 54
437	GUCCACAUGAUAA CAGAGAA	1057	UUCUCUGUUAUCA UGUGGAC	1677	TTCTCTGTTATCA TGTGGAC	Exon 54
438	GUCCACAUGAUAA CAGAGAAU	1058	AUUCUCUGUUAUC AUGUGGAC	1678	ATTCTCTGTTATC ATGTGGAC	Exon 54
439	GUCCACAUGAUAA CAGAGAAUA	1059	UAUUCUCUGUUAU CAUGUGGAC	1679	TATTCTCTGTTAT CATGTGGAC	Exon 54
440	GUCCACAUGAUAA CAGAGAAUAU	1060	AUAUUCUCUGUUA UCAUGUGGAC	1680	ATATTCTCTGTTA TCATGTGGAC	Exon 54
441	CCACAUGAUAACA GAGAAUA	1061	UAUUCUCUGUUAU CAUGUGG	1681	TATTCTCTGTTAT CATGTGG	Exon 54
442	GAAGAAACUCAUA GAUUACUGCAA	1062	UUGCAGUAAUCUA UGAGUUUCUUC	1682	TTGCAGTAATCTA TGAGTTTCTTC	Exon 55
443	GAAGCUGAAACAA CUGCCAAUGUCC	1063	GGACAUUGGCAGU UGUUUCAGCUUC	1683	GGACATTGGCAGT TGTTTCAGCTTC	Exon 55
444	AAGCUGAAACAAC UGCCAAUGUCC	1064	GGACAUUGGCAGU UGUUUCAGCUU	1684	GGACATTGGCAGT TGTTTCAGCTT	Exon 55
445	AAGCUGAAACAAC UGCCAAUGUCCU	1065	AGGACAUUGGCAG UUGUUUCAGCUU	1685	AGGACATTGGCAG TTGTTTCAGCTT	Exon 55
446	AGCUGAAACAACU GCCAAUGUC	1066	GACAUUGGCAGUU GUUUCAGCU	1686	GACATTGGCAGTT GTTTCAGCT	Exon 55
447	AGCUGAAACAACU GCCAAUGUCC	1067	GGACAUUGGCAGU UGUUUCAGCU	1687	GGACATTGGCAGT TGTTTCAGCT	Exon 55
448	AGCUGAAACAACU GCCAAUGUCCU	1068	AGGACAUUGGCAG UUGUUUCAGCU	1688	AGGACATTGGCAG TTGTTTCAGCT	Exon 55
449	AGCUGAAACAACU GCCAAUGUCCUA	1069	UAGGACAUUGGCA GUUGUUUCAGCU	1689	TAGGACATTGGCA GTTGTTTCAGCT	Exon 55
450	GCUGAAACAACUG CCAAUGUC	1070	GACAUUGGCAGUU GUUUCAGC	1690	GACATTGGCAGTT GTTTCAGC	Exon 55
451	GCUGAAACAACUG CCAAUGUCC	1071	GGACAUUGGCAGU UGUUUCAGC	1691	GGACATTGGCAGT TGTTTCAGC	Exon 55
452	GCUGAAACAACUG CCAAUGUCCU	1072	AGGACAUUGGCAG UUGUUUCAGC	1692	AGGACATTGGCAG TTGTTTCAGC	Exon 55
453	CAACUGCCAAUGU CCUACAGGAUGC	1073	GCAUCCUGUAGGA CAUUGGCAGUUG	1693	GCATCCTGTAGGA CATTGGCAGTTG	Exon 55
454	AACUGCCAAUGUC CUACAGGAUGC	1074	GCAUCCUGUAGGA CAUUGGCAGUU	1694	GCATCCTGTAGGA CATTGGCAGTT	Exon 55
455	ACUGCCAAUGUCC UACAGGAUGC	1075	GCAUCCUGUAGGA CAUUGGCAGU	1695	GCATCCTGTAGGA CATTGGCAGT	Exon 55
456	CUGCCAAUGUCCU ACAGGAU	1076	AUCCUGUAGGACA UUGGCAG	1696	ATCCTGTAGGACA TTGGCAG	Exon 55
457	CUGCCAAUGUCCU ACAGGAUGC	1077	GCAUCCUGUAGGA CAUUGGCAG	1697	GCATCCTGTAGGA CATTGGCAG	Exon 55
458	UGCCAAUGUCCUA CAGGAUGC	1078	GCAUCCUGUAGGA CAUUGGCA	1698	GCATCCTGTAGGA CATTGGCA	Exon 55
459	GCCAAUGUCCUAC AGGAUGC	1079	GCAUCCUGUAGGA CAUUGGC	1699	GCATCCTGTAGGA CATTGGC	Exon 55
460	CCAAUGUCCUACA GGAUGCU	1080	AGCAUCCUGUAGG ACAUUGG	1700	AGCATCCTGTAGG ACATTGG	Exon 55
461	AGAGCUGAUGAAA CAAUGGCAAG	1081	CUUGCCAUUGUUU CAUCAGCUCU	1701	CTTGCCATTGTTT CATCAGCTCT	Exon 55/intron 55 junction
462	AGAGCUGAUGAAA CAAUGGCAAGU	1082	ACUUGCCAUUGUU UCAUCAGCUCU	1702	ACTTGCCATTGTT TCATCAGCTCT	Exon 55/intron 55 junction
463	AGAGCUGAUGAAA CAAUGGCAAGUA	1083	UACUUGCCAUUGU UUCAUCAGCUCU	1703	TACTTGCCATTGT TTCATCAGCTCT	Exon 55/intron 55 junction
464	GAGCUGAUGAAAC AAUGGCAAGU	1084	ACUUGCCAUUGUU UCAUCAGCUC	1704	ACTTGCCATTGTT TCATCAGCTC	Exon 55/intron 55 junction
465	GAGCUGAUGAAAC AAUGGCAAGUA	1085	UACUUGCCAUUGU UUCAUCAGCUC	1705	TACTTGCCATTGT TTCATCAGCTC	Exon 55/intron 55 junction
466	GAGCUGAUGAAAC AAUGGCAAGUAA	1086	UUACUUGCCAUUG UUUCAUCAGCUC	1706	TTACTTGCCATTG TTTCATCAGCTC	Exon 55/intron 55 junction

467	AGCUGAUGAAACA AUGGCAAGUAAG	1087	CUUACUUGCCAUU GUUUCAUCAGCU	1707	CTTACTTGCCATT GTTTCATCAGCT	Exon 55/intron 55 junction
468	GCUGAUGAAACAA UGGCAAGUAAG	1088	CUUACUUGCCAUU GUUUCAUCAGC	1708	CTTACTTGCCATT GTTTCATCAGC	Exon 55/intron 55 junction
469	GCUGAUGAAACAA UGGCAAGUAAGU	1089	ACUUACUUGCCAU UGUUUCAUCAGC	1709	ACTTACTTGCCAT TGTTTCATCAGC	Exon 55/intron 55 junction
470	CUGAUGAAACAAU GGCAAGUAAGU	1090	ACUUACUUGCCAU UGUUUCAUCAG	1710	ACTTACTTGCCAT TGTTTCATCAG	Exon 55/intron 55 junction
471	UAUCACAACCUGG AUGAAAACAGCC	1091	GGCUGUUUUCAUC CAGGUUGUGAUA	1711	GGCTGTTTTCATC CAGGTTGTGATA	Exon 56
472	AUCACAACCUGGA UGAAAACAGCC	1092	GGCUGUUUUCAUC CAGGUUGUGAU	1712	GGCTGTTTTCATC CAGGTTGTGAT	Exon 56
473	AUCACAACCUGGA UGAAAACAGCCA	1093	UGGCUGUUUUCAU CCAGGUUGUGAU	1713	TGGCTGTTTTCAT CCAGGTTGTGAT	Exon 56
474	UCACAACCUGGAU GAAAACAGCC	1094	GGCUGUUUUCAUC CAGGUUGUGA	1714	GGCTGTTTTCATC CAGGTTGTGA	Exon 56
475	UCACAACCUGGAU GAAAACAGCCA	1095	UGGCUGUUUUCAU CCAGGUUGUGA	1715	TGGCTGTTTTCAT CCAGGTTGTGA	Exon 56
476	UCACAACCUGGAU GAAAACAGCCAA	1096	UUGGCUGUUUUCA UCCAGGUUGUGA	1716	TTGGCTGTTTTCA TCCAGGTTGTGA	Exon 56
477	CACAACCUGGAUG AAAACAGCCAAA	1097	UUUGGCUGUUUUC AUCCAGGUUGUG	1717	TTTGGCTGTTTTC ATCCAGGTTGTG	Exon 56
478	ACAACCUGGAUGA AAACAGCCAAAA	1098	UUUUGGCUGUUUU CAUCCAGGUUGU	1718	TTTTGGCTGTTTT CATCCAGGTTGT	Exon 56
479	GGAUGAAAACAGC CAAAAAAUC	1099	GAUUUUUUGGCUG UUUUCAUCC	1719	GATTTTTTGGCTG TTTTCATCC	Exon 56
480	GGAUGAAAACAGC CAAAAAAUCC	1100	GGAUUUUUUGGCU GUUUUCAUCC	1720	GGATTTTTTGGCT GTTTTCATCC	Exon 56
481	GGAUGAAAACAGC CAAAAAAUCCU	1101	AGGAUUUUUUGGC UGUUUUCAUCC	1721	AGGATTTTTTGGC TGTTTTCATCC	Exon 56
482	GGAUGAAAACAGC CAAAAAAUCCUG	1102	CAGGAUUUUUUGG CUGUUUUCAUCC	1722	CAGGATTTTTTGG CTGTTTTCATCC	Exon 56
483	ACAGCCAAAAAAU CCUGAGAUCC	1103	GGAUCUCAGGAUU UUUUGGCUGU	1723	GGATCTCAGGATT TTTTGGCTGT	Exon 56
484	ACAGCCAAAAAAU CCUGAGAUCCC	1104	GGGAUCUCAGGAU UUUUUGGCUGU	1724	GGGATCTCAGGAT TTTTTGGCTGT	Exon 56
485	CCUGAGAUCCCUG GAAGGUUCCGA	1105	UCGGAACCUUCCA GGGAUCUCAGG	1725	TCGGAACCTTCCA GGGATCTCAGG	Exon 56
486	CCUGAGAUCCCUG GAAGGUUCCGAU	1106	AUCGGAACCUUCC AGGGAUCUCAGG	1726	ATCGGAACCTTCC AGGGATCTCAGG	Exon 56
487	CUGAGAUCCCUGG AAGGUUCCGA	1107	UCGGAACCUUCCA GGGAUCUCAG	1727	TCGGAACCTTCCA GGGATCTCAG	Exon 56
488	CUGAGAUCCCUGG AAGGUUCCGAU	1108	AUCGGAACCUUCC AGGGAUCUCAG	1728	ATCGGAACCTTCC AGGGATCTCAG	Exon 56
489	CUGAGAUCCCUGG AAGGUUCCGAUG	1109	CAUCGGAACCUUC CAGGGAUCUCAG	1729	CATCGGAACCTTC CAGGGATCTCAG	Exon 56
490	UGAGAUCCCUGGA AGGUUCCGA	1110	UCGGAACCUUCCA GGGAUCUCA	1730	TCGGAACCTTCCA GGGATCTCA	Exon 56
491	UGAGAUCCCUGGA AGGUUCCGAU	1111	AUCGGAACCUUCC AGGGAUCUCA	1731	ATCGGAACCTTCC AGGGATCTCA	Exon 56
492	UGAGAUCCCUGGA AGGUUCCGAUG	1112	CAUCGGAACCUUC CAGGGAUCUCA	1732	CATCGGAACCTTC CAGGGATCTCA	Exon 56
493	UGAGAUCCCUGGA AGGUUCCGAUGA	1113	UCAUCGGAACCUU CCAGGGAUCUCA	1733	TCATCGGAACCTT CCAGGGATCTCA	Exon 56
494	GAGAUCCCUGGAA GGUUCCGA	1114	UCGGAACCUUCCA GGGAUCUC	1734	TCGGAACCTTCCA GGGATCTC	Exon 56
495	GAGAUCCCUGGAA GGUUCCGAU	1115	AUCGGAACCUUCC AGGGAUCUC	1735	ATCGGAACCTTCC AGGGATCTC	Exon 56
496	GAGAUCCCUGGAA GGUUCCGAUG	1116	CAUCGGAACCUUC CAGGGAUCUC	1736	CATCGGAACCTTC CAGGGATCTC	Exon 56
497	GAGAUCCCUGGAA GGUUCCGAUGA	1117	UCAUCGGAACCUU CCAGGGAUCUC	1737	TCATCGGAACCTT CCAGGGATCTC	Exon 56

498	AGAUCCCUGGAAG GUUCCGAUG	1118	CAUCGGAACCUUC CAGGGAUCU	1738	CATCGGAACCTTC CAGGGATCT	Exon 56
499	AGAUCCCUGGAAG GUUCCGAUGA	1119	UCAUCGGAACCUU CCAGGGAUCU	1739	TCATCGGAACCTT CCAGGGATCT	Exon 56
500	GAUCCCUGGAAGG UUCCGAU	1120	AUCGGAACCUUCC AGGGAUC	1740	ATCGGAACCTTCC AGGGATC	Exon 56
501	GAUCCCUGGAAGG UUCCGAUG	1121	CAUCGGAACCUUC CAGGGAUC	1741	CATCGGAACCTTC CAGGGATC	Exon 56
502	GAUCCCUGGAAGG UUCCGAUGA	1122	UCAUCGGAACCUU CCAGGGAUC	1742	TCATCGGAACCTT CCAGGGATC	Exon 56
503	AUCCCUGGAAGGU UCCGAUGA	1123	UCAUCGGAACCUU CCAGGGAU	1743	TCATCGGAACCTT CCAGGGAT	Exon 56
504	UCCCUGGAAGGUU CCGAUGA	1124	UCAUCGGAACCUU CCAGGGA	1744	TCATCGGAACCTT CCAGGGA	Exon 56
505	AGAUGAUACCAGA AAAGUCCA	1125	UGGACUUUUCUGG UAUCAUCU	1745	TGGACTTTTCTGG TATCATCT	Exon 54
506	AGAUGAUACCAGA AAAGUCCAC	1126	GUGGACUUUUCUG GUAUCAUCU	1746	GTGGACTTTTCTG GTATCATCT	Exon 54
507	AGAUGAUACCAGA AAAGUCCACAUG	1127	CAUGUGGACUUUU CUGGUAUCAUCU	1747	CATGTGGACTTTT CTGGTATCATCT	Exon 54
508	UCCACAUGAUAAC AGAGAAUAUC	1128	GAUAUUCUCUGUU AUCAUGUGGA	1748	GATATTCTCTGTT ATCATGTGGA	Exon 54
509	CUGAAACAACUGC CAAUGUCC	1129	GGACAUUGGCAGU UGUUUCAG	1749	GGACATTGGCAGT TGTTTCAG	Exon 55
510	CUGAAACAACUGC CAAUGUCCU	1130	AGGACAUUGGCAG UUGUUUCAG	1750	AGGACATTGGCAG TTGTTTCAG	Exon 55
511	CUGAAACAACUGC CAAUGUCCUA	1131	UAGGACAUUGGCA GUUGUUUCAG	1751	TAGGACATTGGCA GTTGTTTCAG	Exon 55
512	UGCCAAUGUCCUA CAGGAUG	1132	CAUCCUGUAGGAC AUUGGCA	1752	CATCCTGTAGGAC ATTGGCA	Exon 55
513	CCAAUGUCCUACA GGAUGCUA	1133	UAGCAUCCUGUAG GACAUUGG	1753	TAGCATCCTGTAG GACATTGG	Exon 55
514	CCAAUGUCCUACA GGAUGCUACC	1134	GGUAGCAUCCUGU AGGACAUUGG	1754	GGTAGCATCCTGT AGGACATTGG	Exon 55
515	CUCCAAGGGAGUA AAAGAGCUGAU	1135	AUCAGCUCUUUUA CUCCCUUGGAG	1755	ATCAGCTCTTTTA CTCCCTTGGAG	Exon 55
516	UCCAAGGGAGUAA AAGAGCUGA	1136	UCAGCUCUUUUAC UCCCUUGGA	1756	TCAGCTCTTTTAC TCCCTTGGA	Exon 55
517	UCCAAGGGAGUAA AAGAGCUGAU	1137	AUCAGCUCUUUUA CUCCCUUGGA	1757	ATCAGCTCTTTTA CTCCCTTGGA	Exon 55
518	CCAAGGGAGUAAA AGAGCUG	1138	CAGCUCUUUUACU CCCUUGG	1758	CAGCTCTTTTACT CCCTTGG	Exon 55
519	CCAAGGGAGUAAA AGAGCUGAUGAA	1139	UUCAUCAGCUCUU UUACUCCCUUGG	1759	TTCATCAGCTCTT TTACTCCCTTGG	Exon 55
520	CAAGGGAGUAAAA GAGCUGAUG	1140	CAUCAGCUCUUUU ACUCCCUUG	1760	CATCAGCTCTTTT ACTCCCTTG	Exon 55
521	CAAGGGAGUAAAA GAGCUGAUGAAA	1141	UUUCAUCAGCUCU UUUACUCCCUUG	1761	TTTCATCAGCTCT TTTACTCCCTTG	Exon 55
522	AGGGAGUAAAAGA GCUGAUGA	1142	UCAUCAGCUCUUU UACUCCCU	1762	TCATCAGCTCTTT TACTCCCT	Exon 55
523	AGGGAGUAAAAGA GCUGAUGAA	1143	UUCAUCAGCUCUU UUACUCCCU	1763	TTCATCAGCTCTT TTACTCCCT	Exon 55
524	AAGAGCUGAUGAA ACAAUGGCAA	1144	UUGCCAUUGUUUC AUCAGCUCUU	1764	TTGCCATTGTTTC ATCAGCTCTT	Exon 55
525	AAGAGCUGAUGAA ACAAUGGCAAG	1145	CUUGCCAUUGUUU CAUCAGCUCUU	1765	CTTGCCATTGTTT CATCAGCTCTT	Exon 55/intron 55 junction
526	AAGAGCUGAUGAA ACAAUGGCAAGU	1146	ACUUGCCAUUGUU UCAUCAGCUCUU	1766	ACTTGCCATTGTT TCATCAGCTCTT	Exon 55/intron 55 junction
527	AUGAAACAAUGGC AAGUAAGUC	1147	GACUUACUUGCCA UUGUUUCAU	1767	GACTTACTTGCCA TTGTTTCAT	Exon 55/intron 55 junction
528	UCCAAGGUGAAAU UGAAGCUCACAC	1148	GUGUGAGCUUCAA UUUCACCUUGGA	1768	GTGTGAGCTTCAA TTTCACCTTGGA	Exon 56

529	CCAAGGUGAAAUU GAAGCUCACAC	1149	GUGUGAGCUUCAA UUUCACCUUGG	1769	GTGTGAGCTTCAA TTTCACCTTGG	Exon 56
530	CCAAGGUGAAAUU GAAGCUCACACA	1150	UGUGUGAGCUUCA AUUUCACCUUGG	1770	TGTGTGAGCTTCA ATTTCACCTTGG	Exon 56
531	CAAGGUGAAAUUG AAGCUCACACAG	1151	CUGUGUGAGCUUC AAUUUCACCUUG	1771	CTGTGTGAGCTTC AATTTCACCTTG	Exon 56
532	AAGGUGAAAUUGA AGCUCACACAGA	1152	UCUGUGUGAGCUU CAAUUUCACCUU	1772	TCTGTGTGAGCTT CAATTTCACCTT	Exon 56
533	AGGUGAAAUUGAA GCUCACACAGA	1153	UCUGUGUGAGCUU CAAUUUCACCU	1773	TCTGTGTGAGCTT CAATTTCACCT	Exon 56
534	AGGUGAAAUUGAA GCUCACACAGAU	1154	AUCUGUGUGAGCU UCAAUUUCACCU	1774	ATCTGTGTGAGCT TCAATTTCACCT	Exon 56
535	UUAUCACAACCUG GAUGAAAACAGC	1155	GCUGUUUUCAUCC AGGUUGUGAUAA	1775	GCTGTTTTCATCC AGGTTGTGATAA	Exon 56
536	UGGAUGAAAACAG CCAAAAAAUCC	1156	GGAUUUUUUGGCU GUUUUCAUCCA	1776	GGATTTTTTGGCT GTTTTCATCCA	Exon 56
537	UGGAUGAAAACAG CCAAAAAAUCCU	1157	AGGAUUUUUUGGC UGUUUUCAUCCA	1777	AGGATTTTTTGGC TGTTTTCATCCA	Exon 56
538	CCUGAGAUCCCUG GAAGGUUCCG	1158	CGGAACCUUCCAG GGAUCUCAGG	1778	CGGAACCTTCCAG GGATCTCAGG	Exon 56
539	CUGAGAUCCCUGG AAGGUUCCG	1159	CGGAACCUUCCAG GGAUCUCAG	1779	CGGAACCTTCCAG GGATCTCAG	Exon 56
540	GAGAUCCCUGGAA GGUUCCGAUGAU	1160	AUCAUCGGAACCU UCCAGGGAUCUC	1780	ATCATCGGAACCT TCCAGGGATCTC	Exon 56
541	AGAUCCCUGGAAG GUUCCGAUGAU	1161	AUCAUCGGAACCU UCCAGGGAUCU	1781	ATCATCGGAACCT TCCAGGGATCT	Exon 56
542	GAUCCCUGGAAGG UUCCGAUGAU	1162	AUCAUCGGAACCU UCCAGGGAUC	1782	ATCATCGGAACCT TCCAGGGATC	Exon 56
543	GAUCCCUGGAAGG UUCCGAUGAUGC	1163	GCAUCAUCGGAAC CUUCCAGGGAUC	1783	GCATCATCGGAAC CTTCCAGGGATC	Exon 56
544	AUCCCUGGAAGGU UCCGAUGAU	1164	AUCAUCGGAACCU UCCAGGGAU	1784	ATCATCGGAACCT TCCAGGGAT	Exon 56
545	AUCCCUGGAAGGU UCCGAUGAUGC	1165	GCAUCAUCGGAAC CUUCCAGGGAU	1785	GCATCATCGGAAC CTTCCAGGGAT	Exon 56
546	AUCCCUGGAAGGU UCCGAUGAUGCA	1166	UGCAUCAUCGGAA CCUUCCAGGGAU	1786	TGCATCATCGGAA CCTTCCAGGGAT	Exon 56
547	UCCCUGGAAGGUU CCGAUGAU	1167	AUCAUCGGAACCU UCCAGGGA	1787	ATCATCGGAACCT TCCAGGGA	Exon 56
548	UCCCUGGAAGGUU CCGAUGAUGC	1168	GCAUCAUCGGAAC CUUCCAGGGA	1788	GCATCATCGGAAC CTTCCAGGGA	Exon 56
549	UCCCUGGAAGGUU CCGAUGAUGCA	1169	UGCAUCAUCGGAA CCUUCCAGGGA	1789	TGCATCATCGGAA CCTTCCAGGGA	Exon 56
550	CCCUGGAAGGUUC CGAUGAUGC	1170	GCAUCAUCGGAAC CUUCCAGGG	1790	GCATCATCGGAAC CTTCCAGGG	Exon 56
551	CCCUGGAAGGUUC CGAUGAUGCA	1171	UGCAUCAUCGGAA CCUUCCAGGG	1791	TGCATCATCGGAA CCTTCCAGGG	Exon 56
552	CUGGAAGGUUCCG AUGAUGC	1172	GCAUCAUCGGAAC CUUCCAG	1792	GCATCATCGGAAC CTTCCAG	Exon 56
553	CUGGAAGGUUCCG AUGAUGCA	1173	UGCAUCAUCGGAA CCUUCCAG	1793	TGCATCATCGGAA CCTTCCAG	Exon 56
554	UGGAAGGUUCCGA UGAUGCA	1174	UGCAUCAUCGGAA CCUUCCA	1794	TGCATCATCGGAA CCTTCCA	Exon 56
555	GGCUUACAGAAGC UGAAACAACUGC	1175	GCAGUUGUUUCAG CUUCUGUAAGCC	1795	GCAGTTGTTTCAG CTTCTGTAAGCC	Exon 55
556	GGGAGUAAAAGAG CUGAUGAAA	1176	UUUCAUCAGCUCU UUUACUCCC	1796	TTTCATCAGCTCT TTTACTCCC	Exon 55
557	GGGAGUAAAAGAG CUGAUGAAAC	1177	GUUUCAUCAGCUC UUUUACUCCC	1797	GTTTCATCAGCTC TTTTACTCCC	Exon 55
558	AAAAGAGCUGAUG AAACAAUGGCAA	1178	UUGCCAUUGUUUC AUCAGCUCUUUU	1798	TTGCCATTGTTTC ATCAGCTCTTTT	Exon 55
559	AGGUUCCGAUGAU GCAGUCCU	1179	AGGACUGCAUCAU CGGAACCU	1799	AGGACTGCATCAT CGGAACCT	Exon 56

560	AGGUUCCGAUGAU GCAGUCCUG	1180	CAGGACUGCAUCA UCGGAACCU	1800	CAGGACTGCATCA TCGGAACCT	Exon 56
561	GGUUCCGAUGAUG CAGUCCU	1181	AGGACUGCAUCAU CGGAACC	1801	AGGACTGCATCAT CGGAACC	Exon 56
562	GGUUCCGAUGAUG CAGUCCUG	1182	CAGGACUGCAUCA UCGGAACC	1802	CAGGACTGCATCA TCGGAACC	Exon 56
563	CAGAUGAUACCAG AAAAGUCC	1183	GGACUUUUCUGGU AUCAUCUG	1803	GGACTTTTCTGGT ATCATCTG	Exon 54
564	CAGAUGAUACCAG AAAAGUCCA	1184	UGGACUUUUCUGG UAUCAUCUG	1804	TGGACTTTTCTGG TATCATCTG	Exon 54
565	CAGAUGAUACCAG AAAAGUCCAC	1185	GUGGACUUUUCUG GUAUCAUCUG	1805	GTGGACTTTTCTG GTATCATCTG	Exon 54
566	CAAUGUCCUACAG GAUGCUAC	1186	GUAGCAUCCUGUA GGACAUUG	1806	GTAGCATCCTGTA GGACATTG	Exon 55
567	AAGGGAGUAAAAG AGCUGAUGA	1187	UCAUCAGCUCUUU UACUCCCUU	1807	TCATCAGCTCTTT TACTCCCTT	Exon 55
568	AAGGGAGUAAAAG AGCUGAUGAA	1188	UUCAUCAGCUCUU UUACUCCCUU	1808	TTCATCAGCTCTT TTACTCCCTT	Exon 55
569	AAGGGAGUAAAAG AGCUGAUGAAA	1189	UUUCAUCAGCUCU UUUACUCCCUU	1809	TTTCATCAGCTCT TTTACTCCCTT	Exon 55
570	AAGGGAGUAAAAG AGCUGAUGAAAC	1190	GUUUCAUCAGCUC UUUUACUCCCUU	1810	GTTTCATCAGCTC TTTTACTCCCTT	Exon 55
571	AAAGAGCUGAUGA AACAAUGGCA	1191	UGCCAUUGUUUCA UCAGCUCUUU	1811	TGCCATTGTTTCA TCAGCTCTTT	Exon 55
572	AAAGAGCUGAUGA AACAAUGGCAA	1192	UUGCCAUUGUUUC AUCAGCUCUUU	1812	TTGCCATTGTTTC ATCAGCTCTTT	Exon 55
573	AAAGAGCUGAUGA AACAAUGGCAAG	1193	CUUGCCAUUGUUU CAUCAGCUCUUU	1813	CTTGCCATTGTTT CATCAGCTCTTT	Exon 55/intron 55 junction
574	AUGAAACAAUGGC AAGUAAGUCA	1194	UGACUUACUUGCC AUUGUUUCAU	1814	TGACTTACTTGCC ATTGTTTCAT	Exon 55/intron 55 junction
575	CCAGGGACAAAAC AAAAUAGUUGC	1195	GCAACUAUUUUGU UUUGUCCCUGG	1815	GCAACTATTTTGT TTTGTCCCTGG	Intron 55
576	GCAAUUCUCCAAA UUCACAUUC	1196	GAAUGUGAAUUUG GAGAAUUGC	1816	GAATGTGAATTTG GAGAATTGC	Intron 55
577	CAAUUCUCCAAAU UCACAUUCA	1197	UGAAUGUGAAUUU GGAGAAUUG	1817	TGAATGTGAATTT GGAGAATTG	Intron 55
578	AUUCUCCAAAUUC ACAUUCAUC	1198	GAUGAAUGUGAAU UUGGAGAAU	1818	GATGAATGTGAAT TTGGAGAAT	Intron 55
579	GGUGAAAUUGAAG CUCACACAGAUG	1199	CAUCUGUGUGAGC UUCAAUUUCACC	1819	CATCTGTGTGAGC TTCAATTTCACC	Exon 56
580	CUCACACAGAUGU UUAUCACAACCU	1200	AGGUUGUGAUAAA CAUCUGUGUGAG	1820	AGGTTGTGATAAA CATCTGTGTGAG	Exon 56
581	ACAACCUGGAUGA AAACAGCC	1201	GGCUGUUUUCAUC CAGGUUGU	1821	GGCTGTTTTCATC CAGGTTGT	Exon 56
582	ACAACCUGGAUGA AAACAGCCA	1202	UGGCUGUUUUCAU CCAGGUUGU	1822	TGGCTGTTTTCAT CCAGGTTGT	Exon 56
583	ACAACCUGGAUGA AAACAGCCAA	1203	UUGGCUGUUUUCA UCCAGGUUGU	1823	TTGGCTGTTTTCA TCCAGGTTGT	Exon 56
584	CUGGAUGAAAACA GCCAAAAAAUCC	1204	GGAUUUUUUGGCU GUUUUCAUCCAG	1824	GGATTTTTTGGCT GTTTTCATCCAG	Exon 56
585	AGAUCCCUGGAAG GUUCCGAUGAUG	1205	CAUCAUCGGAACC UUCCAGGGAUCU	1825	CATCATCGGAACC TTCCAGGGATCT	Exon 56
586	GAUCCCUGGAAGG UUCCGAUGAUG	1206	CAUCAUCGGAACC UUCCAGGGAUC	1826	CATCATCGGAACC TTCCAGGGATC	Exon 56
587	AUCCCUGGAAGGU UCCGAUGAUG	1207	CAUCAUCGGAACC UUCCAGGGAU	1827	CATCATCGGAACC TTCCAGGGAT	Exon 56
588	UCCCUGGAAGGUU CCGAUGAUG	1208	CAUCAUCGGAACC UUCCAGGGA	1828	CATCATCGGAACC TTCCAGGGA	Exon 56
589	UCCCUGGAAGGUU CCGAUGAUGCAG	1209	CUGCAUCAUCGGA ACCUUCCAGGGA	1829	CTGCATCATCGGA ACCTTCCAGGGA	Exon 56
590	CCCUGGAAGGUUC CGAUGAUG	1210	CAUCAUCGGAACC UUCCAGGG	1830	CATCATCGGAACC TTCCAGGG	Exon 56

591	CCCUGGAAGGUUC CGAUGAUGCAG	1211	CUGCAUCAUCGGA ACCUUCCAGGG	1831	CTGCATCATCGGA ACCTTCCAGGG	Exon 56
592	CUGGAAGGUUCCG AUGAUGCAG	1212	CUGCAUCAUCGGA ACCUUCCAG	1832	CTGCATCATCGGA ACCTTCCAG	Exon 56
593	UGGAAGGUUCCGA UGAUGCAG	1213	CUGCAUCAUCGGA ACCUUCCA	1833	CTGCATCATCGGA ACCTTCCA	Exon 56
594	GAUGAUGCAGUCC UGUUACAAAGAC	1214	GUCUUUGUAACAG GACUGCAUCAUC	1834	GTCTTTGTAACAG GACTGCATCATC	Exon 56
595	GCUUACAGAAGCU GAAACAACUGCC	1215	GGCAGUUGUUUCA GCUUCUGUAAGC	1835	GGCAGTTGTTTCA GCTTCTGTAAGC	Exon 55
596	GGGAGUAAAAGAG CUGAUGAAACA	1216	UGUUUCAUCAGCU CUUUUACUCCC	1836	TGTTTCATCAGCT CTTTTACTCCC	Exon 55
597	GAGUAAAAGAGCU GAUGAAACAAUG	1217	CAUUGUUUCAUCA GCUCUUUUACUC	1837	CATTGTTTCATCA GCTCTTTTACTC	Exon 55
598	UAAAAGAGCUGAU GAAACAAUGGC	1218	GCCAUUGUUUCAU CAGCUCUUUUA	1838	GCCATTGTTTCAT CAGCTCTTTTA	Exon 55
599	GAUCCAAUUGAAC AAUUCUCAGC	1219	GCUGAGAAUUGUU CAAUUGGAUC	1839	GCTGAGAATTGTT CAATTGGATC	Intron 55
600	AAGGUUCCGAUGA UGCAGUCCUG	1220	CAGGACUGCAUCA UCGGAACCUU	1840	CAGGACTGCATCA TCGGAACCTT	Exon 56
601	CAAGGGAGUAAAA GAGCUGA	1221	UCAGCUCUUUUAC UCCCUUG	1841	TCAGCTCTTTTAC TCCCTTG	Exon 55
602	AGGGAGUAAAAGA GCUGAUGAAACA	1222	UGUUUCAUCAGCU CUUUUACUCCCU	1842	TGTTTCATCAGCT CTTTTACTCCCT	Exon 55
603	GCCAGGGACAAAA CAAAAUAGUUGC	1223	GCAACUAUUUUGU UUUGUCCCUGGC	1843	GCAACTATTTTGT TTTGTCCCTGGC	Intron 55
604	UGCAAUUCUCCAA AUUCACAUUC	1224	GAAUGUGAAUUUG GAGAAUUGCA	1844	GAATGTGAATTTG GAGAATTGCA	Intron 55
605	GCAAUUCUCCAAA UUCACAUUCA	1225	UGAAUGUGAAUUU GGAGAAUUGC	1845	TGAATGTGAATTT GGAGAATTGC	Intron 55
606	AAUUCUCCAAAUU CACAUUCAUC	1226	GAUGAAUGUGAAU UUGGAGAAUU	1846	GATGAATGTGAAT TTGGAGAATT	Intron 55
607	AUUCUCCAAAUUC ACAUUCAUCG	1227	CGAUGAAUGUGAA UUUGGAGAAU	1847	CGATGAATGTGAA TTTGGAGAAT	Intron 55
608	UUCUCCAAAUUCA CAUUCAUCG	1228	CGAUGAAUGUGAA UUUGGAGAA	1848	CGATGAATGTGAA TTTGGAGAA	Intron 55
609	UCUCCAAAUUCAC AUUCAUCG	1229	CGAUGAAUGUGAA UUUGGAGA	1849	CGATGAATGTGAA TTTGGAGA	Intron 55
610	GGUAAUUCUGCAC AUAUUCUUCUUC	1230	GAAGAAGAAUAUG UGCAGAAUUACC	1850	GAAGAAGAATATG TGCAGAATTACC	Intron 55
611	GCUCACACAGAUG UUUAUCACAACC	1231	GGUUGUGAUAAAC AUCUGUGUGAGC	1851	GGTTGTGATAAAC ATCTGTGTGAGC	Exon 56
612	UCACAACCUGGAU GAAAACAG	1232	CUGUUUUCAUCCA GGUUGUGA	1852	CTGTTTTCATCCA GGTTGTGA	Exon 56
613	CACAACCUGGAUG AAAACAGCC	1233	GGCUGUUUUCAUC CAGGUUGUG	1853	GGCTGTTTTCATC CAGGTTGTG	Exon 56
614	CACAACCUGGAUG AAAACAGCCA	1234	UGGCUGUUUUCAU CCAGGUUGUG	1854	TGGCTGTTTTCAT CCAGGTTGTG	Exon 56
615	CACAACCUGGAUG AAAACAGCCAA	1235	UUGGCUGUUUUCA UCCAGGUUGUG	1855	TTGGCTGTTTTCA TCCAGGTTGTG	Exon 56
616	ACAACCUGGAUGA AAACAGCCAAA	1236	UUUGGCUGUUUUC AUCCAGGUUGU	1856	TTTGGCTGTTTTC ATCCAGGTTGT	Exon 56
617	CCUGGAUGAAAAC AGCCAAAAAAUC	1237	GAUUUUUUGGCUG UUUUCAUCCAGG	1857	GATTTTTTGGCTG TTTTCATCCAGG	Exon 56
618	CCCUGGAAGGUUC CGAUGAUGCAGU	1238	ACUGCAUCAUCGG AACCUUCCAGGG	1858	ACTGCATCATCGG AACCTTCCAGGG	Exon 56
619	UGGAAGGUUCCGA UGAUGCAGU	1239	ACUGCAUCAUCGG AACCUUCCA	1859	ACTGCATCATCGG AACCTTCCA	Exon 56
620	UGGAAGGUUCCGA UGAUGCAGUCCU	1240	AGGACUGCAUCAU CGGAACCUUCCA	1860	AGGACTGCATCAT CGGAACCTTCCA	Exon 56
621	GGAAGGUUCCGAU GAUGCAGUCCU	1241	AGGACUGCAUCAU CGGAACCUUCC	1861	AGGACTGCATCAT CGGAACCTTCC	Exon 56

622	GGAAGGUUCCGAU GAUGCAGUCCUG	1242	CAGGACUGCAUCA UCGGAACCUUCC	1862	CAGGACTGCATCA TCGGAACCTTCC	Exon 56
623	GAAGGUUCCGAUG AUGCAGU	1243	ACUGCAUCAUCGG AACCUUC	1863	ACTGCATCATCGG AACCTTC	Exon 56
624	GUUCCGAUGAUGC AGUCCUGUUACA	1244	UGUAACAGGACUG CAUCAUCGGAAC	1864	TGTAACAGGACTG CATCATCGGAAC	Exon 56
625	GGGAGUAAAAGAG CUGAUGAAACAA	1245	UUGUUUCAUCAGC UCUUUUACUCCC	1865	TTGTTTCATCAGC TCTTTTACTCCC	Exon 55
626	GGAUCCAAUUGAA CAAUUCUCAGC	1246	GCUGAGAAUUGUU CAAUUGGAUCC	1866	GCTGAGAATTGTT CAATTGGATCC	Intron 55
627	GAAGGUUCCGAUG AUGCAGUCCUG	1247	CAGGACUGCAUCA UCGGAACCUUC	1867	CAGGACTGCATCA TCGGAACCTTC	Exon 56
628	AGGUUCCGAUGAU GCAGUCCUGUU	1248	AACAGGACUGCAU CAUCGGAACCU	1868	AACAGGACTGCAT CATCGGAACCT	Exon 56
629	GGUUCCGAUGAUG CAGUCCUGUU	1249	AACAGGACUGCAU CAUCGGAACC	1869	AACAGGACTGCAT CATCGGAACC	Exon 56
630	CAAGGGAGUAAAA GAGCUGAU	1250	AUCAGCUCUUUUA CUCCCUUG	1870	ATCAGCTCTTTTA CTCCCTTG	Exon 55
631	AGCACUCUUGUGG AUCCAAUUGAAC	1251	GUUCAAUUGGAUC CACAAGAGUGCU	1871	GTTCAATTGGATC CACAAGAGTGCT	Intron 55
632	GCCAGGGACAAAA CAAAAUAG	1252	CUAUUUUGUUUUG UCCCUGGC	1872	CTATTTTGTTTTG TCCCTGGC	Intron 55
633	UUGCAAUUCUCCA AAUUCACAUUC	1253	GAAUGUGAAUUUG GAGAAUUGCAA	1873	GAATGTGAATTTG GAGAATTGCAA	Intron 55
634	UGCAAUUCUCCAA AUUCACAUUCA	1254	UGAAUGUGAAUUU GGAGAAUUGCA	1874	TGAATGTGAATTT GGAGAATTGCA	Intron 55
635	GCAAUUCUCCAAA UUCACAUUCAU	1255	AUGAAUGUGAAUU UGGAGAAUUGC	1875	ATGAATGTGAATT TGGAGAATTGC	Intron 55
636	CAAUUCUCCAAAU UCACAUUCAUC	1256	GAUGAAUGUGAAU UUGGAGAAUUG	1876	GATGAATGTGAAT TTGGAGAATTG	Intron 55
637	AAUUCUCCAAAUU CACAUUCAUCG	1257	CGAUGAAUGUGAA UUUGGAGAAUU	1877	CGATGAATGTGAA TTTGGAGAATT	Intron 55
638	AUUCUCCAAAUUC ACAUUCAUCGC	1258	GCGAUGAAUGUGA AUUUGGAGAAU	1878	GCGATGAATGTGA ATTTGGAGAAT	Intron 55
639	UUCUCCAAAUUCA CAUUCAUCGC	1259	GCGAUGAAUGUGA AUUUGGAGAA	1879	GCGATGAATGTGA ATTTGGAGAA	Intron 55
640	UCUCCAAAUUCAC AUUCAUCGC	1260	GCGAUGAAUGUGA AUUUGGAGA	1880	GCGATGAATGTGA ATTTGGAGA	Intron 55
641	GUGAAAUUGAAGC UCACACAGAUGU	1261	ACAUCUGUGUGAG CUUCAAUUUCAC	1881	ACATCTGTGTGAG CTTCAATTTCAC	Exon 56
642	UAUCACAACCUGG AUGAAAACAG	1262	CUGUUUUCAUCCA GGUUGUGAUA	1882	CTGTTTTCATCCA GGTTGTGATA	Exon 56
643	AUCACAACCUGGA UGAAAACAG	1263	CUGUUUUCAUCCA GGUUGUGAU	1883	CTGTTTTCATCCA GGTTGTGAT	Exon 56
644	CCUGGAAGGUUCC GAUGAUGCAGUC	1264	GACUGCAUCAUCG GAACCUUCCAGG	1884	GACTGCATCATCG GAACCTTCCAGG	Exon 56
645	CUGGAAGGUUCCG AUGAUGCAGUC	1265	GACUGCAUCAUCG GAACCUUCCAG	1885	GACTGCATCATCG GAACCTTCCAG	Exon 56
646	UGGAAGGUUCCGA UGAUGCAGUC	1266	GACUGCAUCAUCG GAACCUUCCA	1886	GACTGCATCATCG GAACCTTCCA	Exon 56
647	GGAAGGUUCCGAU GAUGCAGUC	1267	GACUGCAUCAUCG GAACCUUCC	1887	GACTGCATCATCG GAACCTTCC	Exon 56
648	GGAGUAAAAGAGC UGAUGAAACAAU	1268	AUUGUUUCAUCAG CUCUUUUACUCC	1888	ATTGTTTCATCAG CTCTTTTACTCC	Exon 55
649	UGUGGAUCCAAUU GAACAAUUC	1269	GAAUUGUUCAAUU GGAUCCACA	1889	GAATTGTTCAATT GGATCCACA	Intron 55
650	AAGGUUCCGAUGA UGCAGUCCUGUU	1270	AACAGGACUGCAU CAUCGGAACCUU	1890	AACAGGACTGCAT CATCGGAACCTT	Exon 56
651	AUAAUGGGGUGGU GAAACUG	1271	CAGUUUCACCACC CCAUUAU	1891	CAGTTTCACCACC CCATTAT	Intron 54
652	GCACUCUUGUGGA UCCAAUUGAACA	1272	UGUUCAAUUGGAU CCACAAGAGUGC	1892	TGTTCAATTGGAT CCACAAGAGTGC	Intron 55

653	GGAUCCAAUUGAA CAAUUCUCAG	1273	CUGAGAAUUGUUC AAUUGGAUCC	1893	CTGAGAATTGTTC AATTGGATCC	Intron 55
654	GCCAGGGACAAAA CAAAAUAGU	1274	ACUAUUUUGUUUU GUCCCUGGC	1894	ACTATTTTGTTTT GTCCCTGGC	Intron 55
655	UUUGCAAUUCUCC AAAUUCACAUUC	1275	GAAUGUGAAUUUG GAGAAUUGCAAA	1895	GAATGTGAATTTG GAGAATTGCAAA	Intron 55
656	UUGCAAUUCUCCA AAUUCACAUUCA	1276	UGAAUGUGAAUUU GGAGAAUUGCAA	1896	TGAATGTGAATTT GGAGAATTGCAA	Intron 55
657	UGCAAUUCUCCAA AUUCACAUUCAU	1277	AUGAAUGUGAAUU UGGAGAAUUGCA	1897	ATGAATGTGAATT TGGAGAATTGCA	Intron 55
658	GCAAUUCUCCAAA UUCACAUUCAUC	1278	GAUGAAUGUGAAU UUGGAGAAUUGC	1898	GATGAATGTGAAT TTGGAGAATTGC	Intron 55
659	CAAUUCUCCAAAU UCACAUUCAUCG	1279	CGAUGAAUGUGAA UUUGGAGAAUUG	1899	CGATGAATGTGAA TTTGGAGAATTG	Intron 55
660	AAUUCUCCAAAUU CACAUUCAUCGC	1280	GCGAUGAAUGUGA AUUUGGAGAAUU	1900	GCGATGAATGTGA ATTTGGAGAATT	Intron 55
661	AUUCUCCAAAUUC ACAUUCAUCGCU	1281	AGCGAUGAAUGUG AAUUUGGAGAAU	1901	AGCGATGAATGTG AATTTGGAGAAT	Intron 55
662	UCUCCAAAUUCAC AUUCAUCGCU	1282	AGCGAUGAAUGUG AAUUUGGAGA	1902	AGCGATGAATGTG AATTTGGAGA	Intron 55
663	UCCAAAUUCACAU UCAUCGC	1283	GCGAUGAAUGUGA AUUUGGA	1903	GCGATGAATGTGA ATTTGGA	Intron 55
664	UUAUCACAACCUG GAUGAAAACAG	1284	CUGUUUUCAUCCA GGUUGUGAUAA	1904	CTGTTTTCATCCA GGTTGTGATAA	Exon 56
665	UAUCACAACCUGG AUGAAAACAGC	1285	GCUGUUUUCAUCC AGGUUGUGAUA	1905	GCTGTTTTCATCC AGGTTGTGATA	Exon 56
666	UGUGGAUCCAAUU GAACAAUUCU	1286	AGAAUUGUUCAAU UGGAUCCACA	1906	AGAATTGTTCAAT TGGATCCACA	Intron 55
667	GUGGAUCCAAUUG AACAAUUC	1287	GAAUUGUUCAAUU GGAUCCAC	1907	GAATTGTTCAATT GGATCCAC	Intron 55
668	UCCAAUUGAACAA UUCUCAGCAU	1288	AUGCUGAGAAUUG UUCAAUUGGA	1908	ATGCTGAGAATTG TTCAATTGGA	Intron 55
669	CCAGGGACAAAAC AAAAUAGU	1289	ACUAUUUUGUUUU GUCCCUGG	1909	ACTATTTTGTTTT GTCCCTGG	Intron 55
670	AAUAAUGGGGUGG UGAAACUG	1290	CAGUUUCACCACC CCAUUAUU	1910	CAGTTTCACCACC CCATTATT	Intron 54
671	UGGAUCCAAUUGA ACAAUUCUCAG	1291	CUGAGAAUUGUUC AAUUGGAUCCA	1911	CTGAGAATTGTTC AATTGGATCCA	Intron 55
672	AGCCAGGGACAAA ACAAAAUAGU	1292	ACUAUUUUGUUUU GUCCCUGGCU	1912	ACTATTTTGTTTT GTCCCTGGCT	Intron 55
673	GCCAGGGACAAAA CAAAAUAGUU	1293	AACUAUUUUGUUU UGUCCCUGGC	1913	AACTATTTTGTTT TGTCCCTGGC	Intron 55
674	UUCUCCAAAUUCA CAUUCAUCGCU	1294	AGCGAUGAAUGUG AAUUUGGAGAA	1914	AGCGATGAATGTG AATTTGGAGAA	Intron 55
675	UCUCCAAAUUCAC AUUCAUCGCUU	1295	AAGCGAUGAAUGU GAAUUUGGAGA	1915	AAGCGATGAATGT GAATTTGGAGA	Intron 55
676	CUCCAAAUUCACA UUCAUCGC	1296	GCGAUGAAUGUGA AUUUGGAG	1916	GCGATGAATGTGA ATTTGGAG	Intron 55
677	UCCAAAUUCACAU UCAUCGCU	1297	AGCGAUGAAUGUG AAUUUGGA	1917	AGCGATGAATGTG AATTTGGA	Intron 55
678	GUAAUUCUGCACA UAUUCUUCUUCC	1298	GGAAGAAGAAUAU GUGCAGAAUUAC	1918	GGAAGAAGAATAT GTGCAGAATTAC	Intron 55
679	UUUAUCACAACCU GGAUGAAAACAG	1299	CUGUUUUCAUCCA GGUUGUGAUAAA	1919	CTGTTTTCATCCA GGTTGTGATAAA	Exon 56
680	GUGGAUCCAAUUG AACAAUUCU	1300	AGAAUUGUUCAAU UGGAUCCAC	1920	AGAATTGTTCAAT TGGATCCAC	Intron 55
681	UCCAAUUGAACAA UUCUCAGCAUU	1301	AAUGCUGAGAAUU GUUCAAUUGGA	1921	AATGCTGAGAATT GTTCAATTGGA	Intron 55
682	CCAGGGACAAAAC AAAAUAGUU	1302	AACUAUUUUGUUU UGUCCCUGG	1922	AACTATTTTGTTT TGTCCCTGG	Intron 55
683	UCCAAAUUCACAU UCAUCGCUU	1303	AAGCGAUGAAUGU GAAUUUGGA	1923	AAGCGATGAATGT GAATTTGGA	Intron 55

684	CCAAAUUCACAUU CAUCGCUUG	1304	CAAGCGAUGAAUG UGAAUUUGG	1924	CAAGCGATGAATG TGAATTTGG	Intron 55
685	UGGUAAUUCUGCA CAUAUUCUUC	1305	GAAGAAUAUGUGC AGAAUUACCA	1925	GAAGAATATGTGC AGAATTACCA	Intron 55
686	GUGGAUCCAAUUG AACAAUUCUCAG	1306	CUGAGAAUUGUUC AAUUGGAUCCAC	1926	CTGAGAATTGTTC AATTGGATCCAC	Intron 55
687	UGGAUCCAAUUGA ACAAUUCUCAGC	1307	GCUGAGAAUUGUU CAAUUGGAUCCA	1927	GCTGAGAATTGTT CAATTGGATCCA	Intron 55
688	GGAUCCAAUUGAA CAAUUCUC	1308	GAGAAUUGUUCAA UUGGAUCC	1928	GAGAATTGTTCAA TTGGATCC	Intron 55
689	CAAGCCAGGGACA AAACAAAAUAG	1309	CUAUUUUGUUUUG UCCCUGGCUUG	1929	CTATTTTGTTTTG TCCCTGGCTTG	Intron 55
690	AAGCCAGGGACAA AACAAAAUAGU	1310	ACUAUUUUGUUUU GUCCCUGGCUU	1930	ACTATTTTGTTTT GTCCCTGGCTT	Intron 55
691	AGCCAGGGACAAA ACAAAAUAGUU	1311	AACUAUUUUGUUU UGUCCCUGGCU	1931	AACTATTTTGTTT TGTCCCTGGCT	Intron 55
692	GCCAGGGACAAAA CAAAAUAGUUG	1312	CAACUAUUUUGUU UUGUCCCUGGC	1932	CAACTATTTTGTT TTGTCCCTGGC	Intron 55
693	UUCUCCAAAUUCA CAUUCAUCGCUU	1313	AAGCGAUGAAUGU GAAUUUGGAGAA	1933	AAGCGATGAATGT GAATTTGGAGAA	Intron 55
694	UCUCCAAAUUCAC AUUCAUCGCUUG	1314	CAAGCGAUGAAUG UGAAUUUGGAGA	1934	CAAGCGATGAATG TGAATTTGGAGA	Intron 55
695	CUCCAAAUUCACA UUCAUCGCU	1315	AGCGAUGAAUGUG AAUUUGGAG	1935	AGCGATGAATGTG AATTTGGAG	Intron 55
696	GUUCCGAUGAUGC AGUCCUG	1316	CAGGACUGCAUCA UCGGAAC	1936	CAGGACTGCATCA TCGGAAC	Exon 56
697	UUCCGAUGAUGCA GUCCUGU	1317	ACAGGACUGCAUC AUCGGAA	1937	ACAGGACTGCATC ATCGGAA	Exon 56
698	UCCGAUGAUGCAG UCCUGUU	1318	AACAGGACUGCAU CAUCGGA	1938	AACAGGACTGCAT CATCGGA	Exon 56
699	UCCGAUGAUGCAG UCCUGUUACAA	1319	UUGUAACAGGACU GCAUCAUCGGA	1939	TTGTAACAGGACT GCATCATCGGA	Exon 56
700	UCCGAUGAUGCAG UCCUGUUACAAA	1320	UUUGUAACAGGAC UGCAUCAUCGGA	1940	TTTGTAACAGGAC TGCATCATCGGA	Exon 56
701	UCCAAUUGAACAA UUCUCAGCAUUU	1321	AAAUGCUGAGAAU UGUUCAAUUGGA	1941	AAATGCTGAGAAT TGTTCAATTGGA	Intron 55
702	CCAGGGACAAAAC AAAAUAGUUG	1322	CAACUAUUUUGUU UUGUCCCUGG	1942	CAACTATTTTGTT TTGTCCCTGG	Intron 55
703	CUCCAAAUUCACA UUCAUCGCUU	1323	AAGCGAUGAAUGU GAAUUUGGAG	1943	AAGCGATGAATGT GAATTTGGAG	Intron 55
704	UCCAAAUUCACAU UCAUCGCUUG	1324	CAAGCGAUGAAUG UGAAUUUGGA	1944	CAAGCGATGAATG TGAATTTGGA	Intron 55
705	UUGGUAAUUCUGC ACAUAUUCUUC	1325	GAAGAAUAUGUGC AGAAUUACCAA	1945	GAAGAATATGTGC AGAATTACCAA	Intron 55
706	UGGUAAUUCUGCA CAUAUUCUUCU	1326	AGAAGAAUAUGUG CAGAAUUACCA	1946	AGAAGAATATGTG CAGAATTACCA	Intron 55
707	UAAUAAUGGGGUG GUGAAAC	1327	GUUUCACCACCCC AUUAUUA	1947	GTTTCACCACCCC ATTATTA	Intron 54
708	UGGAUCCAAUUGA ACAAUUCUC	1328	GAGAAUUGUUCAA UUGGAUCCA	1948	GAGAATTGTTCAA TTGGATCCA	Intron 55
709	CAAGCCAGGGACA AAACAAAAUAGU	1329	ACUAUUUUGUUUU GUCCCUGGCUUG	1949	ACTATTTTGTTTT GTCCCTGGCTTG	Intron 55
710	AGCCAGGGACAAA ACAAAAUAGUUG	1330	CAACUAUUUUGUU UUGUCCCUGGCU	1950	CAACTATTTTGTT TTGTCCCTGGCT	Intron 55
711	UUCCGAUGAUGCA GUCCUGUU	1331	AACAGGACUGCAU CAUCGGAA	1951	AACAGGACTGCAT CATCGGAA	Exon 56
712	UUUGGUAAUUCUG CACAUAUUCUUC	1332	GAAGAAUAUGUGC AGAAUUACCAAA	1952	GAAGAATATGTGC AGAATTACCAAA	Intron 55
713	UUGGUAAUUCUGC ACAUAUUCUUCU	1333	AGAAGAAUAUGUG CAGAAUUACCAA	1953	AGAAGAATATGTG CAGAATTACCAA	Intron 55
714	UGGUAAUUCUGCA CAUAUUCUUCUU	1334	AAGAAGAAUAUGU GCAGAAUUACCA	1954	AAGAAGAATATGT GCAGAATTACCA	Intron 55

715	UGGAUCCAAUUGA ACAAUUCUCA	1335	UGAGAAUUGUUCA AUUGGAUCCA	1955	TGAGAATTGTTCA ATTGGATCCA	Intron 55
716	GUUCCGAUGAUGC AGUCCUGUU	1336	AACAGGACUGCAU CAUCGGAAC	1956	AACAGGACTGCAT CATCGGAAC	Exon 56
717	UUCCGAUGAUGCA GUCCUGUUA	1337	UAACAGGACUGCA UCAUCGGAA	1957	TAACAGGACTGCA TCATCGGAA	Exon 56
718	GGUAAUUCUGCAC AUAUUCUUC	1338	GAAGAAUAUGUGC AGAAUUACC	1958	GAAGAATATGTGC AGAATTACC	Intron 55
719	UCCGAUGAUGCAG UCCUGUUACA	1339	UGUAACAGGACUG CAUCAUCGGA	1959	TGTAACAGGACTG CATCATCGGA	Exon 56
720	GGUAAUUCUGCAC AUAUUCUUCU	1340	AGAAGAAUAUGUG CAGAAUUACC	1960	AGAAGAATATGTG CAGAATTACC	Intron 55
721	UUCCGAUGAUGCA GUCCUGUUACA	1341	UGUAACAGGACUG CAUCAUCGGAA	1961	TGTAACAGGACTG CATCATCGGAA	Exon 56
722	GUAAUUCUGCACA UAUUCUUCUUC	1342	GAAGAAGAAUAUG UGCAGAAUUAC	1962	GAAGAAGAATATG TGCAGAATTAC	Intron 55
723	AUUGAACAAUUCU CAGCAUUUGUAC	1343	GUACAAAUGCUGA GAAUUGUUCAAU	1963	GTACAAATGCTGA GAATTGTTCAAT	Intron 55
724	AUCACAACCUGGA UGAAAACAGC	1344	GCUGUUUUCAUCC AGGUUGUGAU	1964	GCTGTTTTCATCC AGGTTGTGAT	Exon 56
725	UCACAACCUGGAU GAAAACAGC	1345	GCUGUUUUCAUCC AGGUUGUGA	1965	GCTGTTTTCATCC AGGTTGTGA	Exon 56
726	CACAACCUGGAUG AAAACAGC	1346	GCUGUUUUCAUCC AGGUUGUG	1966	GCTGTTTTCATCC AGGTTGTG	Exon 56
727	GAAGGUUCCGAUG AUGCAGUC	1347	GACUGCAUCAUCG GAACCUUC	1967	GACTGCATCATCG GAACCTTC	Exon 56
728	GAAGGUUCCGAUG AUGCAGUCCU	1348	AGGACUGCAUCAU CGGAACCUUC	1968	AGGACTGCATCAT CGGAACCTTC	Exon 56
729	AAGGUUCCGAUGA UGCAGUC	1349	GACUGCAUCAUCG GAACCUU	1969	GACTGCATCATCG GAACCTT	Exon 56
730	AAGGUUCCGAUGA UGCAGUCCU	1350	AGGACUGCAUCAU CGGAACCUU	1970	AGGACTGCATCAT CGGAACCTT	Exon 56
731	GGAGCUUGGGAGG GUUCAAGACG	1351	CGUCUUGAACCCU CCCAAGCUCC	1971	CGTCTTGAACCCT CCCAAGCTCC	Intron 54
732	CCUGAGAUCCCUG GAAGGUUCC	1352	GGAACCUUCCAGG GAUCUCAGG	1972	GGAACCTTCCAGG GATCTCAGG	Exon 56
733	UGGCUGUAAUAAU GGGGUGGU	1353	ACCACCCCAUUAU UACAGCCA	1973	ACCACCCCATTAT TACAGCCA	Intron 54
734	GGCUGUAAUAAUG GGGUGGU	1354	ACCACCCCAUUAU UACAGCC	1974	ACCACCCCATTAT TACAGCC	Intron 54
735	GGCUGUAAUAAUG GGGUGGUG	1355	CACCACCCCAUUA UUACAGCC	1975	CACCACCCCATTA TTACAGCC	Intron 54
736	UUGGCUGUAAUAA UGGGGUGGU	1356	ACCACCCCAUUAU UACAGCCAA	1976	ACCACCCCATTAT TACAGCCAA	Intron 54
737	UUGGCUGUAAUAA UGGGGUGGUG	1357	CACCACCCCAUUA UUACAGCCAA	1977	CACCACCCCATTA TTACAGCCAA	Intron 54
738	AUGGCAAGUAAGU CAGGCAU	1358	AUGCCUGACUUAC UUGCCAU	1978	ATGCCTGACTTAC TTGCCAT	Exon 55/intron 55 junction
739	UGGCUGUAAUAAU GGGGUGGUGAA	1359	UUCACCACCCCAU UAUUACAGCCA	1979	TTCACCACCCCAT TATTACAGCCA	Intron 54
740	GGCUGUAAUAAUG GGGUGGUGAA	1360	UUCACCACCCCAU UAUUACAGCC	1980	TTCACCACCCCAT TATTACAGCC	Intron 54
741	GCUGUAAUAAUGG GGUGGUG	1361	CACCACCCCAUUA UUACAGC	1981	CACCACCCCATTA TTACAGC	Intron 54
742	GGAGCUUGGGAGG GUUCAAGAC	1362	GUCUUGAACCCUC CCAAGCUCC	1982	GTCTTGAACCCTC CCAAGCTCC	Intron 54
743	AUGGAGUUCACUA GGUGCAC	1363	GUGCACCUAGUGA ACUCCAU	1983	GTGCACCTAGTGA ACTCCAT	Intron 54
744	AAUGGCAAGUAAG UCAGGCAU	1364	AUGCCUGACUUAC UUGCCAUU	1984	ATGCCTGACTTAC TTGCCATT	Exon 55/intron 55 junction
745	AUGGCAAGUAAGU CAGGCAUU	1365	AAUGCCUGACUUA CUUGCCAU	1985	AATGCCTGACTTA CTTGCCAT	Exon 55/intron 55 junction

746	UUGGCUGUAAUAA UGGGGUGGUGAA	1366	UUCACCACCCCAU UAUUACAGCCAA	1986	TTCACCACCCCAT TATTACAGCCAA	Intron 54
747	UAAUGGGGUGGUG AAACUGG	1367	CCAGUUUCACCAC CCCAUUA	1987	CCAGTTTCACCAC CCCATTA	Intron 54
748	UGGCAAGUAAGUC AGGCAUUUCCG	1368	CGGAAAUGCCUGA CUUACUUGCCA	1988	CGGAAATGCCTGA CTTACTTGCCA	Exon 55/intron 55 junction
749	GCUGUAAUAAUGG GGUGGUGAA	1369	UUCACCACCCCAU UAUUACAGC	1989	TTCACCACCCCAT TATTACAGC	Intron 54
750	AAUGGCAAGUAAG UCAGGCAUU	1370	AAUGCCUGACUUA CUUGCCAUU	1990	AATGCCTGACTTA CTTGCCATT	Exon 55/intron 55 junction
751	AUGGCAAGUAAGU CAGGCAUUU	1371	AAAUGCCUGACUU ACUUGCCAU	1991	AAATGCCTGACTT ACTTGCCAT	Exon 55/intron 55 junction
752	GCAAGUAAGUCAG GCAUUUCCGCU	1372	AGCGGAAAUGCCU GACUUACUUGC	1992	AGCGGAAATGCCT GACTTACTTGC	Exon 55/intron 55 junction
753	AUAAUGGGGUGGU GAAACUGG	1373	CCAGUUUCACCAC CCCAUUAU	1993	CCAGTTTCACCAC CCCATTAT	Intron 54
754	AAUGGCAAGUAAG UCAGGCA	1374	UGCCUGACUUACU UGCCAUU	1994	TGCCTGACTTACT TGCCATT	Exon 55/intron 55 junction
755	AUGGCAAGUAAGU CAGGCAUUUCCG	1375	CGGAAAUGCCUGA CUUACUUGCCAU	1995	CGGAAATGCCTGA CTTACTTGCCAT	Exon 55/intron 55 junction
756	CGAUGAUGCAGUC CUGUUACAAAGA	1376	UCUUUGUAACAGG ACUGCAUCAUCG	1996	TCTTTGTAACAGG ACTGCATCATCG	Exon 56
757	AAUGGCAAGUAAG UCAGGCAUUU	1377	AAAUGCCUGACUU ACUUGCCAUU	1997	AAATGCCTGACTT ACTTGCCATT	Exon 55/intron 55 junction
758	GCAAGUAAGUCAG GCAUUUCC	1378	GGAAAUGCCUGAC UUACUUGC	1998	GGAAATGCCTGAC TTACTTGC	Exon 55/intron 55 junction
759	GCAAGUAAGUCAG GCAUUUCCGCUU	1379	AAGCGGAAAUGCC UGACUUACUUGC	1999	AAGCGGAAATGCC TGACTTACTTGC	Exon 55/intron 55 junction
760	CAAGUAAGUCAGG CAUUUCCGCU	1380	AGCGGAAAUGCCU GACUUACUUG	2000	AGCGGAAATGCCT GACTTACTTG	Exon 55/intron 55 junction
761	AAUAAUGGGGUGG UGAAACUGG	1381	CCAGUUUCACCAC CCCAUUAUU	2001	CCAGTTTCACCAC CCCATTATT	Intron 54
762	GGCAAGUAAGUCA GGCAUUUC	1382	GAAAUGCCUGACU UACUUGCC	2002	GAAATGCCTGACT TACTTGCC	Exon 55/intron 55 junction
763	CCGAUGAUGCAGU CCUGUUACAAAG	1383	CUUUGUAACAGGA CUGCAUCAUCGG	2003	CTTTGTAACAGGA CTGCATCATCGG	Exon 56
764	GCAAGUAAGUCAG GCAUUUCCG	1384	CGGAAAUGCCUGA CUUACUUGC	2004	CGGAAATGCCTGA CTTACTTGC	Exon 55/intron 55 junction
765	CAAGUAAGUCAGG CAUUUCCGC	1385	GCGGAAAUGCCUG ACUUACUUG	2005	GCGGAAATGCCTG ACTTACTTG	Exon 55/intron 55 junction
766	GUUUGGUAAUUCU GCACAUAUUC	1386	GAAUAUGUGCAGA AUUACCAAAC	2006	GAATATGTGCAGA ATTACCAAAC	Intron 55
767	UAAUAAUGGGGUG GUGAAACUGG	1387	CCAGUUUCACCAC CCCAUUAUUA	2007	CCAGTTTCACCAC CCCATTATTA	Intron 54
768	UGGCAAGUAAGUC AGGCAUUUC	1388	GAAAUGCCUGACU UACUUGCCA	2008	GAAATGCCTGACT TACTTGCCA	Exon 55/intron 55 junction
769	GGCAAGUAAGUCA GGCAUUUCC	1389	GGAAAUGCCUGAC UUACUUGCC	2009	GGAAATGCCTGAC TTACTTGCC	Exon 55/intron 55 junction
770	CCGAUGAUGCAGU CCUGUUA	1390	UAACAGGACUGCA UCAUCGG	2010	TAACAGGACTGCA TCATCGG	Exon 56
771	CGAUGAUGCAGUC CUGUUAC	1391	GUAACAGGACUGC AUCAUCG	2011	GTAACAGGACTGC ATCATCG	Exon 56
772	CCAAAUUCACAUU CAUCGCUUGU	1392	ACAAGCGAUGAAU GUGAAUUUGG	2012	ACAAGCGATGAAT GTGAATTTGG	Intron 55
773	GUUUGGUAAUUCU GCACAUAUUCU	1393	AGAAUAUGUGCAG AAUUACCAAAC	2013	AGAATATGTGCAG AATTACCAAAC	Intron 55
774	GUAAUAAUGGGGU GGUGAAA	1394	UUUCACCACCCCA UUAUUAC	2014	TTTCACCACCCCA TTATTAC	Intron 54
775	GUAAUAAUGGGGU GGUGAAACUG	1395	CAGUUUCACCACC CCAUUAUUAC	2015	CAGTTTCACCACC CCATTATTAC	Intron 54
776	GGCAAGUAAGUCA GGCAUUUCCG	1396	CGGAAAUGCCUGA CUUACUUGCC	2016	CGGAAATGCCTGA CTTACTTGCC	Exon 55/intron 55 junction

777	CCGAUGAUGCAGU CCUGUUACA	1397	UGUAACAGGACUG CAUCAUCGG	2017	TGTAACAGGACTG CATCATCGG	Exon 56
778	GUAAUAAUGGGGU GGUGAAACU	1398	AGUUUCACCACCC CAUUAUUAC	2018	AGTTTCACCACCC CATTATTAC	Intron 54
779	CUCCAAAUUCACA UUCAUCGCUUGU	1399	ACAAGCGAUGAAU GUGAAUUUGGAG	2019	ACAAGCGATGAAT GTGAATTTGGAG	Intron 55

† *Each thymine base (T) in any one of the oligonucleotides and/or target sequences provided in Table 8 may independently and optionally be replaced with a uracil base (U), and/or each U may independently and optionally be replaced with a T. Target sequences listed in Table 8 contain U's, but binding of a DMD-targeting oligonucleotide to RNA and/or DNA is contemplated.*

[000201] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) targets a region of a DMD sequence. In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) targets a region of a DMD RNA (*e.g.*, the Dp427m transcript of SEQ ID NO: 130). In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) comprises a region of complementarity to a DMD RNA (*e.g.*, the Dp427m transcript of SEQ ID NO: 130). In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) comprises a region of complementarity to an exon of a DMD RNA (*e.g.*, SEQ ID NO: 2142, 2152, or 2165). In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) comprises a region of complementarity to an intron of a DMD RNA (*e.g.*, SEQ ID NO: 2145 or 2157). In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) comprises a region of complementarity to a portion of a DMD sequence (*e.g.*, a sequence provided by any one of SEQ ID NOs: 2143, 2144, 2146-2151, 2153-2156, 2158-2164, and 2166-2169). Examples of DMD sequences are provided below. Each of the DMD sequences provided below include thymine nucleotides (T's), but it should be understood that each sequence can represent a DNA sequence or an RNA sequence in which any or all of the T's would be replaced with uracil nucleotides (U's).

[000202] *Homo sapiens* dystrophin (DMD), transcript variant Dp427m, mRNA (NCBI Reference Sequence: NM_004006.2)

TCCTGGCATCAGTTACTGTGTTGACTCACTCAGTGTTGGGATCACTCACTTTCCCCCTACAGGACTCAGATCTGGGA
GGCAATTACCTTCGGAGAAAAACGAATAGGAAAAACTGAAGTGTTACTTTTTTTAAAGCTGCTGAAGTTTGTTGGTT
TCTCATTGTTTTTAAGCCTACTGGAGCAATAAAGTTTGAAGAACTTTTACCAGGTTTTTTTTATCGCTGCCTTGATA
TACACTTTTCAAAATGCTTTGGTGGGAAGAAGTAGAGGACTGTTATGAAAGAGAAGATGTTCAAAAGAAAACATTCA
CAAAATGGGTAAATGCACAATTTTCTAAGTTTGGGAAGCAGCATATTGAGAACCTCTTCAGTGACCTACAGGATGGG
AGGCGCCTCCTAGACCTCCTCGAAGGCCTGACAGGGCAAAAACTGCCAAAAGAAAAAGGATCCACAAGAGTTCATGC
CCTGAACAATGTCAACAAGGCACTGCGGGTTTTGCAGAACAATAATGTTGATTTAGTGAATATTGGAAGTACTGACA
TCGTAGATGGAAATCATAAACTGACTCTTGGTTTGATTTGGAATATAATCCTCCACTGGCAGGTCAAAAATGTAATG
AAAAATATCATGGCTGGATTGCAACAAACCAACAGTGAAAAGATTCTCCTGAGCTGGGTCCGACAATCAACTCGTAA
TTATCCACAGGTTAATGTAATCAACTTCACCACCAGCTGGTCTGATGGCCTGGCTTTGAATGCTCTCATCCATAGTC
ATAGGCCAGACCTATTTGACTGGAATAGTGTGGTTTGCCAGCAGTCAGCCACACAACGACTGGAACATGCATTCAAC
ATCGCCAGATATCAATTAGGCATAGAGAAACTACTCGATCCTGAAGATGTTGATACCACCTATCCAGATAAGAAGTC
CATCTTAATGTACATCACATCACTCTTCCAAGTTTTGCCTCAACAAGTGAGCATTGAAGCCATCCAGGAAGTGGAAA
TGTTGCCAAGGCCACCTAAAGTGACTAAAGAAGAACATTTTCAGTTACATCATCAAATGCACTATTCTCAACAGATC
ACGGTCAGTCTAGCACAGGGATATGAGAGAACTTCTTCCCCTAAGCCTCGATTCAAGAGCTATGCCTACACACAGGC
TGCTTATGTCACCACCTCTGACCCTACACGGAGCCCATTTCCTTCACAGCATTTGGAAGCTCCTGAAGACAAGTCAT
TTGGCAGTTCATTGATGGAGAGTGAAGTAAACCTGGACCGTTATCAAACAGCTTTAGAAGAAGTATTATCGTGGCTT

CTTTCTGCTGAGGACACATTGCAAGCACAAGGAGAGATTTCTAATGATGTGGAAGTGGTGAAAGACCAGTTTCATAC
TCATGAGGGGTACATGATGGATTTGACAGCCCATCAGGGCCGGGTTGGTAATATTCTACAATTGGGAAGTAAGCTGA
TTGGAACAGGAAAATTATCAGAAGATGAAGAAACTGAAGTACAAGAGCAGATGAATCTCCTAAATTCAAGATGGGAA
TGCCTCAGGGTAGCTAGCATGGAAAAACAAAGCAATTTACATAGAGTTTTAATGGATCTCCAGAATCAGAAACTGAA
AGAGTTGAATGACTGGCTAACAAAAACAGAAGAAAGAACAAGGAAAATGGAGGAAGAGCCTCTTGGACCTGATCTTG
AAGACCTAAAACGCCAAGTACAACAACATAAGGTGCTTCAAGAAGATCTAGAACAAGAACAAGTCAGGGTCAATTCT
CTCACTCACATGGTGGTGGTAGTTGATGAATCTAGTGGAGATCACGCAACTGCTGCTTTGGAAGAACAACTTAAGGT
ATTGGGAGATCGATGGGCAAACATCTGTAGATGGACAGAAGACCGCTGGGTTCTTTTACAAGACATCCTTCTCAAAT
GGCAACGTCTTACTGAAGAACAGTGCCTTTTTAGTGCATGGCTTTCAGAAAAAGAAGATGCAGTGAACAAGATTCAC
ACAACTGGCTTTAAAGATCAAAATGAAATGTTATCAAGTCTTCAAAAACTGGCCGTTTTAAAAGCGGATCTAGAAAA
GAAAAAGCAATCCATGGGCAAACTGTATTCACTCAAACAAGATCTTCTTTCAACACTGAAGAATAAGTCAGTGACCC
AGAAGACGGAAGCATGGCTGGATAACTTTGCCCGGTGTTGGGATAATTTAGTCCAAAAACTTGAAAAGAGTACAGCA
CAGATTTCACAGGCTGTCACCACCACTCAGCCATCACTAACACAGACAACTGTAATGGAAACAGTAACTACGGTGAC
CACAAGGGAACAGATCCTGGTAAAGCATGCTCAAGAGGAACTTCCACCACCACCTCCCCAAAAGAAGAGGCAGATTA
CTGTGGATTCTGAAATTAGGAAAAGGTTGGATGTTGATATAACTGAACTTCACAGCTGGATTACTCGCTCAGAAGCT
GTGTTGCAGAGTCCTGAATTTGCAATCTTTCGGAAGGAAGGCAACTTCTCAGACTTAAAAGAAAAAGTCAATGCCAT
AGAGCGAGAAAAAGCTGAGAAGTTCAGAAAACTGCAAGATGCCAGCAGATCAGCTCAGGCCCTGGTGGAACAGATGG
TGAATGAGGGTGTTAATGCAGATAGCATCAAACAAGCCTCAGAACAACTGAACAGCCGGTGGATCGAATTCTGCCAG
TTGCTAAGTGAGAGACTTAACTGGCTGGAGTATCAGAACAACATCATCGCTTTCTATAATCAGCTACAACAATTGGA
GCAGATGACAACTACTGCTGAAAACTGGTTGAAAATCCAACCCACCACCCCATCAGAGCCAACAGCAATTAAAAGTC
AGTTAAAAATTTGTAAGGATGAAGTCAACCGGCTATCAGGTCTTCAACCTCAAATTGAACGATTAAAAATTCAAAGC
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AGTCTTTTCTGATGTGCAGGCCAGAGAGAAAGAGCTACAGACAATTTTTGACACTTTGCCACCAATGCGCTATCAGG
AGACCATGAGTGCCATCAGGACATGGGTCCAGCAGTCAGAAACCAAACTCTCCATACCTCAACTTAGTGTCACCGAC
TATGAAATCATGGAGCAGAGACTCGGGGAATTGCAGGCTTTACAAAGTTCTCTGCAAGAGCAACAAAGTGGCCTATA
CTATCTCAGCACCACTGTGAAAGAGATGTCGAAGAAAGCGCCCTCTGAAATTAGCCGGAAATATCAATCAGAATTTG
AAGAAATTGAGGGACGCTGGAAGAAGCTCTCCTCCCAGCTGGTTGAGCATTGTCAAAAGCTAGAGGAGCAAATGAAT
AAACTCCGAAAAATTCAGAATCACATACAAACCCTGAAGAAATGGATGGCTGAAGTTGATGTTTTTCTGAAGGAGGA
ATGGCCTGCCCTTGGGGATTCAGAAATTCTAAAAAAGCAGCTGAAACAGTGCAGACTTTTAGTCAGTGATATTCAGA
CAATTCAGCCCAGTCTAAACAGTGTCAATGAAGGTGGGCAGAAGATAAAGAATGAAGCAGAGCCAGAGTTTGCTTCG
AGACTTGAGACAGAACTCAAAGAACTTAACACTCAGTGGGATCACATGTGCCAACAGGTCTATGCCAGAAAGGAGGC
CTTGAAGGGAGGTTTGGAGAAAACTGTAAGCCTCCAGAAAGATCTATCAGAGATGCACGAATGGATGACACAAGCTG
AAGAAGAGTATCTTGAGAGAGATTTTGAATATAAAACTCCAGATGAATTACAGAAAGCAGTTGAAGAGATGAAGAGA
GCTAAAGAAGAGGCCCAACAAAAAGAAGCGAAAGTGAAACTCCTTACTGAGTCTGTAAATAGTGTCATAGCTCAAGC
TCCACCTGTAGCACAAGAGGCCTTAAAAAAGGAACTTGAAACTCTAACCACCAACTACCAGTGGCTCTGCACTAGGC
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GCTAGATTCACTTGAAAATTTGATGCGACATTCAGAGGATAACCCAAATCAGATTCGCATATTGGCACAGACCCTAA
CAGATGGCGGAGTCATGGATGAGCTAATCAATGAGGAACTTGAGACATTTAATTCTCGTTGGAGGGAACTACATGAA
GAGGCTGTAAGGAGGCAAAAGTTGCTTGAACAGAGCATCCAGTCTGCCCAGGAGACTGAAAAATCCTTACACTTAAT
CCAGGAGTCCCTCACATTCATTGACAAGCAGTTGGCAGCTTATATTGCAGACAAGGTGGACGCAGCTCAAATGCCTC
AGGAAGCCCAGAAAATCCAATCTGATTTGACAAGTCATGAGATCAGTTTAGAAGAAATGAAGAAACATAATCAGGGG
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TGCCTGCATTGGAAACAAAGAGTGTGGAACAGGAAGTAGTACAGTCACAGCTAAATCATTGTGTGAACTTGTATAAA
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CATCACAAAGTGGATCATTCAGGCTGACACACTTTTGGATGAATCAGAGAAAAAGAAACCCCAGCAAAAAGAAGACG
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TTCACACAGAATTAAGACTGGAAAGGCCTCCATTCCTTTGAAGGAATTGGAGCAGTTTAACTCAGATATACAAAAAT
TGCTTGAACCACTGGAGGCTGAAATTCAGCAGGGGGTGAATCTGAAAGAGGAAGACTTCAATAAAGATATGAATGAA
GACAATGAGGGTACTGTAAAAGAATTGTTGCAAAGAGGAGACAACTTACAACAAAGAATCACAGATGAGAGAAAGCG
AGAGGAAATAAAGATAAAACAGCAGCTGTTACAGACAAAACATAATGCTCTCAAGGATTTGAGGTCTCAAAGAAGAA
AAAAGGCTCTAGAAATTTCTCATCAGTGGTATCAGTACAAGAGGCAGGCTGATGATCTCCTGAAATGCTTGGATGAC
ATTGAAAAAAAATTAGCCAGCCTACCTGAGCCCAGAGATGAAAGGAAAATAAAGGAAATTGATCGGGAATTGCAGAA
GAAGAAAGAGGAGCTGAATGCAGTGCGTAGGCAAGCTGAGGGCTTGTCTGAGGATGGGGCCGCAATGGCAGTGGAGC
CAACTCAGATCCAGCTCAGCAAGCGCTGGCGGGAAATTGAGAGCAAATTTGCTCAGTTTCGAAGACTCAACTTTGCA
CAAATTCACACTGTCCGTGAAGAAACGATGATGGTGATGACTGAAGACATGCCTTTGGAAATTTCTTATGTGCCTTC

TACTTATTTGACTGAAATCACTCATGTCTCACAAGCCCTATTAGAAGTGGAACAACTTCTCAATGCTCCTGACCTCT
GTGCTAAGGACTTTGAAGATCTCTTTAAGCAAGAGGAGTCTCTGAAGAATATAAAAAGATAGTCTACAACAAAGCTCA
GGTCGGATTGACATTATTCATAGCAAGAAGACAGCAGCATTGCAAAGTGCAACGCCTGTGGAAAGGGTGAAGCTACA
GGAAGCTCTCTCCCAGCTTGATTTCCAATGGGAAAAAGTTAACAAAATGTACAAGGACCGACAAGGGCGATTTGACA
GATCTGTTGAGAAATGGCGGCGTTTTCATTATGATATAAAGATATTTAATCAGTGGCTAACAGAAGCTGAACAGTTT
CTCAGAAAGACACAAATTCCTGAGAATTGGGAACATGCTAAATACAAATGGTATCTTAAGGAACTCCAGGATGGCAT
TGGGCAGCGGCAAACTGTTGTCAGAACATTGAATGCAACTGGGGAAGAAATAATTCAGCAATCCTCAAAAACAGATG
CCAGTATTCTACAGGAAAAATTGGGAAGCCTGAATCTGCGGTGGCAGGAGGTCTGCAAACAGCTGTCAGACAGAAAA
AAGAGGCTAGAAGAACAAAAGAATATCTTGTCAGAATTTCAAAGAGATTTAAATGAATTTGTTTTATGGTTGGAGGA
AGCAGATAACATTGCTAGTATCCCACTTGAACCTGGAAAAGAGCAGCAACTAAAAGAAAAGCTTGAGCAAGTCAAGT
TACTGGTGGAAGAGTTGCCCCTGCGCCAGGGAATTCTCAAACAATTAAATGAAACTGGAGGACCCGTGCTTGTAAGT
GCTCCCATAAGCCCAGAAGAGCAAGATAAACTTGAAAATAAGCTCAAGCAGACAAATCTCCAGTGGATAAAGGTTTC
CAGAGCTTTACCTGAGAAACAAGGAGAAATTGAAGCTCAAATAAAAGACCTTGGGCAGCTTGAAAAAAAGCTTGAAG
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TTACGAATTATTTTTTTAAACTTCAGTTTTACTGCATTTTCACAACATATCAGACTTCACCAAATATATGCCTTACT
ATTGTATTATAGTACTGCTTTACTGTGTATCTCAATAAAGCACGCAGTTATGTTAC (SEQ ID NO: 130)

[000203] *Homo sapiens* dystrophin (DMD), transcript variant Dp427m, exon 54 (nucleotide positions 8117-8271 of NCBI Reference Sequence: NM_004006.2; nucleotide positions 1686466-1686620 of NCBI Reference Sequence: NG_012232.1)

CAGTTGGCCAAAGACCTCCGCCAGTGGCAGACAAATGTAGATGTGGCAAATGACTTGGCCCTGAAACTTCTCCGGGA
TTATTCTGCAGATGATACCAGAAAAGTCCACATGATAACAGAGAATATCAATGCCTCTTGGAGAAGCATTCATAAAA
G (SEQ ID NO: 2142)

[000204] *Homo sapiens* dystrophin (DMD), exon 54 target sequence 1 (nucleotide positions 1686541-1686602 of NCBI Reference Sequence: NG_012232.1)

GATTATTCTGCAGATGATACCAGAAAAGTCCACATGATAACAGAGAATATCAATGCCTCTTG (SEQ ID NO: 2143)

[000205] *Homo sapiens* dystrophin (DMD) exon 54/intron 54 junction (nucleotide positions 1686591 to 1686650 of NCBI Reference Sequence: NG_012232.1)

CAATGCCTCTTGGAGAAGCATTCATAAAAGGTATGAATTACATTATTTCTAAAACTACTG (SEQ ID NO: 2144)

[000206] *Homo sapiens* dystrophin (DMD), intron 54 (nucleotide positions 1686621-1716747 of NCBI Reference Sequence: NG_012232.1)

GTATGAATTACATTATTTCTAAAACTACTGTTGGCTGTAATAATGGGGTGGTGAAACTGGATGGACCATGAGGATTT
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TACAATTTAGTTCCTCCATCTTTCTCTTTTTATGGAGTTCACTAGGTGCACCATTCTGATATTTAATAATTGCATCT
GAACATTTGGTCCTTTGCAG (SEQ ID NO: 2145)

[000207] *Homo sapiens* dystrophin (DMD), intron 54 target sequence 1 (nucleotide positions 1686621-1686670 of NCBI Reference Sequence: NG_012232.1)

GTATGAATTACATTATTTCTAAAACTACTGTTGGCTGTAATAATGGGGTG (SEQ ID NO: 2146)

[000208] *Homo sapiens* dystrophin (DMD), intron 54 target sequence 2 (nucleotide positions 1686641-1686695 of NCBI Reference Sequence: NG_012232.1)

AAAACTACTGTTGGCTGTAATAATGGGGTGGTGAAACTGGATGGACCATGAGGAT (SEQ ID NO: 2147)

[000209] *Homo sapiens* dystrophin (DMD), intron 54 target sequence 3 (nucleotide positions 1686710-1686754 of NCBI Reference Sequence: NG_012232.1)

CAGCTAAACTGGAGCTTGGGAGGGTTCAAGACGATAAATACCAAC (SEQ ID NO: 2148)

[000210] *Homo sapiens* dystrophin (DMD), intron 54 target sequence 4 (nucleotide positions 1716672-1716711 of NCBI Reference Sequence: NG_012232.1)

TTCTCTTTTTATGGAGTTCACTAGGTGCACCATTCTGATA (SEQ ID NO: 2149)

[000211] *Homo sapiens* dystrophin (DMD), intron 54 target sequence 5 (nucleotide positions 1716498-1716747 of NCBI Reference Sequence: NG_012232.1)

GTTTATAGAAATCTGTAATTGTCATTCTTGCATGCCTTCCCCCATACAAACGCCTTTAAGTTAAATAAAAATGAAAG
TAAATAGACTGCACAATATTATAGTTGTTGCTTAAAGGAAGAGCTGTAGCAACAACTCACCCCATTGTTGGTATATT
ACAATTTAGTTCCTCCATCTTTCTCTTTTTATGGAGTTCACTAGGTGCACCATTCTGATATTTAATAATTGCATCTG
AACATTTGGTCCTTTGCAG (SEQ ID NO: 2150)

[000212] *Homo sapiens* dystrophin (DMD) intron 54/exon 55 junction (nucleotide positions 1716718-1716777 of NCBI Reference Sequence: NG_012232.1)

AATTGCATCTGAACATTTGGTCCTTTGCAGGGTGAGTGAGCGAGAGGCTGCTTTGGAAGA (SEQ ID NO: 2151)

[000213] *Homo sapiens* dystrophin (DMD), transcript variant Dp427m, exon 55 (nucleotide positions 8272-8461 of NCBI Reference Sequence: NM_004006.2; nucleotide positions 1716748-1716937 of NCBI Reference Sequence: NG_012232.1)

GGTGAGTGAGCGAGAGGCTGCTTTGGAAGAAACTCATAGATTACTGCAACAGTTCCCCCTGGACCTGGAAAAGTTTC
TTGCCTGGCTTACAGAAGCTGAAACAACTGCCAATGTCCTACAGGATGCTACCCGTAAGGAAAGGCTCCTAGAAGAC
TCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAA (SEQ ID NO: 2152)

[000214] *Homo sapiens* dystrophin (DMD), exon 55 target sequence 1 (nucleotide positions 1716757-1716809 of NCBI Reference Sequence: NG_012232.1)

GCGAGAGGCTGCTTTGGAAGAAACTCATAGATTACTGCAACAGTTCCCCCTGG (SEQ ID NO: 2153)

[000215] *Homo sapiens* dystrophin (DMD), exon 55 target sequence 2 (nucleotide positions 1716821-1716887 of NCBI Reference Sequence: NG_012232.1)

TTTCTTGCCTGGCTTACAGAAGCTGAAACAACTGCCAATGTCCTACAGGATGCTACCCGTAAGGAAA (SEQ ID NO: 2154)

[000216] *Homo sapiens* dystrophin (DMD), exon 55 target sequence 3 (nucleotide positions 1716891-1716937 of NCBI Reference Sequence: NG_012232.1)

TCCTAGAAGACTCCAAGGGAGTAAAAGAGCTGATGAAACAATGGCAA (SEQ ID NO: 2155)

[000217] *Homo sapiens* dystrophin (DMD) exon 55/intron 55 junction (nucleotide positions 1716908-1716967 of NCBI Reference Sequence: NG_012232.1)

GGAGTAAAAGAGCTGATGAAACAATGGCAAGTAAGTCAGGCATTTCCGCTTTAGCACTCT (SEQ ID NO: 2156)

[000218] *Homo sapiens* dystrophin (DMD), intron 55 (nucleotide positions 1716938-1837156 of NCBI Reference Sequence: NG_012232.1)

GTAAGTCAGGCATTTCCGCTTTAGCACTCTTGTGGATCCAATTGAACAATTCTCAGCATTTGTACTTGTA
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AATAATTATTTATATTTTGCAATTCTCCAAATTCACATTCATCGCTTGTTTCTTTTGTTTGGTAATTCTG
CACATATTCTTCTTCCTGCTGTCCTGTAG (SEQ ID NO: 2157)

[000219] *Homo sapiens* dystrophin (DMD), intron 55 target sequence 1 (nucleotide positions 1716938-1716987 of NCBI Reference Sequence: NG_012232.1)

GTAAGTCAGGCATTTCCGCTTTAGCACTCTTGTGGATCCAATTGAACAAT (SEQ ID NO: 2158)

[000220] *Homo sapiens* dystrophin (DMD), intron 55 target sequence 2 (nucleotide positions 1716950-1717012 of NCBI Reference Sequence: NG_012232.1)

TTTCCGCTTTAGCACTCTTGTGGATCCAATTGAACAATTCTCAGCATTTGTACTTGTAACTGA (SEQ ID NO: 2159)

[000221] *Homo sapiens* dystrophin (DMD), intron 55 target sequence 3 (nucleotide positions 1717003-1717050 of NCBI Reference Sequence: NG_012232.1)

TTGTAACTGACAAGCCAGGGACAAAACAAAATAGTTGCTTTTATACAG (SEQ ID NO: 2160)

[000222] *Homo sapiens* dystrophin (DMD), intron 55 target sequence 4 (nucleotide positions 1837063-1837116 of NCBI Reference Sequence: NG_012232.1)

TTATTTATATTTTGCAATTCTCCAAATTCACATTCATCGCTTGTTTCTTTTGTT (SEQ ID NO: 2161)

[000223] *Homo sapiens* dystrophin (DMD), intron 55 target sequence 5 (nucleotide positions 1837104-1837153 of NCBI Reference Sequence: NG_012232.1)

TGTTTCTTTTGTTTGGTAATTCTGCACATATTCTTCTTCCTGCTGTCCTG (SEQ ID NO: 2162)

[000224] *Homo sapiens* dystrophin (DMD), intron 55 target sequence 6 (nucleotide positions 1836907-1837156 of NCBI Reference Sequence: NG_012232.1)

CCAACTCATAATGGCAAGGAATAAATCTATTACAACTAATAAGATGCCCATTTTAAATCTACATAATAACAGGAGAA
GGCAATACGCCAAGAAAAGGGATTTGAGATGTATCTTCTTGTTAGTTTAGCCTGATTGAAATGTCTTTTGAACTAAT
AATTATTTATATTTTGCAATTCTCCAAATTCACATTCATCGCTTGTTTCTTTTGTTTGGTAATTCTGCACATATTCT
TCTTCCTGCTGTCCTGTAG (SEQ ID NO: 2163)

[000225] *Homo sapiens* dystrophin (DMD) intron 55/exon 56 junction (nucleotide positions 1837127-1837186 of NCBI Reference Sequence: NG_012232.1)

GCACATATTCTTCTTCCTGCTGTCCTGTAGGACCTCCAAGGTGAAATTGAAGCTCACACA (SEQ ID NO: 2164)

[000226] *Homo sapiens* dystrophin (DMD), transcript variant Dp427m, exon 56 (nucleotide positions 8462-8634 of NCBI Reference Sequence: NM_004006.2; nucleotide positions 1837157-1837329 of NCBI Reference Sequence: NG_012232.1)

GACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATC
CCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTGGATAACATGAACTTCAAGTGGAGTGAACTTCGGA
AAAAGTCTCTCAACATTAG (SEQ ID NO: 2165)

[000227] *Homo sapiens* dystrophin (DMD), exon 56 target sequence 1 (nucleotide positions 1837157-1837281 of NCBI Reference Sequence: NG_012232.1)

GACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATC
CCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTGGATAA (SEQ ID NO: 2166)

[000228] *Homo sapiens* dystrophin (DMD), exon 56 target sequence 2 (nucleotide positions 1837157-1837201 of NCBI Reference Sequence: NG_012232.1)
GACCTCCAAGGTGAAATTGAAGCTCACACAGATGTTTATCACAAC (SEQ ID NO: 2167)

[000229] *Homo sapiens* dystrophin (DMD), exon 56 target sequence 3 (nucleotide positions 1837181-1837237 of NCBI Reference Sequence: NG_012232.1)
CACACAGATGTTTATCACAACCTGGATGAAAACAGCCAAAAAATCCTGAGATCCCTG (SEQ ID NO: 2168)

[000230] *Homo sapiens* dystrophin (DMD), exon 56 target sequence 4 (nucleotide positions 1837225-1837281 of NCBI Reference Sequence: NG_012232.1)
CCTGAGATCCCTGGAAGGTTCCGATGATGCAGTCCTGTTACAAAGACGTTTGGATAA (SEQ ID NO: 2169)

[000231] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) targets a splicing feature in a DMD sequence (*e.g.*, a DMD pre-mRNA). In some embodiments, a splicing feature in a DMD sequence is an exonic splicing enhancer (ESE), a branch point, a splice donor site, or a splice acceptor site in a DMD sequence. In some embodiments, an ESE is in exon 55 of a DMD sequence (*e.g.*, a DMD pre-mRNA). In some embodiments, a branch point is in intron 54 or intron 55 of a DMD sequence (*e.g.*, a DMD pre-mRNA). In some embodiments, a splice donor site is across the junction of exon 54 and intron 54, in intron 54, across the junction of exon 55 and intron 55, or in intron 55 of a DMD sequence (*e.g.*, a DMD pre-mRNA). In some embodiments, a splice acceptor site is in intron 54, across the junction of intron 54 and exon 55, in intron 55, or across the junction of intron 55 and exon 56 of a DMD sequence (*e.g.*, a DMD pre-mRNA). In some embodiments, the oligonucleotide useful for targeting DMD promotes skipping of exon 55, such as by targeting a splicing feature (*e.g.*, an ESE, a branch point, a splice donor site, or a splice acceptor site) in a DMD sequence (*e.g.*, a DMD pre-mRNA). Examples of ESEs, branch points, splice donor sites, and splice acceptor sites are provided in Table 9.

[000232] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) targets an exonic splicing enhancer (ESE) in a DMD sequence. In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) targets an ESE in DMD exon 55 (e.g., an ESE listed in Table 9).

[000233] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping, such as for skipping exon 55) comprises a region of complementarity to a target sequence comprising one or more full or partial ESEs of a DMD transcript (e.g., one or more full or partial ESEs listed in Table 9). In some embodiments, the oligonucleotide comprises a region of complementarity to a target sequence comprising one or more full or partial ESEs of

DMD exon 55. In some embodiments, the oligonucleotide comprises a region of complementarity to a target sequence comprising one or more full or partial ESEs as set forth in any one of SEQ ID NOs: 2020-2027, 2031-2061, and 2064-2080. In some embodiments, the oligonucleotide comprises a region of complementarity to a target sequence comprising at least 4 (e.g., 4, 5, 6, 7, or 8) consecutive nucleotides of an ESE as set forth in any one of SEQ ID NOs: 2020-2027, 2031-2061, and 2064-2080. In some embodiments, the oligonucleotide comprises at least 4 (e.g., 4, 5, 6, 7, or 8) consecutive nucleotides of an ESE antisense sequence as set forth in any one of SEQ ID NOs: 2081-2088, 2092-2122, and 2125-2141.

[000234] In some embodiments, the oligonucleotide comprises a region of complementarity to a target sequence comprising at least 6 (e.g., 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more) nucleotides of one or more ESEs (e.g., 2, 3, 4, or more adjacent ESEs) of DMD exon 55. In some embodiments, the oligonucleotide comprises a region of complementarity to a target sequence comprising at least 6 (e.g., 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more) nucleotides of one or more ESEs (e.g., 2, 3, 4, or more adjacent ESEs) as set forth in any one of SEQ ID NOs: 2020-2027, 2031-2061, and 2064-2080. In some embodiments, the oligonucleotide comprises at least 6 (e.g., 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more) nucleotides of one or more ESE antisense sequences (e.g., antisense sequences of 2, 3, 4, or more adjacent ESEs) as set forth in any one of SEQ ID NOs: 2081-2088, 2092-2122, and 2125-2141.

[000235] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping, such as for skipping exon 55) is 18-35 nucleotides in length, and comprises a region of complementarity to a target sequence comprising at least 4 (e.g., 4, 5, 6, 7, or 8) consecutive nucleotides of an ESE as set forth in any one of SEQ ID NOs: 2020-2027, 2031-2061, and 2064-2080. In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping, such as for skipping exon 55) is 20-30 (e.g., 20, 25, 30) nucleotides in length, and comprises a region of complementarity to a target sequence comprising at least 4 (e.g., 4, 5, 6, 7, or 8) consecutive nucleotides of an ESE as set forth in any one of SEQ ID NOs: 2020-2027, 2031-2061, and 2064-2080. In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping, such as for skipping exon 55) is 20-25 (*i.e.*, 20, 21, 22, 23, 24, or 25) nucleotides in length, and comprises a region of complementarity to a target sequence comprising at least 4 (e.g., 4, 5, 6, 7, or 8) consecutive nucleotides of an ESE as set forth in any one of SEQ ID NOs: 2020-2027, 2031-2061, and 2064-2080. In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) is 30 nucleotides in length, and comprises a region of complementarity to a target sequence comprising at least 4 (e.g., 4, 5,

6, 7, or 8) consecutive nucleotides of an ESE as set forth in any one of SEQ ID NOs: 2020-2027, 2031-2061, and 2064-2080.

[000236] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) targets a branch point in a DMD sequence. In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) targets a branch point in DMD intron 54 or intron 55 (e.g., a branch point listed in Table 9).

[000237] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping, such as for skipping exon 55) comprises a region of complementarity to a target sequence comprising a full or partial branch point of a DMD transcript (e.g., a full or partial branch point listed in Table 9). In some embodiments, the oligonucleotide comprises a region of complementarity to a target sequence comprising a full or partial branch point of DMD intron 54 or intron 55. In some embodiments, the oligonucleotide comprises a region of complementarity to a target sequence comprising a full or partial branch point as set forth in SEQ ID NO: 2029. In some embodiments, the oligonucleotide comprises a region of complementarity to a target sequence comprising at least 4 (e.g., 4, 5, 6, or 7) consecutive nucleotides of a branch point as set forth in SEQ ID NO: 2029. In some embodiments, the oligonucleotide comprises at least 4 (e.g., 4, 5, 6, or 7) consecutive nucleotides of a branch point antisense sequence as set forth in SEQ ID NO: 2090.

[000238] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping, such as for skipping exon 55) is 18-35 nucleotides in length, and comprises a region of complementarity to a target sequence comprising at least 4 (e.g., 4, 5, 6, or 7) consecutive nucleotides of a branch point as set forth in SEQ ID NO: 2029. In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping, such as for skipping exon 55) is 20-30 (e.g., 20, 25, 30) nucleotides in length, and comprises a region of complementarity to a target sequence comprising at least 4 (e.g., 4, 5, 6, or 7) consecutive nucleotides of a branch point as set forth in SEQ ID NO: 2029. In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping, such as for skipping exon 55) is 20-25 (*i.e.*, 20, 21, 22, 23, 24, or 25) nucleotides in length, and comprises a region of complementarity to a target sequence comprising at least 4 (e.g., 4, 5, 6, or 7) consecutive nucleotides of a branch point as set forth in SEQ ID NO: 2029. In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) is 30 nucleotides in length, and comprises a region of complementarity to a target sequence comprising at least 4 (e.g., 4, 5, 6, or 7) consecutive nucleotides of a branch point as set forth in SEQ ID NO: 2029.

[000239] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) targets a splice donor site in a DMD sequence. In some embodiments, an

oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) targets a splice donor site across the junction of exon 54 and intron 54, in intron 54, across the junction of exon 55 and intron 55, or in intron 55 (e.g., a splice donor site listed in Table 9).

[000240] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping, such as for skipping exon 55) comprises a region of complementarity to a target sequence comprising a full or partial splice donor site of a DMD transcript (e.g., a full or partial splice donor site listed in Table 9). In some embodiments, the oligonucleotide comprises a region of complementarity to a target sequence comprising a full or partial splice donor site across the junction of exon 54 and intron 54, in intron 54, across the junction of exon 55 and intron 55, or in intron 55 of DMD. In some embodiments, the oligonucleotide comprises a region of complementarity to a target sequence comprising a full or partial splice donor site as set forth in SEQ ID NO: 2028 or 2062. In some embodiments, the oligonucleotide comprises a region of complementarity to a target sequence comprising at least 4 (*e.g.*, 4, 5, 6, 7, or 8) consecutive nucleotides of a splice donor site as set forth in SEQ ID NO: 2028 or 2062. In some embodiments, the oligonucleotide comprises at least 4 (*e.g.*, 4, 5, 6, 7, or 8) consecutive nucleotides of a splice donor site antisense sequence as set forth in SEQ ID NO: 2089 or 2123.

[000241] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping, such as for skipping exon 55) is 18-35 nucleotides in length, and comprises a region of complementarity to a target sequence comprising at least 4 (*e.g.*, 4, 5, 6, 7, or 8) consecutive nucleotides of a splice donor site as set forth in SEQ ID NO: 2028 or 2062. In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping, such as for skipping exon 55) is 20-30 (e.g., 20, 25, 30) nucleotides in length, and comprises a region of complementarity to a target sequence comprising at least 4 (*e.g.*, 4, 5, 6, 7, or 8) consecutive nucleotides of a splice donor site as set forth in SEQ ID NO: 2028 or 2062. In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping, such as for skipping exon 55) is 20-25 (*i.e.*, 20, 21, 22, 23, 24, or 25) nucleotides in length, and comprises a region of complementarity to a target sequence comprising at least 4 (*e.g.*, 4, 5, 6, 7, or 8) consecutive nucleotides of a splice donor site as set forth in SEQ ID NO: 2028 or 2062. In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) is 30 nucleotides in length, and comprises a region of complementarity to a target sequence comprising at least 4 (*e.g.*, 4, 5, 6, 7, or 8) consecutive nucleotides of a splice donor site as set forth in SEQ ID NO: 2028 or 2062.

[000242] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) targets a splice acceptor site in a DMD sequence. In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) targets a splice acceptor site

in intron 54, across the junction of intron 54 and exon 55, in intron 55, or across the junction of intron 55 and exon 56 (e.g., a splice acceptor site listed in Table 9).

[000243] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping, such as for skipping exon 55) comprises a region of complementarity to a target sequence comprising a full or partial splice acceptor site of a DMD transcript (e.g., a full or partial splice acceptor site listed in Table 9). In some embodiments, the oligonucleotide comprises a region of complementarity to a target sequence comprising a full or partial splice acceptor site in intron 54, across the junction of intron 54 and exon 55, in intron 55, or across the junction of intron 55 and exon 56 of DMD. In some embodiments, the oligonucleotide comprises a region of complementarity to a target sequence comprising a full or partial splice acceptor site as set forth in SEQ ID NO: 2030 or 2063. In some embodiments, the oligonucleotide comprises a region of complementarity to a target sequence comprising at least 4 (*e.g.*, 4, 5, 6, 7, 8, 9, 10, or 11) consecutive nucleotides of a splice acceptor site as set forth in SEQ ID NO: 2030 or 2063. In some embodiments, the oligonucleotide comprises at least 4 (*e.g.*, 4, 5, 6, 7, 8, 9, 10, or 11) consecutive nucleotides of a splice acceptor site antisense sequence as set forth in SEQ ID NO: 2091 or 2124.

[000244] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping, such as for skipping exon 55) is 18-35 nucleotides in length, and comprises a region of complementarity to a target sequence comprising at least 4 (*e.g.*, 4, 5, 6, 7, 8, 9, 10, or 11) consecutive nucleotides of a splice acceptor site as set forth in SEQ ID NO: 2030 or 2063. In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping, such as for skipping exon 55) is 20-30 (e.g., 20, 25, 30) nucleotides in length, and comprises a region of complementarity to a target sequence comprising at least 4 (*e.g.*, 4, 5, 6, 7, 8, 9, 10, or 11) consecutive nucleotides of a splice acceptor site as set forth in SEQ ID NO: 2030 or 2063. In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping, such as for skipping exon 55) is 20-25 (*i.e.*, 20, 21, 22, 23, 24, or 25) nucleotides in length, and comprises a region of complementarity to a target sequence comprising at least 4 (*e.g.*, 4, 5, 6, 7, 8, 9, 10, or 11) consecutive nucleotides of a splice acceptor site as set forth in SEQ ID NO: 2030 or 2063. In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) is 30 nucleotides in length, and comprises a region of complementarity to a target sequence comprising at least 4 (*e.g.*, 4, 5, 6, 7, 8, 9, 10, or 11) consecutive nucleotides of a splice acceptor site as set forth in SEQ ID NO: 2030 or 2063.

[000245] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) comprises a region of complementarity to a junction of an exon and an intron of a DMD RNA (*e.g.*, any one of the exon/intron junctions provided by SEQ ID NOs: 2144, 2151,

2156, and 2164). In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) comprises a region of complementarity to at least 10 (*e.g.*, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or more) consecutive nucleosides of a junction of an exon and an intron of a DMD RNA (*e.g.*, any one of the exon/intron junctions provided by SEQ ID NOs: 2144, 2151, 2156, and 2164). In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) is complementary to any one of SEQ ID NOs: 2144, 2151, 2156, and 2164.

[000246] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) comprises a region of complementarity to a target sequence of a DMD RNA (*e.g.*, a target sequence provided by any one of SEQ ID NOs: 2143, 2146-2150, 2153-2155, 2158-2163, and 2166-2169). In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) comprises a region of complementarity to at least 10 (*e.g.*, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or more) consecutive nucleosides of a target sequence of a DMD RNA (*e.g.*, a target sequence provided by any one of SEQ ID NOs: 2143, 2146-2150, 2153-2155, 2158-2163, and 2166-2169). In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) is complementary to any one of SEQ ID NOs: 2143, 2146-2150, 2153-2155, 2158-2163, and 2166-2169.

Table 9. Example target sequence motifs

Location in DMD	Type	SEQ ID NO:	Motif Sequence†	SEQ ID NO:	Motif Antisense Sequence†
Exon 54	ESE	2020	ATTCTGC	2081	GCAGAAT
Exon 54	ESE	2021	CTGCAGA	2082	TCTGCAG
Exon 54	ESE	2022	TGCAGA	2083	TCTGCA
Exon 54	ESE	2023	CAGATGA	2084	TCATCTG
Exon 54	ESE	2024	CCACATG	2085	CATGTGG
Exon 54	ESE	2025	CACATGA	2086	TCATGTG
Exon 54	ESE	2026	CAGAGAA	2087	TTCTCTG
Exon 54	ESE	2027	TCAATGC	2088	GCATTGA
Across exon 54/intron 54 junction	Splice Donor	2028	AGGTATG	2089	CATACCT
Intron 54	Branch Point	2029	TTCTGAT	2090	ATCAGAA
Across intron 54/exon 55 junction	Splice Acceptor	2030	TCCTTTGCAGG	2091	CCTGCAAAGG A
Exon 55	ESE	2031	CGAGAGG	2092	CCTCTCG
Exon 55	ESE	2032	GGCTGCTT	2093	AAGCAGCC
Exon 55	ESE	2033	GATTACTG	2094	CAGTAATC
Exon 55	ESE	2034	TTACTGC	2095	GCAGTAA
Exon 55	ESE	2035	TGCAAC	2096	GTTGCA
Exon 55	ESE	2036	CCCCCTG	2097	CAGGGGG
Exon 55	ESE	2037	CCCCTGG	2098	CCAGGGG
Exon 55	ESE	2038	CCCTGGA	2099	TCCAGGG
Exon 55	ESE	2039	GTTTCTTG	2100	CAAGAAAC
Exon 55	ESE	2040	TTTCTTG	2101	CAAGAAA
Exon 55	ESE	2041	TGCCTGG	2102	CCAGGCA
Exon 55	ESE	2042	GGCTTACA	2103	TGTAAGCC
Exon 55	ESE	2043	TTACAGA	2104	TCTGTAA

Location in DMD	Type	SEQ ID NO:	Motif Sequence†	SEQ ID NO:	Motif Antisense Sequence†
Exon 55	ESE	2044	TACAGA	2105	TCTGTA
Exon 55	ESE	2045	ACAGAAG	2106	CTTCTGT
Exon 55	ESE	2046	CTGCCAA	2107	TTGGCAG
Exon 55	ESE	2047	TGCCAATG	2108	CATTGGCA
Exon 55	ESE	2048	GTCCTACA	2109	TGTAGGAC
Exon 55	ESE	2049	CTACAGG	2110	CCTGTAG
Exon 55	ESE	2050	TACAGGA	2111	TCCTGTA
Exon 55	ESE	2051	GGATGCTA	2112	TAGCATCC
Exon 55	ESE	2052	CTACCCG	2113	CGGGTAG
Exon 55	ESE	2053	TACCCGTA	2114	TACGGGTA
Exon 55	ESE	2054	GGCTCCTA	2115	TAGGAGCC
Exon 55	ESE	2055	CTAGAAG	2116	CTTCTAG
Exon 55	ESE	2056	AGACTCC	2117	GGAGTCT
Exon 55	ESE	2057	GACTCCAA	2118	TTGGAGTC
Exon 55	ESE	2058	CTCCAAG	2119	CTTGGAG
Exon 55	ESE	2059	CCAAGGG	2120	CCCTTGG
Exon 55	ESE	2060	CTGATGA	2121	TCATCAG
Exon 55	ESE	2061	ACAATGG	2122	CCATTGT
Across exon 55/intron 55 junction	Splice Donor	2062	AAGTAAG	2123	CTTACTT
Across intron 55/exon 56 junction	Splice Acceptor	2063	TCCTGTAGG	2124	CCTACAGGA
Exon 56	ESE	2064	GACCTCCA	2125	TGGAGGTC
Exon 56	ESE	2058	CTCCAAG	2119	CTTGGAG
Exon 56	ESE	2065	CCAAGGT	2126	ACCTTGG
Exon 56	ESE	2066	TCACACA	2127	TGTGTGA
Exon 56	ESE	2067	CACACAG	2128	CTGTGTG
Exon 56	ESE	2068	ACACAGA	2129	TCTGTGT
Exon 56	ESE	2069	CACAGA	2130	TCTGTG
Exon 56	ESE	2070	CAGATGT	2131	ACATCTG
Exon 56	ESE	2071	TCACAAC	2132	GTTGTGA
Exon 56	ESE	2072	CAGCCAA	2133	TTGGCTG
Exon 56	ESE	2073	AAATCCTG	2134	CAGGATTT
Exon 56	ESE	2074	CTGAGAT	2135	ATCTCAG
Exon 56	ESE	2075	GATCCCTG	2136	CAGGGATC
Exon 56	ESE	2076	TCCCTGG	2137	CCAGGGA
Exon 56	ESE	2038	CCCTGGA	2099	TCCAGGG
Exon 56	ESE	2077	GGTTCCGA	2138	TCGGAACC
Exon 56	ESE	2078	CCGATGA	2139	TCATCGG
Exon 56	ESE	2079	TTACAAA	2140	TTTGTAA
Exon 56	ESE	2080	AAGACGT	2141	ACGTCTT

† *Each thymine base (T) in any one of the sequences provided in Table 9 may independently and optionally be replaced with a uracil base (U). Motif sequences and antisense sequences listed in Table 9 contain T's, but binding of a motif sequence in RNA and/or DNA is contemplated.*

[000247] In some embodiments, any one of the oligonucleotides useful for targeting DMD (*e.g.*, for exon skipping) is a phosphorodiamidate morpholino oligomer (PMO).

[000248] In some embodiments, the oligonucleotide may have region of complementarity to a mutant DMD allele, for example, a DMD allele with at least one mutation in any of exons 1-79 of DMD in humans that leads to a frameshift and improper RNA splicing/processing.

[000249] In some embodiments, any one of the oligonucleotides can be in salt form, e.g., as sodium, potassium, or magnesium salts.

[000250] In some embodiments, the 5' or 3' nucleoside (e.g., terminal nucleoside) of any one of the oligonucleotides described herein is conjugated to an amine group, optionally via a spacer. In some embodiments, the spacer comprises an aliphatic moiety. In some embodiments, the spacer comprises a polyethylene glycol moiety. In some embodiments, a phosphodiester linkage is present between the spacer and the 5' or 3' nucleoside of the oligonucleotide. In some embodiments, the 5' or 3' nucleoside (e.g., terminal nucleoside) of any of the oligonucleotides described herein is conjugated to a spacer that is a substituted or unsubstituted aliphatic, substituted or unsubstituted heteroaliphatic, substituted or unsubstituted carbocyclylene, substituted or unsubstituted heterocyclylene, substituted or unsubstituted arylene, substituted or unsubstituted heteroarylene, -O-, -N(R^A)-, -S-, -C(=O)-, -C(=O)O-, -C(=O)NR^A-, -NR^AC(=O)-, -NR^AC(=O)R^A-, -C(=O)R^A-, -NR^AC(=O)O-, -NR^AC(=O)N(R^A)-, -OC(=O)-, -OC(=O)O-, -OC(=O)N(R^A)-, -$S(O)_2$NR^A-, -N$R^A$$S(O)_2$-, or a combination thereof; each R^A is independently hydrogen or substituted or unsubstituted alkyl. In certain embodiments, the spacer is a substituted or unsubstituted alkylene, substituted or unsubstituted heterocyclylene, substituted or unsubstituted heteroarylene, -O-, -N(R^A)-, or -C(=O)N$(R^A)_2$, or a combination thereof.

[000251] In some embodiments, the 5' or 3' nucleoside of any one of the oligonucleotides described herein is conjugated to a compound of the formula -NH_2-$(CH_2)_n$-, wherein n is an integer from 1 to 12. In some embodiments, n is 6, 7, 8, 9, 10, 11, or 12. In some embodiments, a phosphodiester linkage is present between the compound of the formula NH_2-$(CH_2)_n$- and the 5' or 3' nucleoside of the oligonucleotide. In some embodiments, a compound of the formula NH_2-$(CH_2)_6$- is conjugated to the oligonucleotide via a reaction between 6-amino-1-hexanol (NH_2-$(CH_2)_6$-OH) and the 5' phosphate of the oligonucleotide.

[000252] In some embodiments, the oligonucleotide is conjugated to a targeting agent, e.g., a muscle targeting agent such as an anti-TfR1 antibody, e.g., via the amine group.

a. Oligonucleotide Size/Sequence

[000253] Oligonucleotides may be of a variety of different lengths, e.g., depending on the format. In some embodiments, an oligonucleotide is 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 75, or more nucleotides in length. In some embodiments, the oligonucleotide is 8 to 50 nucleotides in length, 8 to 40 nucleotides in length, 8 to 30 nucleotides in length, 10 to 15 nucleotides in length, 10 to 20 nucleotides in length, 15 to 25 nucleotides in length, 21 to 23 nucleotides in lengths, 20 to 25 nucleotides in length, etc.

[000254] In some embodiments, a nucleic acid sequence of an oligonucleotide for purposes of the present disclosure is "complementary" to a target nucleic acid when it is specifically hybridizable to the target nucleic acid. In some embodiments, an oligonucleotide hybridizing to

a target nucleic acid (e.g., an mRNA or pre-mRNA molecule) results in modulation of activity or expression of the target (e.g., decreased mRNA translation, altered pre-mRNA splicing, exon skipping, target mRNA degradation, etc.). In some embodiments, a nucleic acid sequence of an oligonucleotide has a sufficient degree of complementarity to its target nucleic acid such that it does not hybridize non-target sequences under conditions in which avoidance of non-specific binding is desired, *e.g.*, under physiological conditions. Thus, in some embodiments, an oligonucleotide may be at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% complementary to the consecutive nucleotides of a target nucleic acid. In some embodiments a complementary nucleotide sequence need not be 100% complementary to that of its target to be specifically hybridizable or specific for a target nucleic acid. In certain embodiments, oligonucleotides comprise one or more mismatched nucleobases relative to the target nucleic acid. In certain embodiments, activity relating to the target is reduced by such mismatch, but activity relating to a non-target is reduced by a greater amount (*i.e.*, selectivity for the target nucleic acid is increased and off-target effects are decreased).

[000255] In some embodiments, an oligonucleotide comprises region of complementarity to a target nucleic acid that is in the range of 8 to 15, 8 to 30, 8 to 40, or 10 to 50, or 5 to 50, 15 to 20, 20 to 25, or 5 to 40 nucleotides in length. In some embodiments, a region of complementarity of an oligonucleotide to a target nucleic acid is 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 nucleotides in length. In some embodiments, the region of complementarity is complementary with at least 8 consecutive nucleotides of a target nucleic acid. In some embodiments, an oligonucleotide may contain 1, 2 or 3 base mismatches compared to the portion of the consecutive nucleotides of target nucleic acid. In some embodiments the oligonucleotide may have up to 3 mismatches over 15 bases, or up to 2 mismatches over 10 bases.

[000256] In some embodiments, the oligonucleotide is complementary (e.g., at least 85% at least 90%, at least 95%, or 100%) to a target sequence of the any one of the oligonucleotides described herein (e.g., the oligonucleotides listed in Table 8). In some embodiments, the oligonucleotide is complementary (e.g., at least 85% at least 90%, at least 95%, or 100%) to a target sequence of the any one of the oligonucleotides provided by SEQ ID NO: 780-2019. In some embodiments, such target sequence is 100% complementary to an oligonucleotide listed in Table 8. In some embodiments, such target sequence is 100% complementary to an oligonucleotide provided by SEQ ID NO: 780-2019. In some embodiments, the oligonucleotide is complementary (e.g., at least 85% at least 90%, at least 95%, or 100%) to a target sequence

provided herein (e.g., a target sequence listed in Table 8). In some embodiments, the oligonucleotide is complementary (e.g., at least 85% at least 90%, at least 95%, or 100%) to any one of SEQ ID NO: 160-779.

[000257] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) comprises a region of complementarity to a target sequence of a DMD RNA (*e.g.*, a target sequence provided by any one of SEQ ID NOs: 160-779). In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) comprises a region of complementarity to at least 8 (*e.g.*, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or more) consecutive nucleosides of a target sequence of a DMD RNA (*e.g.*, a target sequence provided by any one of SEQ ID NOs: 160-779). In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) is complementary to any one of SEQ ID NOs: 160-779.

[000258] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) comprises a sequence comprising at least 8 (e.g., 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or more) consecutive nucleobases of a DMD-targeting sequence provided herein (e.g., an antisense sequence listed in Table 8). In some embodiments, the oligonucleotide comprises a sequence comprising at least 8 (e.g., 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or more) consecutive nucleobases of any one of SEQ ID NOs: 780-2019. In some embodiments, the oligonucleotide comprises the sequence of any one of SEQ ID NOs: 780-2019.

[000259] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) comprises a region of complementarity to a target sequence of a DMD RNA (*e.g.*, a target sequence provided by any one of SEQ ID NOs: 160, 162-166, 168, 169, 173, 178-180, 243-251, 253, 255, 256, 262-266, 268, 270-272, 274, 282-284, 289-291, 294, 295, 319, 343, 347, 351, 356-358, 364, 366, 367, 398, 401, 453-455, 462, 463, 526, 573, 748, and 755). In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) comprises a region of complementarity to at least 8 (*e.g.*, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or more) consecutive nucleosides of a target sequence of a DMD RNA (*e.g.*, a target sequence provided by any one of SEQ ID NOs: 160, 162-166, 168, 169, 173, 178-180, 243-251, 253, 255, 256, 262-266, 268, 270-272, 274, 282-284, 289-291, 294, 295, 319, 343, 347, 351, 356-358, 364, 366, 367, 398, 401, 453-455, 462, 463, 526, 573, 748, and 755). In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) is complementary to any one of SEQ ID NOs: 160, 162-166, 168, 169, 173, 178-180, 243-251, 253, 255, 256, 262-266, 268, 270-272, 274, 282-284, 289-291, 294, 295, 319, 343, 347, 351, 356-358, 364, 366, 367, 398, 401, 453-455, 462, 463, 526, 573, 748, and 755.

[000260] In some embodiments, an oligonucleotide useful for targeting DMD (*e.g.*, for exon skipping) comprises a sequence comprising at least 8 (e.g., 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or more) contiguous nucleobases of a DMD-targeting sequence provided herein (e.g., a sequence of any one of SEQ ID NOs: 1400, 1402-1406, 1408, 1409, 1413, 1418-1420, 1483-1491, 1493, 1495, 1496, 1502-1506, 1508, 1510-1512, 1514, 1522-1524, 1529-1531, 1534, 1535, 1559, 1583, 1587, 1591, 1596, 1597, 1598, 1604, 1606, 1607, 1638, 1641, 1693-1695, 1702, 1703, 1766, 1813, 1988, and 1995). In some embodiments, the oligonucleotide comprises at least 8 (*e.g.*, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or more) consecutive nucleosides of a DMD-targeting sequence provided herein (*e.g.*, a sequence of any one of SEQ ID NOs: 1400, 1402-1406, 1408, 1409, 1413, 1418-1420, 1483-1491, 1493, 1495, 1496, 1502-1506, 1508, 1510-1512, 1514, 1522-1524, 1529-1531, 1534, 1535, 1559, 1583, 1587, 1591, 1596, 1597, 1598, 1604, 1606, 1607, 1638, 1641, 1693-1695, 1702, 1703, 1766, 1813, 1988, and 1995). In some embodiments, the oligonucleotide comprises the sequence of any one of SEQ ID NOs: 1400, 1402-1406, 1408, 1409, 1413, 1418-1420, 1483-1491, 1493, 1495, 1496, 1502-1506, 1508, 1510-1512, 1514, 1522-1524, 1529-1531, 1534, 1535, 1559, 1583, 1587, 1591, 1596, 1597, 1598, 1604, 1606, 1607, 1638, 1641, 1693-1695, 1702, 1703, 1766, 1813, 1988, and 1995.

[000261] In some embodiments, it should be appreciated that methylation of the nucleobase uracil at the C5 position forms thymine. Thus, in some embodiments, a nucleotide or nucleoside having a C5 methylated uracil (or 5-methyl-uracil) may be equivalently identified as a thymine nucleotide or nucleoside.

[000262] In some embodiments, any one or more of the thymine bases (T's) in any one of the oligonucleotides provided herein (e.g., the oligonucleotides listed in Table 8) may independently and optionally be uracil bases (U's), and/or any one or more of the U's in the oligonucleotides provided herein may independently and optionally be T's. In some embodiments, any one or more of the thymine bases (T's) in any one of the oligonucleotides provided by SEQ ID NOs: 1400-2019 or in an oligonucleotide complementary to any one of SEQ ID NOs: 160-779 may optionally be uracil bases (U's), and/or any one or more of the U's in the oligonucleotides may optionally be T's. In some embodiments, any one or more of the uracil bases (U's) in any one of the oligonucleotides provided by SEQ ID NOs: 780-1399 or in an oligonucleotide complementary to any one of SEQ ID NOs: 160-779 may optionally be thymine bases (T's), and/or any one or more of the T's in the oligonucleotides may optionally be U's.

b. Oligonucleotide Modifications:

[000263] The oligonucleotides described herein may be modified, e.g., comprise a modified sugar moiety, a modified internucleoside linkage, a modified nucleotide or nucleoside and/or (e.g., and) combinations thereof. In addition, in some embodiments, oligonucleotides may exhibit one or more of the following properties: do not mediate alternative splicing; are not immune stimulatory; are nuclease resistant; have improved cell uptake compared to unmodified oligonucleotides; are not toxic to cells or mammals; have improved endosomal exit internally in a cell; minimizes TLR stimulation; or avoid pattern recognition receptors. Any of the modified chemistries or formats of oligonucleotides described herein can be combined with each other. For example, one, two, three, four, five, or more different types of modifications can be included within the same oligonucleotide.

[000264] In some embodiments, certain nucleotide or nucleoside modifications may be used that make an oligonucleotide into which they are incorporated more resistant to nuclease digestion than the native oligodeoxynucleotide or oligoribonucleotide molecules; these modified oligonucleotides survive intact for a longer time than unmodified oligonucleotides. Specific examples of modified oligonucleotides include those comprising modified backbones, for example, modified internucleoside linkages such as phosphorothioates, phosphotriesters, methyl phosphonates, short chain alkyl or cycloalkyl intersugar linkages or short chain heteroatomic or heterocyclic intersugar linkages. Accordingly, oligonucleotides of the disclosure can be stabilized against nucleolytic degradation such as by the incorporation of a modification, e.g., a nucleotide or nucleoside modification.

[000265] In some embodiments, an oligonucleotide may be of up to 50 or up to 100 nucleotides in length in which 2 to 10, 2 to 15, 2 to 16, 2 to 17, 2 to 18, 2 to 19, 2 to 20, 2 to 25, 2 to 30, 2 to 40, 2 to 45, or more nucleotides or nucleosides of the oligonucleotide are modified nucleotides/nucleosides. The oligonucleotide may be of 8 to 30 nucleotides in length in which 2 to 10, 2 to 15, 2 to 16, 2 to 17, 2 to 18, 2 to 19, 2 to 20, 2 to 25, 2 to 30 nucleotides or nucleosides of the oligonucleotide are modified nucleotides/nucleosides. The oligonucleotide may be of 8 to 15 nucleotides in length in which 2 to 4, 2 to 5, 2 to 6, 2 to 7, 2 to 8, 2 to 9, 2 to 10, 2 to 11, 2 to 12, 2 to 13, 2 to 14 nucleotides or nucleosides of the oligonucleotide are modified nucleotides/nucleosides. Optionally, the oligonucleotides may have every nucleotide or nucleoside except 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides/nucleosides modified. Oligonucleotide modifications are described further herein.

c. Modified Nucleosides

[000266] In some embodiments, the oligonucleotide described herein comprises at least one nucleoside modified at the 2' position of the sugar. In some embodiments, an

oligonucleotide comprises at least one 2'-modified nucleoside. In some embodiments, all of the nucleosides in the oligonucleotide are 2'-modified nucleosides.

[000267] In some embodiments, the oligonucleotide described herein comprises one or more non-bicyclic 2'-modified nucleosides, e.g., 2'-deoxy, 2'-fluoro (2'-F), 2'-O-methyl (2'-O-Me), 2'-O-methoxyethyl (2'-MOE), 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 nucleoside.

[000268] In some embodiments, the oligonucleotide described herein comprises one or more 2'-4' bicyclic nucleosides in which the ribose ring comprises a bridge moiety connecting two atoms in the ring, *e.g.*, connecting the 2'-O atom to the 4'-C atom via a methylene (LNA) bridge, an ethylene (ENA) bridge, or a (S)-constrained ethyl (cEt) bridge. Examples of LNAs are described in International Patent Application Publication WO/2008/043753, published on April 17, 2008, and entitled "*RNA Antagonist Compounds For The Modulation Of PCSK9*", the contents of which are incorporated herein by reference in its entirety. Examples of ENAs are provided in International Patent Publication No. WO 2005/042777, published on May 12, 2005, and entitled "*APP/ENA Antisense*"; Morita et al., Nucleic Acid Res., Suppl 1:241-242, 2001; Surono et al., Hum. Gene Ther., 15:749-757, 2004; Koizumi, Curr. Opin. Mol. Ther., 8:144-149, 2006 and Horie et al., Nucleic Acids Symp. Ser (Oxf), 49:171-172, 2005; the disclosures of which are incorporated herein by reference in their entireties. Examples of cEt are provided in US Patents 7,101,993; 7,399,845 and 7,569,686, each of which is herein incorporated by reference in its entirety.

[000269] In some embodiments, the oligonucleotide comprises a modified nucleoside disclosed in one of the following United States Patent or Patent Application Publications: US Patent 7,399,845, issued on July 15, 2008, and entitled "6-*Modified Bicyclic Nucleic Acid Analogs*"; US Patent 7,741,457, issued on June 22, 2010, and entitled "*6-Modified Bicyclic Nucleic Acid Analogs*"; US Patent 8,022,193, issued on September 20, 2011, and entitled "*6-Modified Bicyclic Nucleic Acid Analogs*"; US Patent 7,569,686, issued on August 4, 2009, and entitled "*Compounds And Methods For Synthesis Of Bicyclic Nucleic Acid Analogs*"; US Patent 7,335,765, issued on February 26, 2008, and entitled "*Novel Nucleoside And Oligonucleotide Analogues*"; US Patent 7,314,923, issued on January 1, 2008, and entitled "*Novel Nucleoside And Oligonucleotide Analogues*"; US Patent 7,816,333, issued on October 19, 2010, and entitled "*Oligonucleotide Analogues And Methods Utilizing The Same*" and US Publication Number 2011/0009471 now US Patent 8,957,201, issued on February 17, 2015, and entitled "*Oligonucleotide Analogues And Methods Utilizing The Same*", the entire contents of each of which are incorporated herein by reference for all purposes.

[000270] In some embodiments, the oligonucleotide comprises at least one modified nucleoside that results in an increase in Tm of the oligonucleotide in a range of 1°C, 2 °C, 3°C, 4 °C, or 5°C compared with an oligonucleotide that does not have the at least one modified nucleoside. The oligonucleotide may have a plurality of modified nucleosides that result in a total increase in Tm of the oligonucleotide in a range of 2 °C, 3 °C, 4 °C, 5 °C, 6 °C, 7 °C, 8 °C, 9 °C, 10 °C, 15 °C, 20 °C, 25 °C, 30 °C, 35 °C, 40 °C, 45 °C or more compared with an oligonucleotide that does not have the modified nucleoside.

[000271] The oligonucleotide may comprise a mix of nucleosides of different kinds. For example, an oligonucleotide may comprise a mix of 2'-deoxyribonucleosides or ribonucleosides and 2'-fluoro modified nucleosides. An oligonucleotide may comprise a mix of deoxyribonucleosides or ribonucleosides and 2'-O-Me modified nucleosides. An oligonucleotide may comprise a mix of 2'-fluoro modified nucleosides and 2'-O-Me modified nucleosides. An oligonucleotide may comprise a mix of 2'-4' bicyclic nucleosides and 2'-MOE, 2'-fluoro, or 2'-O-Me modified nucleosides. An oligonucleotide may comprise a mix of non-bicyclic 2'-modified nucleosides (e.g., 2'-MOE, 2'-fluoro, or 2'-O-Me) and 2'-4' bicyclic nucleosides (e.g., LNA, ENA, cEt).

[000272] The oligonucleotide may comprise alternating nucleosides of different kinds. For example, an oligonucleotide may comprise alternating 2'-deoxyribonucleosides or ribonucleosides and 2'-fluoro modified nucleosides. An oligonucleotide may comprise alternating deoxyribonucleosides or ribonucleosides and 2'-O-Me modified nucleosides. An oligonucleotide may comprise alternating 2'-fluoro modified nucleosides and 2'-O-Me modified nucleosides. An oligonucleotide may comprise alternating 2'-4' bicyclic nucleosides and 2'-MOE, 2'-fluoro, or 2'-O-Me modified nucleosides. An oligonucleotide may comprise alternating non-bicyclic 2'-modified nucleosides (e.g., 2'-MOE, 2'-fluoro, or 2'-O-Me) and 2'-4' bicyclic nucleosides (e.g., LNA, ENA, cEt).

[000273] In some embodiments, an oligonucleotide described herein comprises a 5′-vinylphosphonate modification, one or more abasic residues, and/or one or more inverted abasic residues.

d. Internucleoside Linkages / Backbones

[000274] In some embodiments, oligonucleotide may contain a phosphorothioate or other modified internucleoside linkage. In some embodiments, the oligonucleotide comprises phosphorothioate internucleoside linkages. In some embodiments, the oligonucleotide comprises phosphorothioate internucleoside linkages between at least two nucleosides. In some embodiments, the oligonucleotide comprises phosphorothioate internucleoside linkages between all nucleosides. For example, in some embodiments, oligonucleotides comprise modified

internucleoside linkages at the first, second, and/or (e.g., and) third internucleoside linkage at the 5' or 3' end of the nucleotide sequence.

[000275] Phosphorus-containing linkages that may be used include, but are not limited to, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl phosphonates comprising 3'alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates comprising 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein the adjacent pairs of nucleoside units are linked 3'-5' to 5'-3' or 2'-5' to 5'-2'; see US patent nos. 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5, 177,196; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455, 233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,306; 5,550,111; 5,563, 253; 5,571,799; 5,587,361; and 5,625,050.

[000276] In some embodiments, oligonucleotides may have heteroatom backbones, such as methylene(methylimino) or MMI backbones; amide backbones (see De Mesmaeker et al. Ace. Chem. Res. 1995, 28:366-374); morpholino backbones (see Summerton and Weller, U.S. Pat. No. 5,034,506); or peptide nucleic acid (PNA) backbones (wherein the phosphodiester backbone of the oligonucleotide is replaced with a polyamide backbone, the nucleotides being bound directly or indirectly to the aza nitrogen atoms of the polyamide backbone, see Nielsen et al., Science 1991, 254, 1497).

e. Stereospecific Oligonucleotides

[000277] In some embodiments, internucleotidic phosphorus atoms of oligonucleotides are chiral, and the properties of the oligonucleotides by adjusted based on the configuration of the chiral phosphorus atoms. In some embodiments, appropriate methods may be used to synthesize P-chiral oligonucleotide analogs in a stereocontrolled manner (e.g., as described in Oka N, Wada T, Stereocontrolled synthesis of oligonucleotide analogs containing chiral internucleotidic phosphorus atoms. Chem Soc Rev. 2011 Dec;40(12):5829-43.) In some embodiments, phosphorothioate containing oligonucleotides comprise nucleoside units that are joined together by either substantially all Sp or substantially all Rp phosphorothioate intersugar linkages are provided. In some embodiments, such phosphorothioate oligonucleotides having substantially chirally pure intersugar linkages are prepared by enzymatic or chemical synthesis, as described, for example, in US Patent 5,587,261, issued on December 12, 1996, the contents of which are incorporated herein by reference in their entirety. In some embodiments, chirally controlled oligonucleotides provide selective cleavage patterns of a target nucleic acid. For example, in some embodiments, a chirally controlled oligonucleotide provides single site

cleavage within a complementary sequence of a nucleic acid, as described, for example, in US Patent Application Publication 20170037399 A1, published on February 2, 2017, entitled "CHIRAL DESIGN", the contents of which are incorporated herein by reference in their entirety.

f. Morpholinos

[000278] In some embodiments, the oligonucleotide may be a morpholino-based compounds. Morpholino-based oligomeric compounds are described in Dwaine A. Braasch and David R. Corey, Biochemistry, 2002, 41(14), 4503-4510); Genesis, volume 30, issue 3, 2001; Heasman, J., Dev. Biol., 2002, 243, 209-214; Nasevicius et al., Nat. Genet., 2000, 26, 216-220; Lacerra et al., Proc. Natl. Acad. Sci., 2000, 97, 9591-9596; and U.S. Pat. No. 5,034,506, issued Jul. 23, 1991. In some embodiments, the morpholino-based oligomeric compound is a phosphorodiamidate morpholino oligomer (PMO) (e.g., as described in Iverson, Curr. Opin. Mol. Ther., 3:235-238, 2001; and Wang et al., J. Gene Med., 12:354-364, 2010; the disclosures of which are incorporated herein by reference in their entireties).

g. Peptide Nucleic Acids (PNAs)

[000279] In some embodiments, both a sugar and an internucleoside linkage (the backbone) of the nucleotide units of an oligonucleotide are replaced with novel groups. In some embodiments, the base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound, an oligonucleotide mimetic that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, for example, an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. Representative publication that report the preparation of PNA compounds include, but are not limited to, US patent nos. 5,539,082; 5,714,331; and 5,719,262, each of which is herein incorporated by reference. Further teaching of PNA compounds can be found in Nielsen *et al.*, Science, 1991, 254, 1497-1500.

h. Mixmers

[000280] In some embodiments, an oligonucleotide described herein may be a mixmer or comprise a mixmer sequence pattern. In general, mixmers are oligonucleotides that comprise both naturally and non-naturally occurring nucleosides or comprise two different types of non-naturally occurring nucleosides typically in an alternating pattern. Mixmers generally have higher binding affinity than unmodified oligonucleotides and may be used to specifically bind a target molecule, *e.g.*, to block a binding site on the target molecule. Generally, mixmers do not recruit an RNase to the target molecule and thus do not promote cleavage of the target molecule.

Such oligonucleotides that are incapable of recruiting RNase H have been described, for example, see WO2007/112754 or WO2007/112753.

[000281] In some embodiments, the mixmer comprises or consists of a repeating pattern of nucleoside analogues and naturally occurring nucleosides, or one type of nucleoside analogue and a second type of nucleoside analogue. However, a mixmer need not comprise a repeating pattern and may instead comprise any arrangement of modified nucleoside s and naturally occurring nucleoside s or any arrangement of one type of modified nucleoside and a second type of modified nucleoside. The repeating pattern, may, for instance be every second or every third nucleoside is a modified nucleoside, such as LNA, and the remaining nucleoside s are naturally occurring nucleosides, such as DNA, or are a 2′ substituted nucleoside analogue such as 2′-MOE or 2′ fluoro analogues, or any other modified nucleoside described herein. It is recognized that the repeating pattern of modified nucleoside, such as LNA units, may be combined with modified nucleoside at fixed positions—*e.g.* at the 5′ or 3′ termini.

[000282] In some embodiments, a mixmer does not comprise a region of more than 5, more than 4, more than 3, or more than 2 consecutive naturally occurring nucleosides, such as DNA nucleosides. In some embodiments, the mixmer comprises at least a region consisting of at least two consecutive modified nucleosides, such as at least two consecutive LNAs. In some embodiments, the mixmer comprises at least a region consisting of at least three consecutive modified nucleoside units, such as at least three consecutive LNAs.

[000283] In some embodiments, the mixmer does not comprise a region of more than 7, more than 6, more than 5, more than 4, more than 3, or more than 2 consecutive nucleoside analogues, such as LNAs. In some embodiments, LNA units may be replaced with other nucleoside analogues, such as those referred to herein.

[000284] Mixmers may be designed to comprise a mixture of affinity enhancing modified nucleosides, such as in non-limiting example LNA nucleosides and 2'-O-Me nucleosides. In some embodiments, a mixmer comprises modified internucleoside linkages (*e.g.*, phosphorothioate internucleoside linkages or other linkages) between at least two, at least three, at least four, at least five or more nucleosides.

[000285] A mixmer may be produced using any suitable method. Representative U.S. patents, U.S. patent publications, and PCT publications that teach the preparation of mixmers include U.S. patent publication Nos. US20060128646, US20090209748, US20090298916, US20110077288, and US20120322851, and U.S. patent No. 7687617.

[000286] In some embodiments, a mixmer comprises one or more morpholino nucleosides. For example, in some embodiments, a mixmer may comprise morpholino

nucleosides mixed (*e.g.*, in an alternating manner) with one or more other nucleosides (*e.g.*, DNA, RNA nucleosides) or modified nucleosides (*e.g.*, LNA, 2'-O-Me nucleosides).

[000287] In some embodiments, mixmers are useful for splice correcting or exon skipping, for example, as reported in Touznik A., et al., *LNA/DNA mixmer-based antisense oligonucleotides correct alternative splicing of the SMN2 gene and restore SMN protein expression in type 1 SMA fibroblasts* Scientific Reports, volume 7, Article number: 3672 (2017), Chen S. et al., *Synthesis of a Morpholino Nucleic Acid (MNA)-Uridine Phosphoramidite, and Exon Skipping Using MNA/2'-O-Methyl Mixmer Antisense Oligonucleotide*, Molecules 2016, 21, 1582, the contents of each which are incorporated herein by reference.

i. Multimers

[000288] In some embodiments, molecular payloads may comprise multimers (e.g., concatemers) of 2 or more oligonucleotides connected by a linker. In this way, in some embodiments, the oligonucleotide loading of a complex can be increased beyond the available linking sites on a targeting agent (e.g., available thiol sites on an antibody) or otherwise tuned to achieve a particular payload loading content. Oligonucleotides in a multimer can be the same or different (e.g., targeting different genes or different sites on the same gene or products thereof).

[000289] In some embodiments, multimers comprise 2 or more oligonucleotides linked together by a cleavable linker. However, in some embodiments, multimers comprise 2 or more oligonucleotides linked together by a non-cleavable linker. In some embodiments, a multimer comprises 2, 3, 4, 5, 6, 7, 8, 9, 10 or more oligonucleotides linked together. In some embodiments, a multimer comprises 2 to 5, 2 to 10 or 4 to 20 oligonucleotides linked together.

[000290] In some embodiments, a multimer comprises 2 or more oligonucleotides linked end-to-end (in a linear arrangement). In some embodiments, a multimer comprises 2 or more oligonucleotides linked end-to-end via an oligonucleotide based linker (e.g., poly-dT linker, an abasic linker). In some embodiments, a multimer comprises a 5' end of one oligonucleotide linked to a 3' end of another oligonucleotide. In some embodiments, a multimer comprises a 3' end of one oligonucleotide linked to a 3' end of another oligonucleotide. In some embodiments, a multimer comprises a 5' end of one oligonucleotide linked to a 5' end of another oligonucleotide. Still, in some embodiments, multimers can comprise a branched structure comprising multiple oligonucleotides linked together by a branching linker.

[000291] Further examples of multimers that may be used in the complexes provided herein are disclosed, for example, in US Patent Application Number 2015/0315588 A1, entitled *Methods of delivering multiple targeting oligonucleotides to a cell using cleavable linkers*, which was published on November 5, 2015; US Patent Application Number 2015/0247141 A1, entitled *Multimeric Oligonucleotide Compounds*, which was published on September 3, 2015,

US Patent Application Number US 2011/0158937 A1, entitled *Immunostimulatory Oligonucleotide Multimers*, which was published on June 30, 2011; and US Patent Number 5,693,773, entitled *Triplex-Forming Antisense Oligonucleotides Having Abasic Linkers Targeting Nucleic Acids Comprising Mixed Sequences Of Purines And Pyrimidines,* which issued on December 2, 1997, the contents of each of which are incorporated herein by reference in their entireties.

C. Linkers

[000292] Complexes described herein generally comprise a linker that covalently links any one of the anti-TfR1 antibodies described herein to a molecular payload. A linker comprises at least one covalent bond. In some embodiments, a linker may be a single bond, e.g., a disulfide bond or disulfide bridge, that covalently links an anti-TfR1 antibody to a molecular payload. However, in some embodiments, a linker may covalently link any one of the anti-TfR1 antibodies described herein to a molecular payload through multiple covalent bonds. In some embodiments, a linker may be a cleavable linker. However, in some embodiments, a linker may be a non-cleavable linker. A linker is typically stable *in vitro* and *in vivo*, and may be stable in certain cellular environments. Additionally, typically a linker does not negatively impact the functional properties of either the anti-TfR1 antibody or the molecular payload. Examples and methods of synthesis of linkers are known in the art (see, e.g. Kline, T. et al. "Methods to Make Homogenous Antibody Drug Conjugates." Pharmaceutical Research, 2015, 32:11, 3480–3493.; Jain, N. et al. "Current ADC Linker Chemistry" Pharm Res. 2015, 32:11, 3526–3540.; McCombs, J.R. and Owen, S.C. "Antibody Drug Conjugates: Design and Selection of Linker, Payload and Conjugation Chemistry" AAPS J. 2015, 17:2, 339–351.).

[000293] A linker typically will contain two different reactive species that allow for attachment to both the anti-TfR1 antibody and a molecular payload. In some embodiments, the two different reactive species may be a nucleophile and/or an electrophile. In some embodiments, a linker contains two different electrophiles or nucleophiles that are specific for two different nucleophiles or electrophiles. In some embodiments, a linker is covalently linked to an anti-TfR1 antibody via conjugation to a lysine residue or a cysteine residue of the anti-TfR1 antibody. In some embodiments, a linker is covalently linked to a cysteine residue of an anti-TfR1 antibody via a maleimide-containing linker, wherein optionally the maleimide-containing linker comprises a maleimidocaproyl or maleimidomethyl cyclohexane-1-carboxylate group. In some embodiments, a linker is covalently linked to a cysteine residue of an anti-TfR1 antibody or thiol functionalized molecular payload via a 3-arylpropionitrile functional group. In some embodiments, a linker is covalently linked to a lysine residue of an anti-TfR1 antibody. In some embodiments, a linker is covalently linked to an anti-TfR1 antibody and/or (e.g., and) a

molecular payload, independently, via an amide bond, a carbamate bond, a hydrazide, a triazole, a thioether, and/or a disulfide bond.

i. Cleavable Linkers

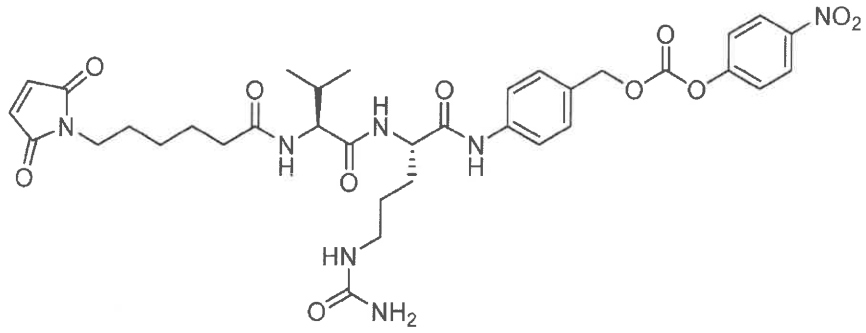
[000294] A cleavable linker may be a protease-sensitive linker, a pH-sensitive linker, or a glutathione-sensitive linker. These linkers are typically cleavable only intracellularly and are preferably stable in extracellular environments, e.g., extracellular to a muscle cell.

[000295] Protease-sensitive linkers are cleavable by protease enzymatic activity. These linkers typically comprise peptide sequences and may be 2-10 amino acids, about 2-5 amino acids, about 5-10 amino acids, about 10 amino acids, about 5 amino acids, about 3 amino acids, or about 2 amino acids in length. In some embodiments, a peptide sequence may comprise naturally-occurring amino acids, e.g. cysteine, alanine, or non-naturally-occurring or modified amino acids. Non-naturally occurring amino acids include β-amino acids, homo-amino acids, proline derivatives, 3-substituted alanine derivatives, linear core amino acids, N-methyl amino acids, and others known in the art. In some embodiments, a protease-sensitive linker comprises a valine-citrulline or alanine-citrulline sequence. In some embodiments, a protease-sensitive linker can be cleaved by a lysosomal protease, e.g. cathepsin B, and/or (e.g., and) an endosomal protease.

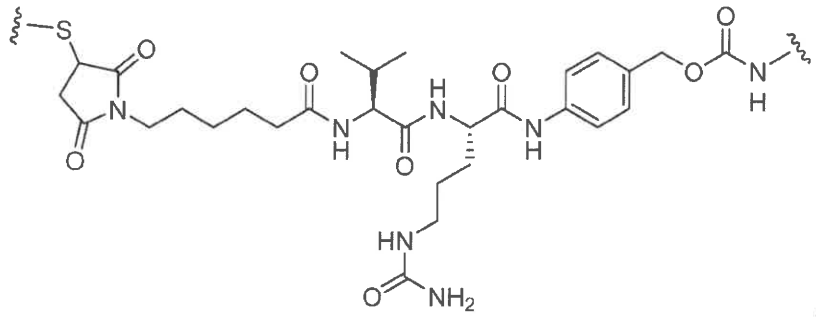
[000296] A pH-sensitive linker is a covalent linkage that readily degrades in high or low pH environments. In some embodiments, a pH-sensitive linker may be cleaved at a pH in a range of 4 to 6. In some embodiments, a pH-sensitive linker comprises a hydrazone or cyclic acetal. In some embodiments, a pH-sensitive linker is cleaved within an endosome or a lysosome.

[000297] In some embodiments, a glutathione-sensitive linker comprises a disulfide moiety. In some embodiments, a glutathione-sensitive linker is cleaved by a disulfide exchange reaction with a glutathione species inside a cell. In some embodiments, the disulfide moiety further comprises at least one amino acid, e.g., a cysteine residue.

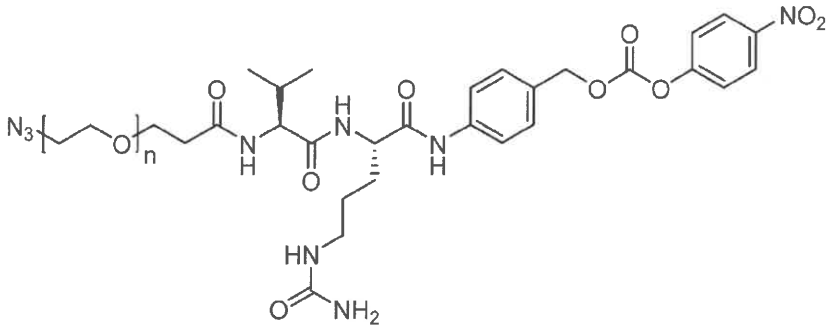
[000298] In some embodiments, a linker comprises a valine-citrulline sequence (e.g., as described in US Patent 6,214,345, incorporated herein by reference). In some embodiments, before conjugation, a linker comprises a structure of:



[000299] In some embodiments, after conjugation, a linker comprises a structure of:



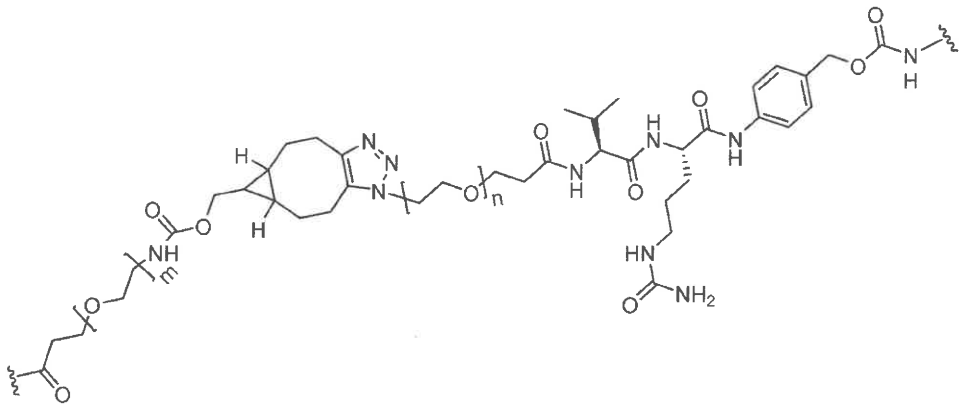
[000300] In some embodiments, before conjugation, a linker comprises a structure of:



(A)

wherein n is any number from 0-10. In some embodiments, n is 3.

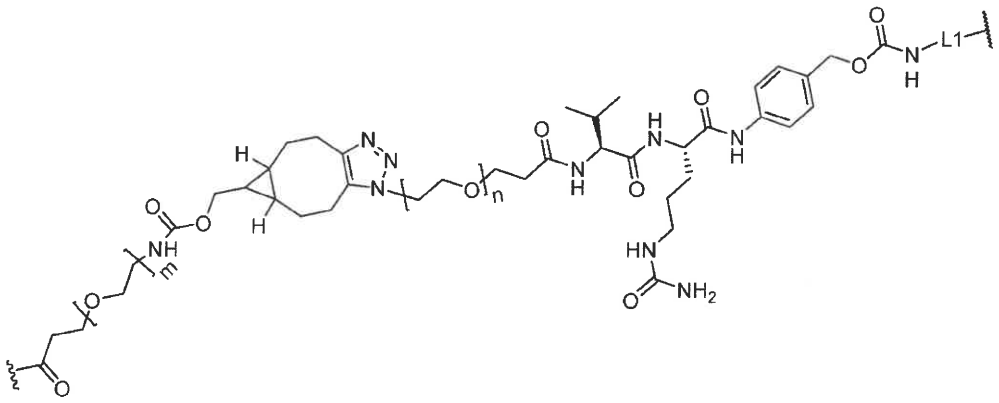
[000301] In some embodiments, a linker comprises a structure of:



(H),

wherein n is any number from 0-10, wherein m is any number from 0-10. In some embodiments, n is 3 and/or (e.g., and) m is 4.

[000302] In some embodiments, a linker comprises a structure of:



(I),

wherein n is any number from 0-10, wherein m is any number from 0-10. In some embodiments, n is 3 and/or (e.g., and) m is 4.

ii. Non-cleavable Linkers

[000303] In some embodiments, non-cleavable linkers may be used. Generally, a non-cleavable linker cannot be readily degraded in a cellular or physiological environment. In some embodiments, a non-cleavable linker comprises an optionally substituted alkyl group, wherein the substitutions may include halogens, hydroxyl groups, oxygen species, and other common substitutions. In some embodiments, a linker may comprise an optionally substituted alkyl, an optionally substituted alkylene, an optionally substituted arylene, a heteroarylene, a peptide sequence comprising at least one non-natural amino acid, a truncated glycan, a sugar or sugars that cannot be enzymatically degraded, an azide, an alkyne-azide, a peptide sequence comprising a LPXT sequence, a thioether, a biotin, a biphenyl, repeating units of polyethylene glycol or equivalent compounds, acid esters, acid amides, sulfamides, and/or an alkoxy-amine linker. In some embodiments, sortase-mediated ligation can be utilized to covalently link an anti-TfR1 antibody comprising a LPXT sequence to a molecular payload comprising a $(G)_n$ sequence (see, e.g. Proft T. Sortase-mediated protein ligation: an emerging biotechnology tool for protein modification and immobilization. Biotechnol Lett. 2010, 32(1):1-10.).

[000304] In some embodiments, a linker may comprise a substituted alkylene, an optionally substituted alkenylene, an optionally substituted alkynylene, an optionally substituted cycloalkylene, an optionally substituted cycloalkenylene, an optionally substituted arylene, an optionally substituted heteroarylene further comprising at least one heteroatom selected from N, O, and S,; an optionally substituted heterocyclylene further comprising at least one heteroatom selected from N, O, and S, an imino, an optionally substituted nitrogen species, an optionally substituted oxygen species O, an optionally substituted sulfur species, or a poly(alkylene oxide), e.g. polyethylene oxide or polypropylene oxide. In some embodiments, a linker may be a non-cleavable N-gamma-maleimidobutyryl-oxysuccinimide ester (GMBS) linker.

iii. Linker conjugation

[000305] In some embodiments, a linker is covalently linked to an anti-TfR1 antibody and/or (e.g., and) molecular payload via a phosphate, thioether, ether, carbon-carbon, carbamate, or amide bond. In some embodiments, a linker is covalently linked to an oligonucleotide through a phosphate or phosphorothioate group, e.g. a terminal phosphate of an oligonucleotide backbone. In some embodiments, a linker is covalently linked to an anti-TfR1 antibody, through a lysine or cysteine residue present on the anti-TfR1 antibody.

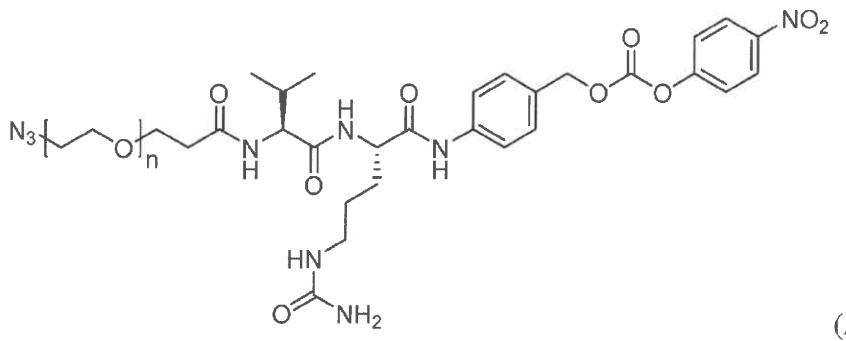
[000306] In some embodiments, a linker, or a portion thereof is covalently linked to an anti-TfR1 antibody and/or (e.g., and) molecular payload by a cycloaddition reaction between an azide and an alkyne to form a triazole, wherein the azide or the alkyne may be located on the anti-TfR1 antibody, molecular payload, or the linker. In some embodiments, an alkyne may be a cyclic alkyne, *e.g.*, a cyclooctyne. In some embodiments, an alkyne may be bicyclononyne (also known as bicyclo[6.1.0]nonyne or BCN) or substituted bicyclononyne. In some embodiments, a cyclooctyne is as described in International Patent Application Publication WO2011136645, published on November 3, 2011, entitled, "*Fused Cyclooctyne Compounds And Their Use In Metal-free Click Reactions*". In some embodiments, an azide may be a sugar or carbohydrate molecule that comprises an azide. In some embodiments, an azide may be 6-azido-6-deoxygalactose or 6-azido-N-acetylgalactosamine. In some embodiments, a sugar or carbohydrate molecule that comprises an azide is as described in International Patent Application Publication WO2016170186, published on October 27, 2016, entitled, "*Process For The Modification Of A Glycoprotein Using A Glycosyltransferase That Is Or Is Derived From A β(1,4)-N-Acetylgalactosaminyltransferase*". In some embodiments, a cycloaddition reaction between an azide and an alkyne to form a triazole, wherein the azide or the alkyne may be located on the anti-TfR1 antibody, molecular payload, or the linker is as described in International Patent Application Publication WO2014065661, published on May 1, 2014, entitled, "*Modified antibody, antibody-conjugate and process for the preparation thereof*"; or International Patent Application Publication WO2016170186, published on October 27, 2016, entitled, "*Process For The Modification Of A Glycoprotein Using A Glycosyltransferase That Is Or Is Derived From A β(1,4)-N-Acetylgalactosaminyltransferase*".

[000307] In some embodiments, a linker comprises a spacer, *e.g.*, a polyethylene glycol spacer or an acyl/carbomoyl sulfamide spacer, *e.g.*, a HydraSpace™ spacer. In some embodiments, a spacer is as described in Verkade, J.M.M. et al., "*A Polar Sulfamide Spacer Significantly Enhances the Manufacturability, Stability, and Therapeutic Index of Antibody-Drug Conjugates*", Antibodies, 2018, 7, 12.

[000308] In some embodiments, a linker is covalently linked to an anti-TfR1 antibody and/or (e.g., and) molecular payload by the Diels-Alder reaction between a dienophile and a diene/hetero-diene, wherein the dienophile or the diene/hetero-diene may be located on the anti-TfR1 antibody, molecular payload, or the linker. In some embodiments a linker is covalently linked to an anti-TfR1 antibody and/or (e.g., and) molecular payload by other pericyclic reactions such as an ene reaction. In some embodiments, a linker is covalently linked to an anti-TfR1 antibody and/or (e.g., and) molecular payload by an amide, thioamide, or sulfonamide bond reaction. In some embodiments, a linker is covalently linked to an anti-TfR1 antibody and/or (e.g., and) molecular payload by a condensation reaction to form an oxime, hydrazone, or semicarbazide group existing between the linker and the anti-TfR1 antibody and/or (e.g., and) molecular payload.

[000309] In some embodiments, a linker is covalently linked to an anti-TfR1 antibody and/or (e.g., and) molecular payload by a conjugate addition reaction between a nucleophile, e.g. an amine or a hydroxyl group, and an electrophile, e.g. a carboxylic acid, carbonate, or an aldehyde. In some embodiments, a nucleophile may exist on a linker and an electrophile may exist on an anti-TfR1 antibody or molecular payload prior to a reaction between a linker and an anti-TfR1 antibody or molecular payload. In some embodiments, an electrophile may exist on a linker and a nucleophile may exist on an anti-TfR1 antibody or molecular payload prior to a reaction between a linker and an anti-TfR1 antibody or molecular payload. In some embodiments, an electrophile may be an azide, pentafluorophenyl, a silicon centers, a carbonyl, a carboxylic acid, an anhydride, an isocyanate, a thioisocyanate, a succinimidyl ester, a sulfosuccinimidyl ester, a maleimide, an alkyl halide, an alkyl pseudohalide, an epoxide, an episulfide, an aziridine, an aryl, an activated phosphorus center, and/or an activated sulfur center. In some embodiments, a nucleophile may be an optionally substituted alkene, an optionally substituted alkyne, an optionally substituted aryl, an optionally substituted heterocyclyl, a hydroxyl group, an amino group, an alkylamino group, an anilido group, and/or a thiol group.

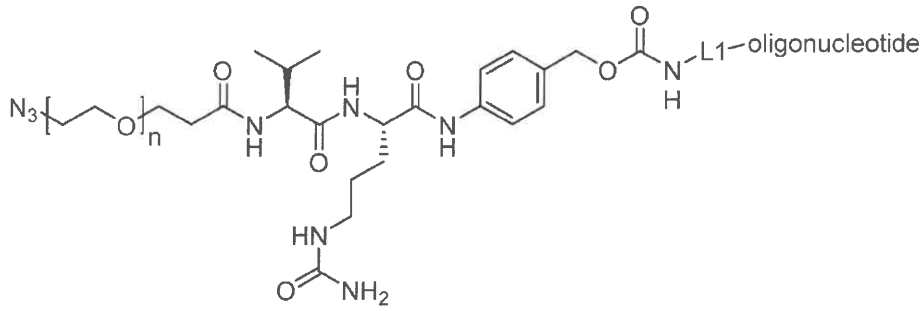
[000310] In some embodiments, a linker comprises a valine-citrulline sequence covalently linked to a reactive chemical moiety (e.g., an azide moiety or a BCN moiety for click chemistry). In some embodiments, a linker comprising a valine-citrulline sequence covalently linked to a reactive chemical moiety (e.g., an azide moiety for click chemistry) comprises a structure of:



(A)

wherein n is any number from 0-10. In some embodiments, n is 3.

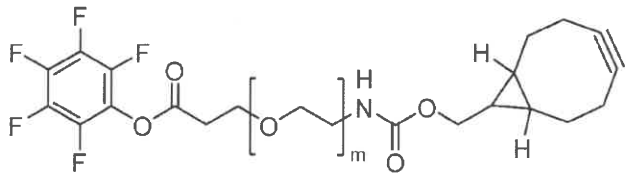
[000311] In some embodiments, a linker comprising the structure of Formula (A) is covalently linked (e.g., optionally via additional chemical moieties) to a molecular payload (e.g., an oligonucleotide). In some embodiments, a linker comprising the structure of Formula (A) is covalently linked to an oligonucleotide, e.g., through a nucleophilic substitution with amine-L1-oligonucleotides forming a carbamate bond, yielding a compound comprising a structure of:



(B)

wherein n is any number from 0-10. In some embodiments, n is 3.

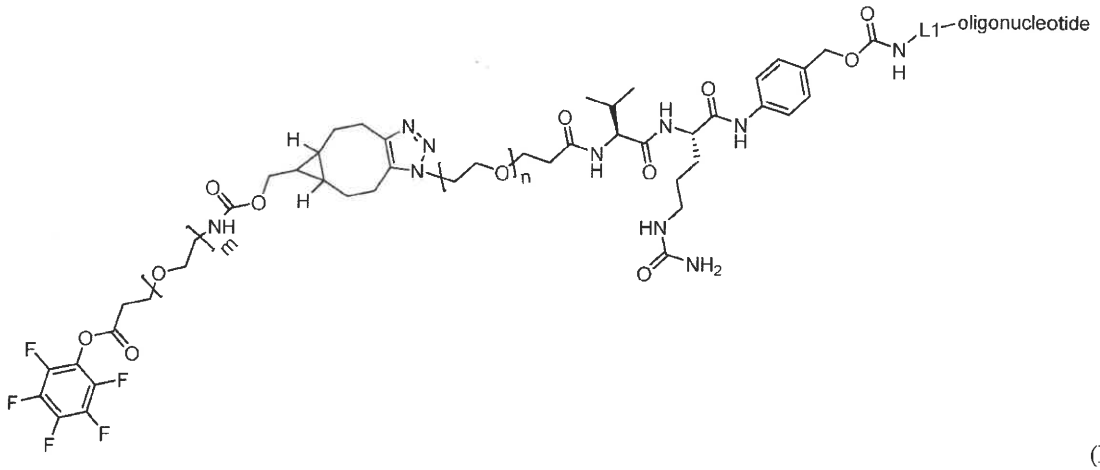
[000312] In some embodiments, the compound of Formula (B) is further covalently linked via a triazole to additional moieties, wherein the triazole is formed by a click reaction between the azide of Formula (A) or Formula (B) and an alkyne provided on a bicyclononyne. In some embodiments, a compound comprising a bicyclononyne comprises a structure of:



(C)

wherein m is any number from 0-10. In some embodiments, m is 4.

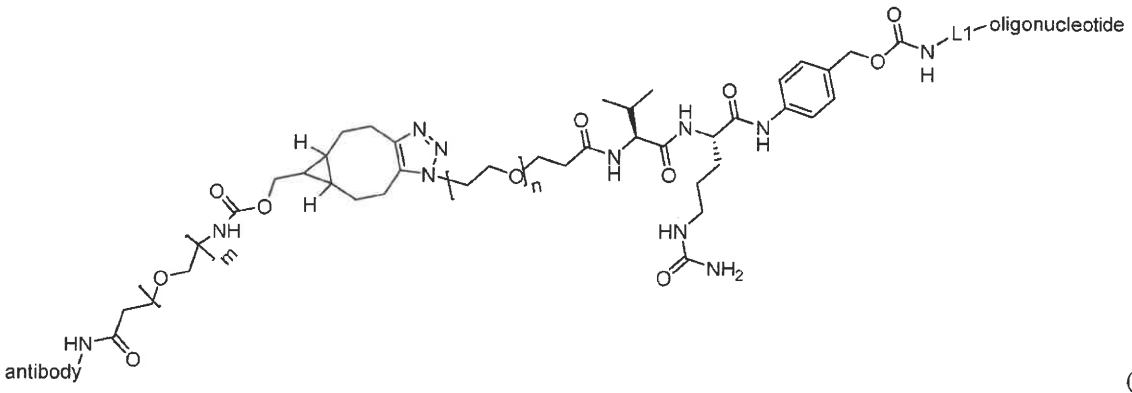
[000313] In some embodiments, the azide of the compound of structure (B) forms a triazole via a click reaction with the alkyne of the compound of structure (C), forming a compound comprising a structure of:



(D),

wherein n is any number from 0-10, and wherein m is any number from 0-10. In some embodiments, n is 3 and m is 4.

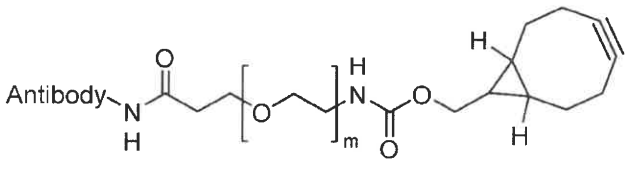
[000314] In some embodiments, the compound of structure (D) is further covalently linked to a lysine of the anti-TfR1 antibody, forming a complex comprising a structure of:



(E),

wherein n is any number from 0-10, wherein m is any number from 0-10. In some embodiments, n is 3 and/or (e.g., and) m is 4. It should be understood that the amide shown adjacent the anti-TfR1 antibody in Formula (E) results from a reaction with an amine of the anti-TfR1 antibody, such as a lysine epsilon amine.

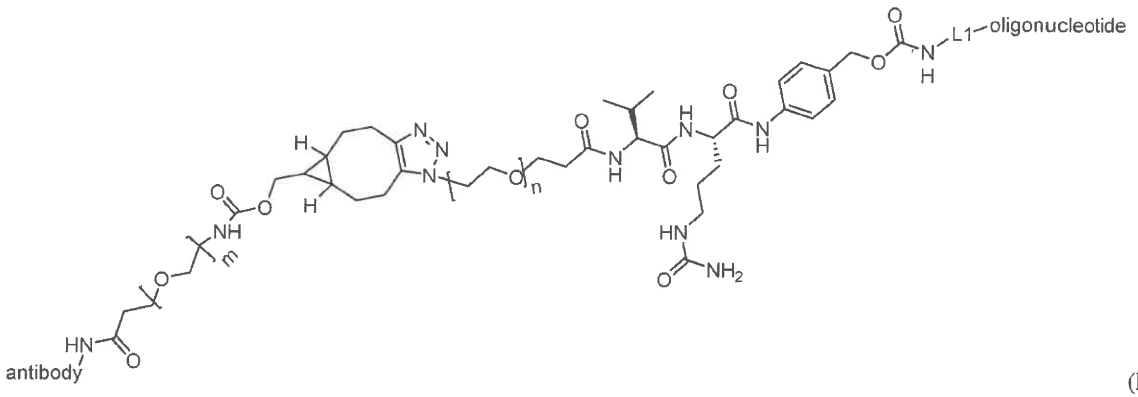
[000315] In some embodiments, the compound of Formula (C) is further covalently linked to a lysine of the anti-TfR1 antibody, forming a compound comprising a structure of:



(F),

wherein m is 0-15 (e.g., 4). It should be understood that the amide shown adjacent the anti-TfR1 antibody in Formula (F) results from a reaction with an amine of the anti-TfR1 antibody, such as a lysine epsilon amine.

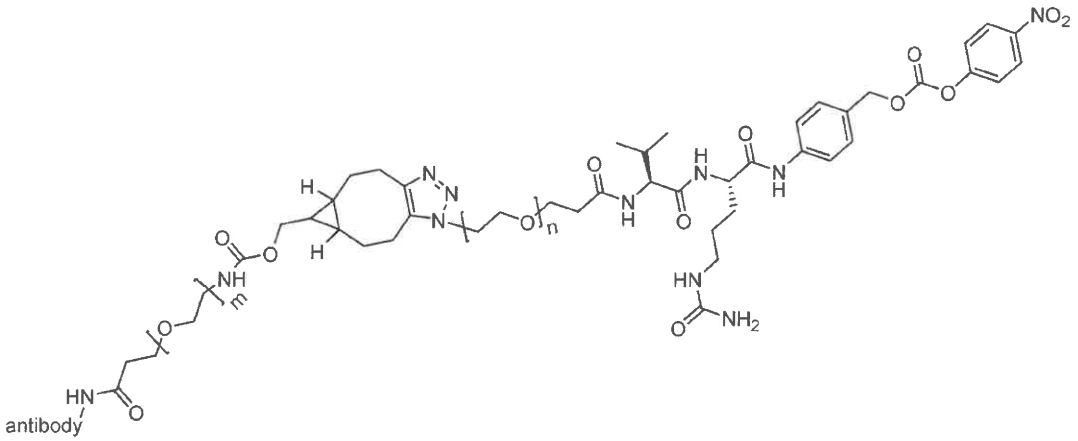
[000316] In some embodiments, the azide of the compound of structure (B) forms a triazole via a click reaction with the alkyne of the compound of structure (F), forming a complex comprising a structure of:



(E),

wherein n is any number from 0-10, wherein m is any number from 0-10. In some embodiments, n is 3 and/or (e.g., and) m is 4. It should be understood that the amide shown adjacent the anti-TfR1 antibody in Formula (E) results from a reaction with an amine of the anti-TfR1 antibody, such as a lysine epsilon amine.

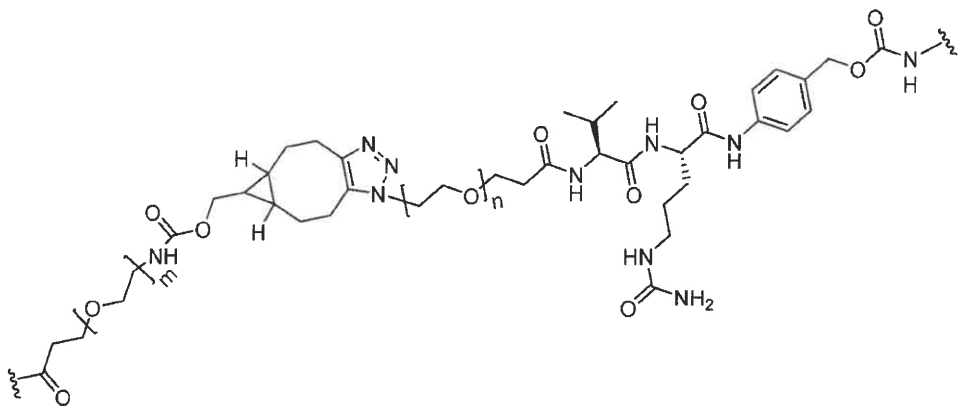
[000317] In some embodiments, the azide of the compound of structure (A) forms a triazole via a click reaction with the alkyne of the compound of structure (F), forming a compound comprising a structure of:



(G),

wherein n is any number from 0-10, wherein m is any number from 0-10. In some embodiments, n is 3 and/or (e.g., and) m is 4. In some embodiments, an oligonucleotide is covalently linked to a compound comprising a structure of formula (G), thereby forming a complex comprising a structure of formula (E). It should be understood that the amide shown adjacent the anti-TfR1 antibody in Formula (G) results from a reaction with an amine of the anti-TfR1 antibody, such as a lysine epsilon amine.

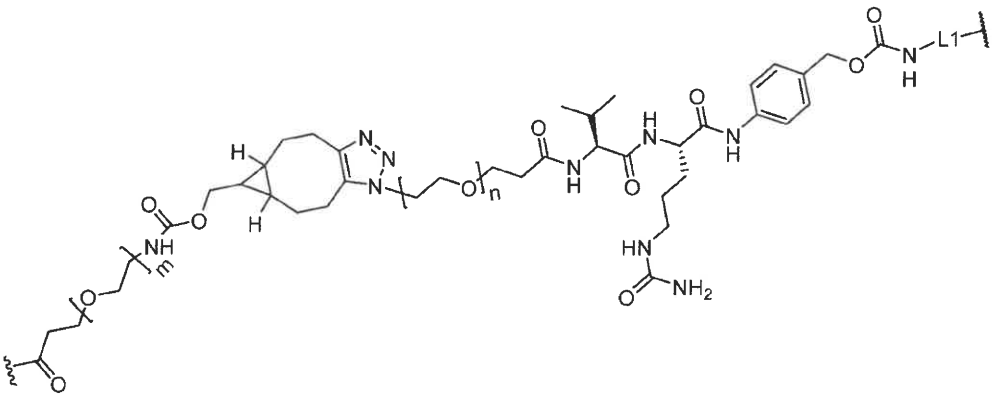
[000318] In some embodiments, in any one of the complexes described herein, the anti-TfR1 antibody is covalently linked via a lysine of the anti-TfR1 antibody to a molecular payload (e.g., an oligonucleotide) via a linker comprising a structure of:



(H),

wherein n is any number from 0-10, wherein m is any number from 0-10. In some embodiments, n is 3 and/or (e.g., and) m is 4.

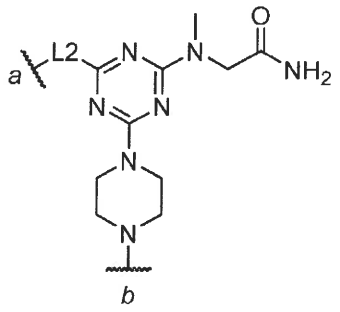
[000319] In some embodiments, in any one of the complexes described herein, the anti-TfR1 antibody is covalently linked via a lysine of the anti-TfR1 antibody to a molecular payload (e.g., an oligonucleotide) via a linker comprising a structure of:

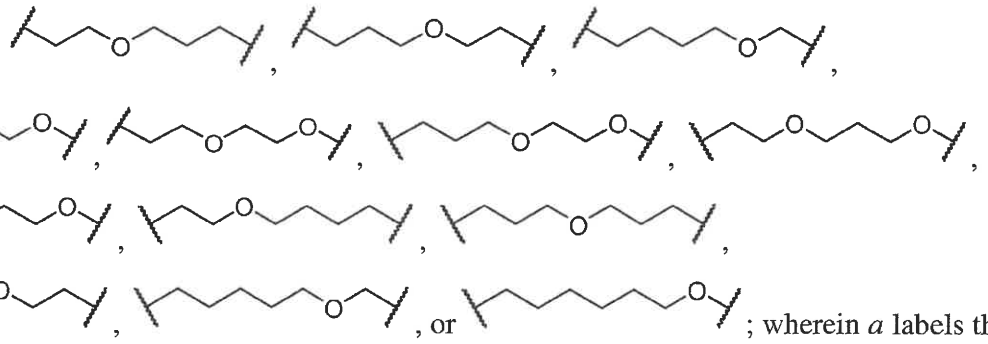


(I),

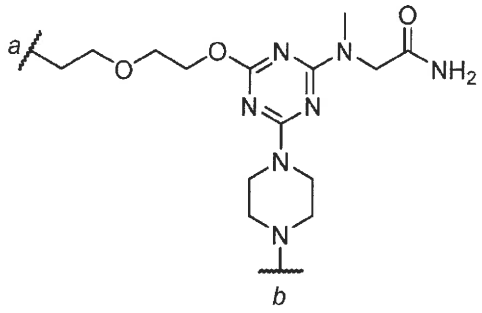
wherein n is any number from 0-10, wherein m is any number from 0-10. In some embodiments, n is 3 and/or (e.g., and) m is 4.

[000320] In some embodiments, in formulae (B), (D), (E), and (I), L1 is a spacer that is a substituted or unsubstituted aliphatic, substituted or unsubstituted heteroaliphatic, substituted or unsubstituted carbocyclylene, substituted or unsubstituted heterocyclylene, substituted or unsubstituted arylene, substituted or unsubstituted heteroarylene, -O-, -N(R^A)-, -S-, -C(=O)-, -C(=O)O-, -C(=O)NR^A-, -NR^AC(=O)-, -NR^AC(=O)R^A-, -C(=O)R^A-, -NR^AC(=O)O-, -NR^AC(=O)N(R^A)-, -OC(=O)-, -OC(=O)O-, -OC(=O)N(R^A)-, -S(O)$_2$NR^A-, -NR^AS(O)$_2$-, or a combination thereof, wherein each R^A is independently hydrogen or substituted or unsubstituted alkyl. In some embodiments, L1 is

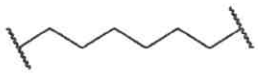


wherein L2 is ; wherein *a* labels the site directly linked to the carbamate moiety of formulae (B), (D), (E), and (I); and *b* labels the site covalently linked (directly or via additional chemical moieties) to the oligonucleotide.

[000321] In some embodiments, L1 is:



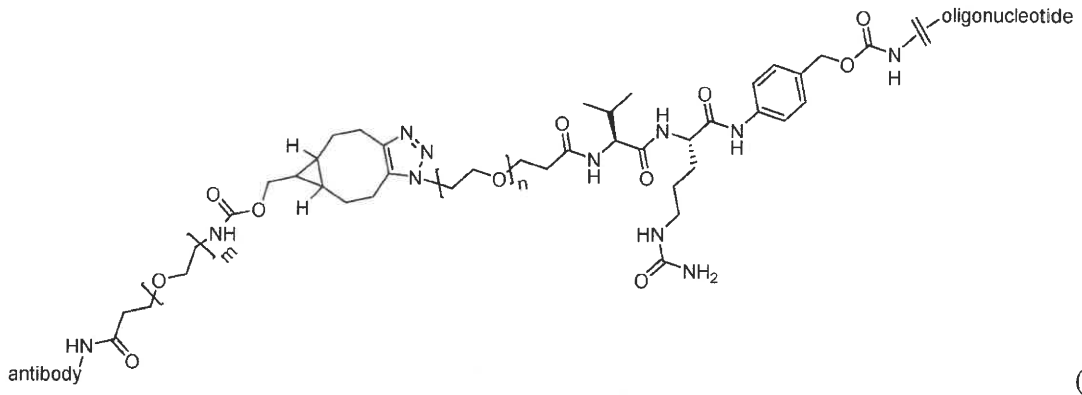
wherein *a* labels the site directly linked to the carbamate moiety of formulae (B), (D), (E), and (I); and *b* labels the site covalently linked (directly or via additional chemical moieties) to the oligonucleotide.

[000322] In some embodiments, L1 is .

[000323] In some embodiments, L1 is linked to a 5' phosphate of the oligonucleotide. In some embodiments, the phosphate is a phosphodiester. In some embodiments, L1 is linked to a 5' phosphorothioate of the oligonucleotide. In some embodiments, L1 is linked to a 5' phosphonoamidate of the oligonucleotide. In some embodiments, L1 is linked via a phosphorodiamidate linkage to the 5' end of the oligonucleotide.

[000324] In some embodiments, L1 is optional (e.g., need not be present).

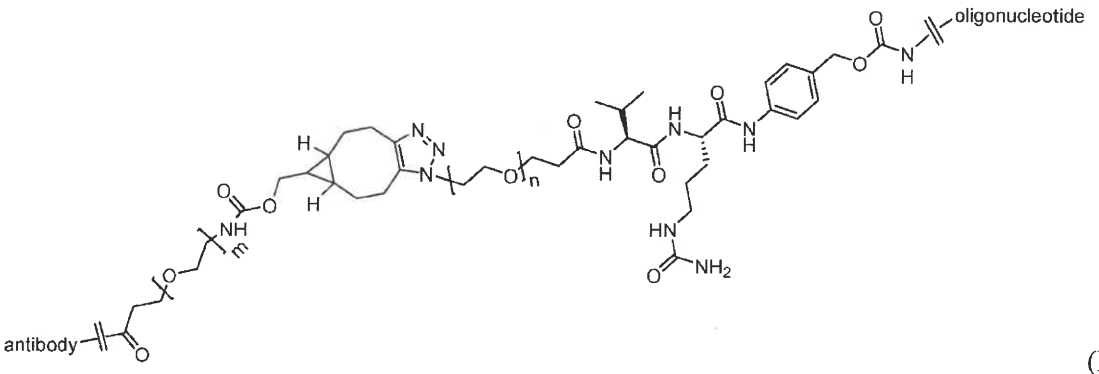
[000325] In some embodiments, any one of the complexes described herein has a structure of:



(J),

wherein n is 0-15 (e.g., 3) and m is 0-15 (e.g., 4). It should be understood that the amide shown adjacent the anti-TfR1 antibody in Formula (J) results from a reaction with an amine of the anti-TfR1 antibody, such as a lysine epsilon amine.

[000326] In some embodiments, any one of the complexes described herein has a structure of:



(K),

wherein n is 0-15 (e.g., 3) and m is 0-15 (e.g., 4).

[000327] In some embodiments, the oligonucleotide is modified to comprise an amine group at the 5' end, the 3' end, or internally (e.g., as an amine functionalized nucleobase), prior to linking to a compound, *e.g.*, a compound of formula (A) or formula (G).

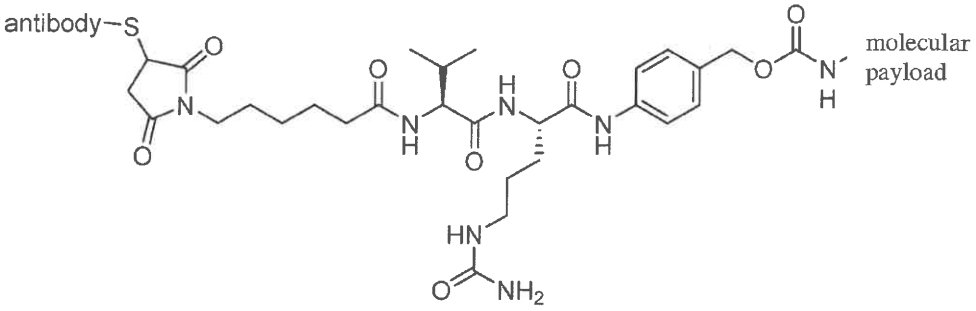
[000328] Although linker conjugation is described in the context of anti-TfR1 antibodies and oligonucleotide molecular payloads, it should be understood that use of such linker conjugation on other muscle-targeting agents, such as other muscle-targeting antibodies, and/or on other molecular payloads is contemplated.

D. Examples of Antibody-Molecular Payload Complexes

[000329] Further provided herein are non-limiting examples of complexes comprising any one the anti-TfR1 antibodies described herein covalently linked to any of the molecular payloads (e.g., an oligonucleotide) described herein. In some embodiments, the anti-TfR1 antibody (e.g., any one of the anti-TfR1 antibodies provided in Tables 2-7) is covalently linked to a molecular payload (e.g., an oligonucleotide such as the oligonucleotides provided in Table 8) via a linker. Any of the linkers described herein may be used. In some embodiments, if the molecular

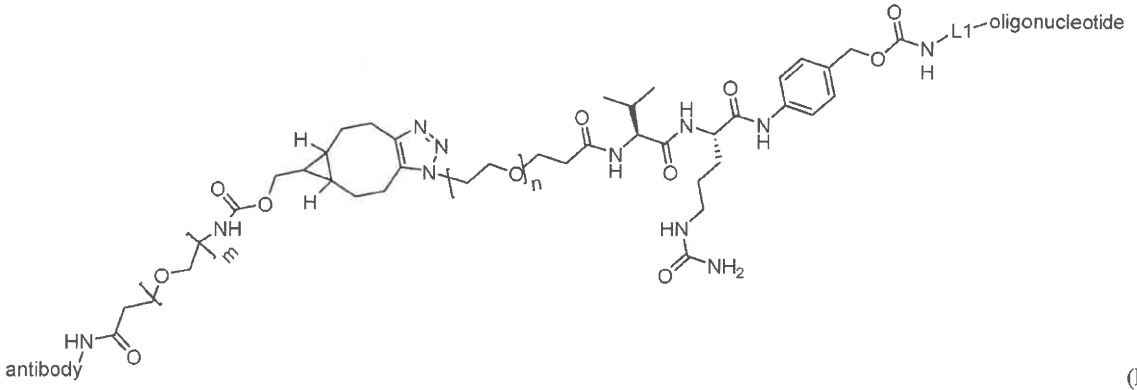
payload is an oligonucleotide, the linker is linked to the 5′ end of the oligonucleotide, the 3′ end of the oligonucleotide, or to an internal site of the oligonucleotide. In some embodiments, the linker is linked to the anti-TfR1 antibody via a thiol-reactive linkage (e.g., via a cysteine in the anti-TfR1 antibody). In some embodiments, the linker (e.g., a linker comprising a valine-citrulline sequence) is linked to the antibody (e.g., an anti-TfR1 antibody described herein) via an amine group (e.g., via a lysine in the antibody). In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000330] An example of a structure of a complex comprising an anti-TfR1 antibody covalently linked to a molecular payload via a linker is provided below:



wherein the linker is linked to the antibody via a thiol-reactive linkage (e.g., via a cysteine in the antibody). In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000331] Another example of a structure of a complex comprising an anti-TfR1 antibody covalently linked to a molecular payload via a linker is provided below:



(E)

wherein n is a number between 0-10, wherein m is a number between 0-10, wherein the linker is linked to the antibody via an amine group (e.g., on a lysine residue), and/or (e.g., and) wherein the linker is linked to the oligonucleotide (e.g., at the 5' end, 3' end, or internally). In some embodiments, the linker is linked to the antibody via a lysine, the linker is linked to the

oligonucleotide at the 5' end, n is 3, and m is 4. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779). It should be understood that the amide shown adjacent the anti-TfR1 antibody in Formula (E) results from a reaction with an amine of the anti-TfR1 antibody, such as a lysine epsilon amine.

[000332] It should be appreciated that antibodies can be linked to molecular payloads with different stoichiometries, a property that may be referred to as a drug to antibody ratios (DAR) with the "drug" being the molecular payload. In some embodiments, one molecular payload is linked to an antibody (DAR = 1). In some embodiments, two molecular payloads are linked to an antibody (DAR = 2). In some embodiments, three molecular payloads are linked to an antibody (DAR = 3). In some embodiments, four molecular payloads are linked to an antibody (DAR = 4). In some embodiments, a mixture of different complexes, each having a different DAR, is provided. In some embodiments, an average DAR of complexes in such a mixture may be in a range of 1 to 3, 1 to 4, 1 to 5 or more. An average DAR of complexes in a mixture need not be an integer value. DAR may be increased by conjugating molecular payloads to different sites on an antibody and/or (e.g., and) by conjugating multimers to one or more sites on antibody. For example, a DAR of 2 may be achieved by conjugating a single molecular payload to two different sites on an antibody or by conjugating a dimer molecular payload to a single site of an antibody.

[000333] In some embodiments, the complex described herein comprises an anti-TfR1 antibody described herein (e.g., the antibodies provided in Tables 2-7) covalently linked to a molecular payload. In some embodiments, the complex described herein comprises an anti-TfR1 antibody described herein (e.g., the antibodies provided in Tables 2-7) covalently linked to molecular payload via a linker (e.g., a linker comprising a valine-citrulline sequence). In some embodiments, the linker (e.g., a linker comprising a valine-citrulline sequence) is linked to the antibody (e.g., an anti-TfR1 antibody described herein) via a thiol-reactive linkage (e.g., via a cysteine in the antibody). In some embodiments, the linker (e.g., a linker comprising a valine-citrulline sequence) is linked to the antibody (e.g., an anti-TfR1 antibody described herein) via an amine group (e.g., via a lysine in the antibody). In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000334] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a

CDR-H1, a CDR-H2, a CDR-H3, a CDR-L1, a CDR-L2, and a CDR-L3 of any one of the antibodies listed in Table 2. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000335] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a VH comprising the amino acid sequence of SEQ ID NO: 69, SEQ ID NO: 71, or SEQ ID NO: 72, and a VL comprising the amino acid sequence of SEQ ID NO: 70. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000336] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a VH comprising the amino acid sequence of SEQ ID NO: 73 or SEQ ID NO: 76, and a VL comprising the amino acid sequence of SEQ ID NO: 74. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000337] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a VH comprising the amino acid sequence of SEQ ID NO: 73 or SEQ ID NO: 76, and a VL comprising the amino acid sequence of SEQ ID NO: 75. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000338] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a VH comprising the amino acid sequence of SEQ ID NO: 77, and a VL comprising the amino acid sequence of SEQ ID NO: 78. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000339] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a VH comprising the amino acid sequence of SEQ ID NO: 77 or SEQ ID NO: 79, and a VL comprising the amino acid sequence of SEQ ID NO: 80. In some embodiments, the molecular

payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000340] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a VH comprising the amino acid sequence of SEQ ID NO: 154, and a VL comprising the amino acid sequence of SEQ ID NO: 155. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000341] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 84, SEQ ID NO: 86 or SEQ ID NO: 87 and a light chain comprising the amino acid sequence of SEQ ID NO: 85. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000342] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 88 or SEQ ID NO: 91, and a light chain comprising the amino acid sequence of SEQ ID NO: 89. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000343] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 88 or SEQ ID NO: 91, and a light chain comprising the amino acid sequence of SEQ ID NO: 90. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000344] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 92 or SEQ ID NO: 94, and a light chain comprising the amino acid sequence of SEQ ID NO: 95. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide

listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000345] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 92, and a light chain comprising the amino acid sequence of SEQ ID NO: 93. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000346] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 156, and a light chain comprising the amino acid sequence of SEQ ID NO: 157. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000347] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 97, SEQ ID NO: 98, or SEQ ID NO: 99 and a light chain comprising the amino acid sequence of SEQ ID NO: 85. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000348] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 100 or SEQ ID NO: 101 and a light chain comprising the amino acid sequence of SEQ ID NO: 89. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000349] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 100 or SEQ ID NO: 101 and a light chain comprising the amino acid sequence of SEQ ID NO: 90. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide

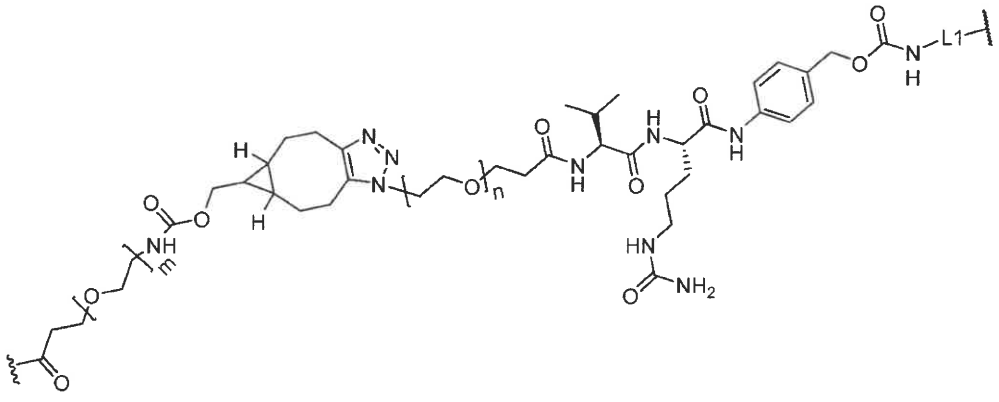
listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000350] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 102 and a light chain comprising the amino acid sequence of SEQ ID NO: 93. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000351] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 102 or SEQ ID NO: 103 and a light chain comprising the amino acid sequence of SEQ ID NO: 95. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

[000352] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to a molecular payload, wherein the anti-TfR1 antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 158 or SEQ ID NO: 159 and a light chain comprising the amino acid sequence of SEQ ID NO: 157. In some embodiments, the molecular payload is a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779).

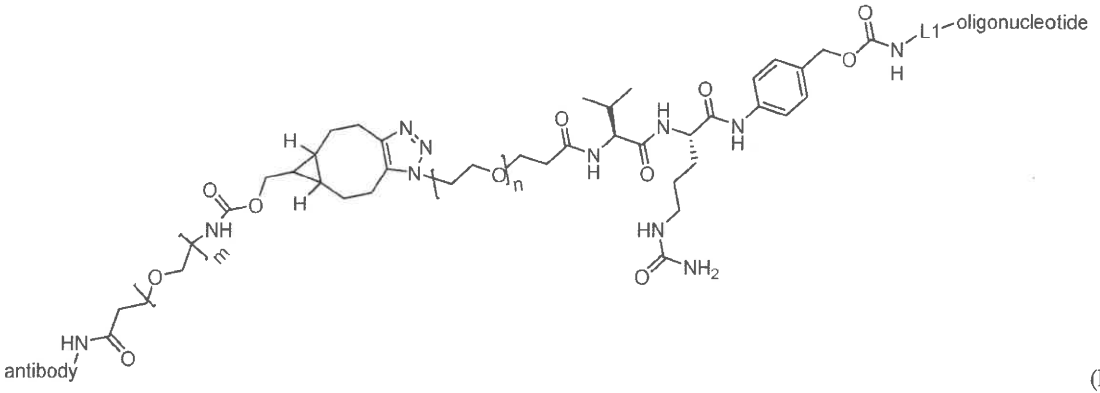
[000353] In any of the example complexes described herein, in some embodiments, the anti-TfR1 antibody is covalently linked to the molecular payload via a linker comprising a structure of:



(I)

wherein n is 3, m is 4.

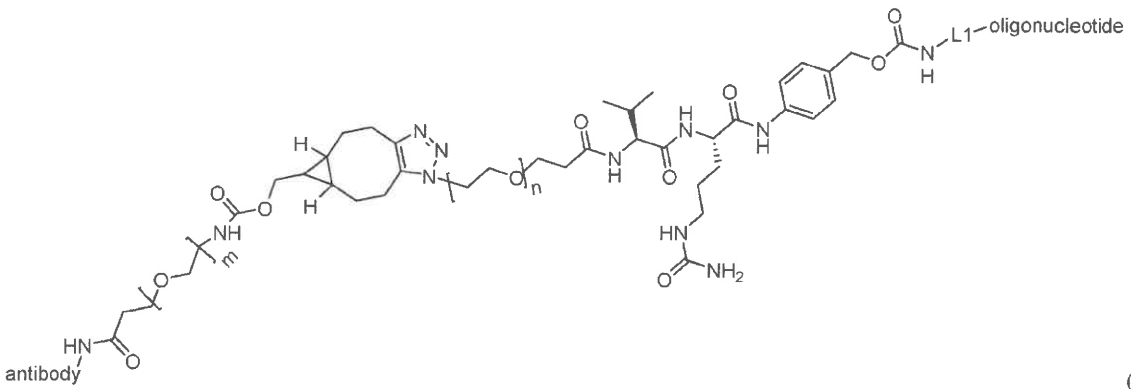
[000354] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to the 5' end of a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779) via a lysine in the anti-TfR1 antibody, wherein the anti-TfR1 antibody comprises a CDR-H1, a CDR-H2, a CDR-H3, a CDR-L1, a CDR-L2, and a CDR-L3 of any one of the antibodies listed in Table 2, wherein the complex has a structure of:



(E)

wherein n is 3 and m is 4. It should be understood that the amide shown adjacent the anti-TfR1 antibody in Formula (E) results from a reaction with an amine of the anti-TfR1 antibody, such as a lysine epsilon amine.

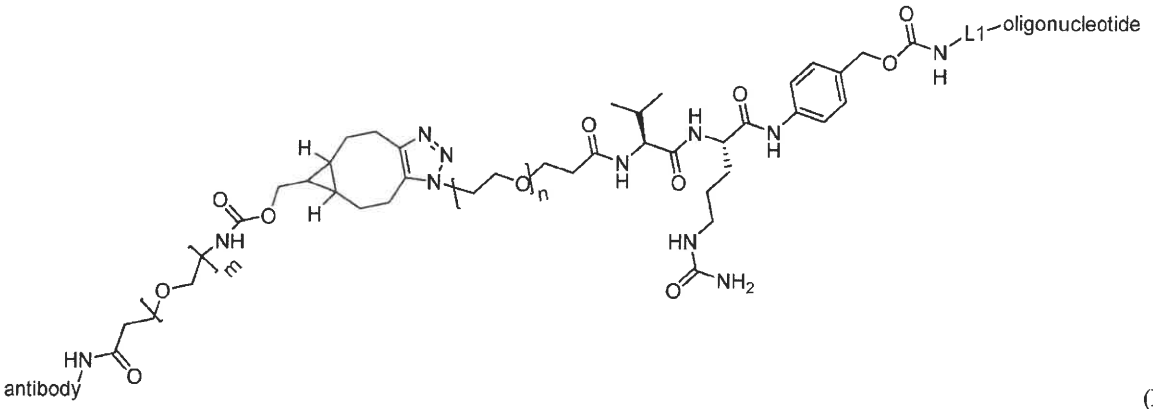
[000355] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to the 5' end of a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779) via a lysine in the anti-TfR1 antibody, wherein the anti-TfR1 antibody comprises a VH and VL of any one of the antibodies listed in Table 3, wherein the complex has a structure of:



(E)

wherein n is 3 and m is 4. It should be understood that the amide shown adjacent the anti-TfR1 antibody in Formula (E) results from a reaction with an amine of the anti-TfR1 antibody, such as a lysine epsilon amine.

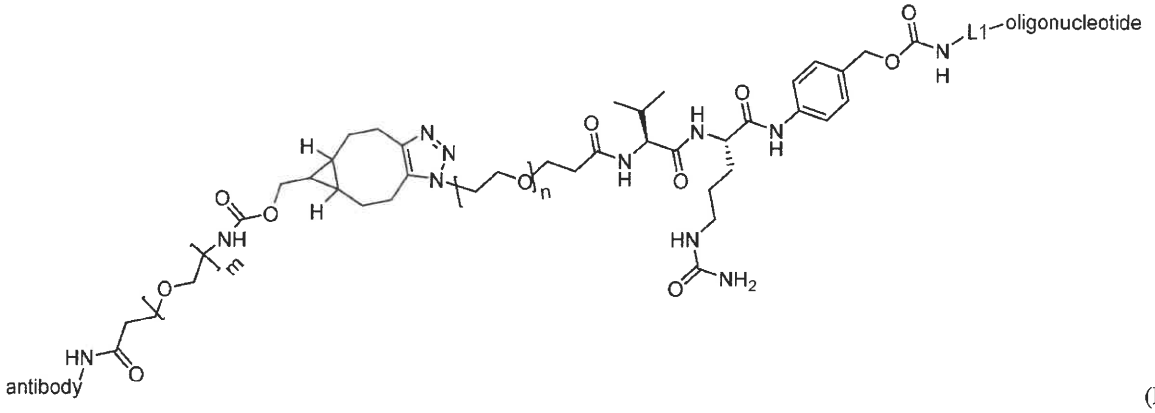
[000356] In some embodiments, the complex described herein comprises an anti-TfR1 antibody covalently linked to the 5' end of a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779) via a lysine in the anti-TfR1 antibody, wherein the anti-TfR1 antibody comprises a heavy chain and light chain of any one of the antibodies listed in Table 4, wherein the complex has a structure of:



(E)

wherein n is 3 and m is 4. It should be understood that the amide shown adjacent the anti-TfR1 antibody in Formula (E) results from a reaction with an amine of the anti-TfR1 antibody, such as a lysine epsilon amine.

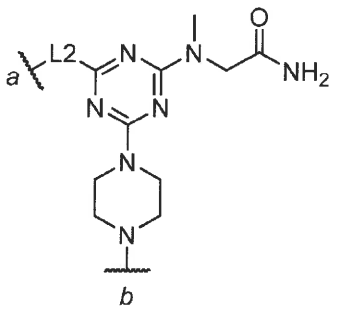
[000357] In some embodiments, the complex described herein comprises an anti-TfR1 Fab covalently linked to the 5' end of a DMD-targeting oligonucleotide (e.g., a DMD-targeting oligonucleotide listed in Table 8, provided by any one of SEQ ID NO: 780-2019, or complementary to any one of SEQ ID NO: 160-779) via a lysine in the anti-TfR1 antibody, wherein the anti-TfR1 Fab comprises a heavy chain and light chain of any one of the antibodies listed in Table 5, wherein the complex has a structure of:

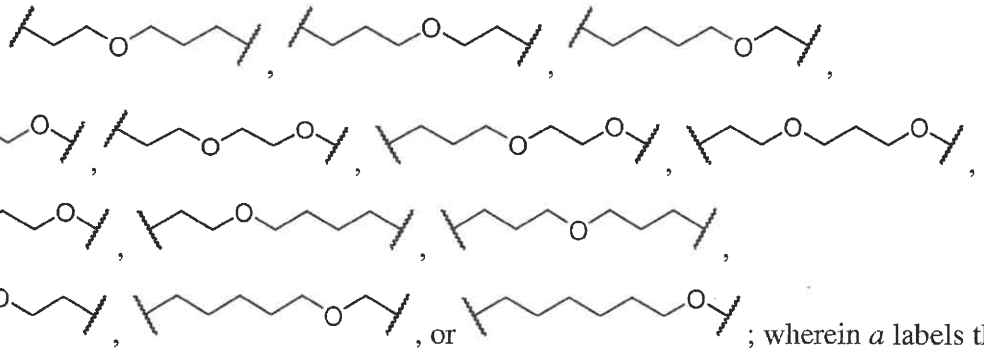


(E)

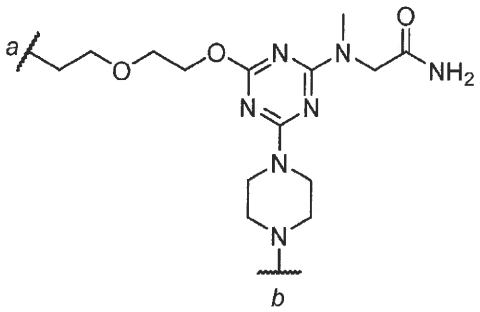
wherein n is 3 and m is 4. It should be understood that the amide shown adjacent the anti-TfR1 antibody in Formula (E) results from a reaction with an amine of the anti-TfR1 antibody, such as a lysine epsilon amine.

[000358] In some embodiments, in any one of the examples of complexes described herein, L1 is:



wherein L2 is ; wherein *a* labels the site directly linked to the carbamate moiety of formulae (B), (D), (E), and (I); and *b* labels the site covalently linked (directly or via additional chemical moieties) to the oligonucleotide.

[000359] In some embodiments, L1 is:



wherein *a* labels the site directly linked to the carbamate moiety of formulae (B), (D), (E), and (I); and *b* labels the site covalently linked (directly or via additional chemical moieties) to the oligonucleotide.

[000360] In some embodiments, L1 is linked to a 5' phosphate of the oligonucleotide. In some embodiments, the phosphate is a phosphodiester. In some embodiments, L1 is linked to a 5' phosphorothioate of the oligonucleotide. In some embodiments, L1 is linked to a 5' phosphonoamidate of the oligonucleotide. In some embodiments, L1 is linked via a phosphorodiamidate linkage to the 5' end of the oligonucleotide.

[000361] In some embodiments, L1 is optional (e.g., need not be present).

III. Formulations

[000362] Complexes provided herein may be formulated in any suitable manner. Generally, complexes provided herein are formulated in a manner suitable for pharmaceutical use. For example, complexes can be delivered to a subject using a formulation that minimizes degradation, facilitates delivery and/or (e.g., and) uptake, or provides another beneficial property to the complexes in the formulation. In some embodiments, provided herein are compositions comprising complexes and pharmaceutically acceptable carriers. Such compositions can be suitably formulated such that when administered to a subject, either into the immediate environment of a target cell or systemically, a sufficient amount of the complexes enter target muscle cells. In some embodiments, complexes are formulated in buffer solutions such as phosphate-buffered saline solutions, liposomes, micellar structures, and capsids.

[000363] It should be appreciated that, in some embodiments, compositions may include separately one or more components of complexes provided herein (e.g., muscle-targeting agents, linkers, molecular payloads, or precursor molecules of any one of them).

[000364] In some embodiments, complexes are formulated in water or in an aqueous solution (e.g., water with pH adjustments). In some embodiments, complexes are formulated in basic buffered aqueous solutions (e.g., PBS). In some embodiments, formulations as disclosed herein comprise an excipient. In some embodiments, an excipient confers to a composition improved stability, improved absorption, improved solubility and/or (e.g., and) therapeutic enhancement of the active ingredient. In some embodiments, an excipient is a buffering agent (*e.g.*, sodium citrate, sodium phosphate, a tris base, or sodium hydroxide) or a vehicle (*e.g.*, a buffered solution, petrolatum, dimethyl sulfoxide, or mineral oil).

[000365] In some embodiments, a complex or component thereof (e.g., oligonucleotide or antibody) is lyophilized for extending its shelf-life and then made into a solution before use (*e.g.*, administration to a subject). Accordingly, an excipient in a composition comprising a complex, or component thereof, described herein may be a lyoprotectant (*e.g.*, mannitol, lactose, polyethylene glycol, or polyvinyl pyrolidone), or a collapse temperature modifier (*e.g.*, dextran, ficoll, or gelatin).

[000366] In some embodiments, a pharmaceutical composition is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, administration. Typically, the route of administration is intravenous or subcutaneous.

[000367] Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol,

propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. In some embodiments, formulations include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, and sodium chloride in the composition. Sterile injectable solutions can be prepared by incorporating the complexes in a required amount in a selected solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization.

[000368] In some embodiments, a composition may contain at least about 0.1% of the complex, or component thereof, or more, although the percentage of the active ingredient(s) may be between about 1% and about 80% or more of the weight or volume of the total composition. Factors such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations will be contemplated by one skilled in the art of preparing such pharmaceutical formulations, and as such, a variety of dosages and treatment regimens may be desirable.

IV. Methods of Use / Treatment

[000369] Complexes comprising a muscle-targeting agent covalently linked to a molecular payload as described herein are effective in treating a subject having a dystrophinopathy, e.g., Duchenne muscular dystrophy. In some embodiments, complexes comprise a molecular payload that is an oligonucleotide, *e.g.*, an antisense oligonucleotide that facilitates exon skipping of a pre-mRNA expressed from a mutated DMD allele.

[000370] In some embodiments, a subject may be a human subject, a non-human primate subject, a rodent subject, or any suitable mammalian subject. In some embodiments, a subject may have Duchenne muscular dystrophy or other dystrophinopathy. In some embodiments, a subject has a mutated DMD allele, which may optionally comprise at least one mutation in a DMD exon that causes a frameshift mutation and leads to improper RNA splicing/processing. In some embodiments, a subject is suffering from symptoms of a severe dystrophinopathy, e.g. muscle atrophy or muscle loss. In some embodiments, a subject has an asymptomatic increase in serum concentration of creatine phosphokinase (CK) and/or (e.g., and) muscle cramps with myoglobinuria. In some embodiments, a subject has a progressive muscle disease, such as Duchenne or Becker muscular dystrophy or DMD-associated dilated cardiomyopathy (DCM). In some embodiments, a subject is not suffering from symptoms of a dystrophinopathy.

[000371] In some embodiments, a subject has a mutation in a DMD gene that is amenable to exon 55 skipping. In some embodiments, a complex comprising a muscle-targeting agent covalently linked to a molecular payload as described herein is effective in treating a subject having a mutation in a DMD gene that is amenable to exon 55 skipping. In some embodiments,

a complex comprises a molecular payload that is an oligonucleotide, *e.g.*, an antisense oligonucleotide that facilitates skipping of exon 55 of a pre-mRNA, such as in a pre-mRNA encoded from a mutated DMD gene (*e.g.*, a mutated DMD gene that is amenable to exon 55 skipping).

[000372] An aspect of the disclosure includes methods involving administering to a subject an effective amount of a complex as described herein. In some embodiments, an effective amount of a pharmaceutical composition that comprises a complex comprising a muscle-targeting agent covalently linked to a molecular payload can be administered to a subject in need of treatment. In some embodiments, a pharmaceutical composition comprising a complex as described herein may be administered by a suitable route, which may include intravenous administration, e.g., as a bolus or by continuous infusion over a period of time. In some embodiments, administration may be performed by intramuscular, intraperitoneal, intracerebrospinal, subcutaneous, intra-articular, intrasynovial, or intrathecal routes. In some embodiments, a pharmaceutical composition may be in solid form, aqueous form, or a liquid form. In some embodiments, an aqueous or liquid form may be nebulized or lyophilized. In some embodiments, a nebulized or lyophilized form may be reconstituted with an aqueous or liquid solution.

[000373] Compositions for intravenous administration may contain various carriers such as vegetable oils, dimethylactamide, dimethyformamide, ethyl lactate, ethyl carbonate, isopropyl myristate, ethanol, and polyols (glycerol, propylene glycol, liquid polyethylene glycol, and the like). For intravenous injection, water soluble antibodies can be administered by the drip method, whereby a pharmaceutical formulation containing the antibody and a physiologically acceptable excipients is infused. Physiologically acceptable excipients may include, for example, 5% dextrose, 0.9% saline, Ringer's solution or other suitable excipients. Intramuscular preparations, e.g., a sterile formulation of a suitable soluble salt form of the antibody, can be dissolved and administered in a pharmaceutical excipient such as Water-for-Injection, 0.9% saline, or 5% glucose solution.

[000374] In some embodiments, a pharmaceutical composition that comprises a complex comprising a muscle-targeting agent covalently linked to a molecular payload is administered via site-specific or local delivery techniques. Examples of these techniques include implantable depot sources of the complex, local delivery catheters, site specific carriers, direct injection, or direct application.

[000375] In some embodiments, a pharmaceutical composition that comprises a complex comprising a muscle-targeting agent covalently linked to a molecular payload is administered at an effective concentration that confers therapeutic effect on a subject. Effective amounts vary,

as recognized by those skilled in the art, depending on the severity of the disease, unique characteristics of the subject being treated, e.g., age, physical conditions, health, or weight, the duration of the treatment, the nature of any concurrent therapies, the route of administration and related factors. These related factors are known to those in the art and may be addressed with no more than routine experimentation. In some embodiments, an effective concentration is the maximum dose that is considered to be safe for the patient. In some embodiments, an effective concentration will be the lowest possible concentration that provides maximum efficacy.

[000376] Empirical considerations, e.g., the half-life of the complex in a subject, generally will contribute to determination of the concentration of pharmaceutical composition that is used for treatment. The frequency of administration may be empirically determined and adjusted to maximize the efficacy of the treatment.

[000377] The efficacy of treatment may be assessed using any suitable methods. In some embodiments, the efficacy of treatment may be assessed by evaluation of observation of symptoms associated with a dystrophinopathy, e.g., muscle atrophy or muscle weakness, through measures of a subject's self-reported outcomes, e.g., mobility, self-care, usual activities, pain/discomfort, and anxiety/depression, or by quality-of-life indicators, e.g., lifespan.

[000378] In some embodiments, a pharmaceutical composition that comprises a complex comprising a muscle-targeting agent covalently linked to a molecular payload described herein is administered to a subject at an effective concentration sufficient to modulate activity or expression of a target gene by at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90% or at least 95% relative to a control, e.g. baseline level of gene expression prior to treatment.

ADDITIONAL EMBODIMENTS

1. A complex comprising an anti-transferrin receptor 1 (TfR1) antibody covalently linked to a molecular payload configured for inducing skipping of exon 55 in a DMD pre-mRNA, wherein the anti-TfR1 antibody is an antibody identified in any one of Tables 2-7.

2. The complex of embodiment 1, wherein the anti-TfR1 antibody comprises:

(i) a heavy chain complementarity determining region 1 (CDR-H1) of SEQ ID NO: 33, a heavy chain complementarity determining region 2 (CDR-H2) of SEQ ID NO: 34, a heavy chain complementarity determining region 3 (CDR-H3) of SEQ ID NO: 35, a light chain complementarity determining region 1 (CDR-L1) of SEQ ID NO: 36, a light chain complementarity determining region 2 (CDR-L2) of SEQ ID NO: 37, and a light chain complementarity determining region 3 (CDR-L3) of SEQ ID NO: 32;

(ii) a CDR-H1 of SEQ ID NO: 7, a CDR-H2 of SEQ ID NO: 8, a CDR-H3 of SEQ ID NO: 9, a CDR-L1 of SEQ ID NO: 10, a CDR-L2 of SEQ ID NO: 11, and a CDR-L3 of SEQ ID NO: 6;

(iii) a CDR-H1 of SEQ ID NO: 7, a CDR-H2 of SEQ ID NO: 20, a CDR-H3 of SEQ ID NO: 9, a CDR-L1 of SEQ ID NO: 10, a CDR-L2 of SEQ ID NO: 11, and a CDR-L3 of SEQ ID NO: 6;

(iv) a CDR-H1 of SEQ ID NO: 7, a CDR-H2 of SEQ ID NO: 24, a CDR-H3 of SEQ ID NO: 9, a CDR-L1 of SEQ ID NO: 10, a CDR-L2 of SEQ ID NO: 11, and a CDR-L3 of SEQ ID NO: 6;

(v) a CDR-H1 of SEQ ID NO: 51, a CDR-H2 of SEQ ID NO: 52, a CDR-H3 of SEQ ID NO: 53, a CDR-L1 of SEQ ID NO: 54, a CDR-L2 of SEQ ID NO: 55, and a CDR-L3 of SEQ ID NO: 50;

(vi) a CDR-H1 of SEQ ID NO: 64, a CDR-H2 of SEQ ID NO: 52, a CDR-H3 of SEQ ID NO: 53, a CDR-L1 of SEQ ID NO: 54, a CDR-L2 of SEQ ID NO: 55, and a CDR-L3 of SEQ ID NO: 50; or

(vii) a CDR-H1 of SEQ ID NO: 67, a CDR-H2 of SEQ ID NO: 52, a CDR-H3 of SEQ ID NO: 53, a CDR-L1 of SEQ ID NO: 54, a CDR-L2 of SEQ ID NO: 55, and a CDR-L3 of SEQ ID NO: 50.

3. The complex of embodiment 1 or embodiment 2, wherein the anti-TfR1 antibody comprises:

(i) a heavy chain variable region (VH) comprising an amino acid sequence at least 85% identical to SEQ ID NO: 76; and/or a light chain variable region (VL) comprising an amino acid sequence at least 85% identical to SEQ ID NO: 75;

(ii) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 69; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 70;

(iii) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 71; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 70;

(iv) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 72; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 70;

(v) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 73; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 74;

(vi) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 73; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 75;

(vii) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 76; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 74;

(viii) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 77; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 78;

(ix) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 79; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 80; or

(x) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 77; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 80.

4. The complex of any one of embodiments 1 to 3, wherein the anti-TfR1 antibody comprises:

(i) a VH comprising the amino acid sequence of SEQ ID NO: 76 and a VL comprising the amino acid sequence of SEQ ID NO: 75;

(ii) a VH comprising the amino acid sequence of SEQ ID NO: 69 and a VL comprising the amino acid sequence of SEQ ID NO: 70;

(iii) a VH comprising the amino acid sequence of SEQ ID NO: 71and a VL comprising the amino acid sequence of SEQ ID NO: 70;

(iv) a VH comprising the amino acid sequence of SEQ ID NO: 72 and a VL comprising the amino acid sequence of SEQ ID NO: 70;

(v) a VH comprising the amino acid sequence of SEQ ID NO: 73 and a VL comprising the amino acid sequence of SEQ ID NO: 74;

(vi) a VH comprising the amino acid sequence of SEQ ID NO: 73 and a VL comprising the amino acid sequence of SEQ ID NO: 75;

(vii) a VH comprising the amino acid sequence of SEQ ID NO: 76 and a VL comprising the amino acid sequence of SEQ ID NO: 74;

(viii) a VH comprising the amino acid sequence of SEQ ID NO: 77 and a VL comprising the amino acid sequence of SEQ ID NO: 78;

(ix) a VH comprising the amino acid sequence of SEQ ID NO: 79 and a VL comprising the amino acid sequence of SEQ ID NO: 80; or

(x) a VH comprising the amino acid sequence of SEQ ID NO: 77 and a VL comprising the amino acid sequence of SEQ ID NO: 80.

5. The complex of any one of embodiments 1 to 4, wherein the anti-TfR1 antibody is a Fab fragment, a Fab' fragment, a F(ab')2 fragment, an scFv, an Fv, or a full-length IgG.

6. The complex of embodiment 5, wherein the anti-TfR1 antibody is a Fab fragment.

7. The complex of embodiment 6, wherein the anti-TfR1 antibody comprises:

(i) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 101; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 90;

(ii) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 97; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 85;

(iii) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 98; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 85;

(iv) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 99; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 85;

(v) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 100; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 89;

(vi) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 100; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 90;

(vii) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 101; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 89;

(viii) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 102; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 93;

(ix) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 103; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 95; or

(x) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 102; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 95.

8. The complex of embodiment 6 or embodiment 7, wherein the anti-TfR1 antibody comprises:

(i) a heavy chain comprising the amino acid sequence of SEQ ID NO: 101; and a light chain comprising the amino acid sequence of SEQ ID NO: 90;

(ii) a heavy chain comprising the amino acid sequence of SEQ ID NO: 97; and a light chain comprising the amino acid sequence of SEQ ID NO: 85;

(iii) a heavy chain comprising the amino acid sequence of SEQ ID NO: 98; and a light chain comprising the amino acid sequence of SEQ ID NO: 85;

(iv) a heavy chain comprising the amino acid sequence of SEQ ID NO: 99; and a light chain comprising the amino acid sequence of SEQ ID NO: 85;

(v) a heavy chain comprising the amino acid sequence of SEQ ID NO: 100; and a light chain comprising the amino acid sequence of SEQ ID NO: 89;

(vi) a heavy chain comprising the amino acid sequence of SEQ ID NO: 100; and a light chain comprising the amino acid sequence of SEQ ID NO: 90;

(vii) a heavy chain comprising the amino acid sequence of SEQ ID NO: 101; and a light chain comprising the amino acid sequence of SEQ ID NO: 89;

(viii) a heavy chain comprising the amino acid sequence of SEQ ID NO: 102; and a light chain comprising the amino acid sequence of SEQ ID NO: 93;

(ix) a heavy chain comprising the amino acid sequence of SEQ ID NO: 103; and a light chain comprising the amino acid sequence of SEQ ID NO: 95; or

(x) a heavy chain comprising the amino acid sequence of SEQ ID NO: 102; and a light chain comprising the amino acid sequence of SEQ ID NO: 95.

9. The complex of any one of embodiments 1 to 8, wherein the anti-TfR1 antibody does not specifically bind to the transferrin binding site of the transferrin receptor 1 and/or wherein the anti-TfR1 antibody does not inhibit binding of transferrin to the transferrin receptor 1.

10. The complex of any one of embodiments 1 to 9, wherein the molecular payload comprises an oligonucleotide.

11. The complex of embodiment 10, wherein the oligonucleotide promotes antisense-mediated exon skipping in the DMD pre-RNA.

12. The complex of embodiment 10 or 11, wherein the oligonucleotide comprises a region of complementarity to a splicing feature of the DMD pre-mRNA.

13. The complex of embodiment 12, wherein the splicing feature is an exonic splicing enhancer (ESE) of the DMD pre-mRNA.

14. The complex of embodiment 13, wherein the splicing feature is in exon 55 of the DMD pre-mRNA, optionally wherein the ESE comprises a sequence of any one of SEQ ID NOs: 2031-2061.

15. The complex of embodiment 12, wherein the splicing feature is a branch point, a splice donor site, or a splice acceptor site.

16. The complex of embodiment 15, wherein the splicing feature is across the junction of exon 54 and intron 54, in intron 54, across the junction of intron 54 and exon 55, across the junction of exon 55 and intron 55, in intron 55, or across the junction of intron 55 and exon 56 of the DMD pre-mRNA, optionally wherein the splicing feature comprises a sequence of any one of SEQ ID NOs: 2028-2030, 2062, and 2063.

17. The complex of any one of embodiments 12 to 16, wherein the region of complementarity comprises at least 4 consecutive nucleosides complementary to the splicing feature.

18. The complex of any one of embodiments 1 to 9, wherein the molecular payload comprises an oligonucleotide comprising a sequence complementary to any one of SEQ ID NOs: 160-779 or comprising a sequence of any one of SEQ ID NOs: 780-2019, wherein each thymine base (T) may independently and optionally be replaced with a uracil base (U), and each U may independently and optionally be replaced with a T.

19. The complex of any one of embodiments 10 to 18, wherein the oligonucleotide comprises at least one modified internucleoside linkage.

20. The complex of embodiment 19, wherein the at least one modified internucleoside linkage is a phosphorothioate linkage.

21. The complex of any one of embodiments 10 to 20, wherein the oligonucleotide comprises one or more modified nucleosides.

22. The complex of embodiment 21, wherein the one or more modified nucleosides are 2'-modified nucleosides.

23. The complex of any one of embodiments 10 to 18, wherein the oligonucleotide comprises one or more phosphorodiamidate morpholinos, optionally wherein the oligonucleotide is a phosphorodiamidate morpholino oligomer (PMO).

24. The complex of any one of embodiments 1 to 23, wherein the anti-TfR1 antibody is covalently linked to the molecular payload via a cleavable linker.

25. The complex of embodiment 24, wherein the cleavable linker comprises a valine-citrulline sequence.

26. The complex of any one of embodiments 1 to 25, wherein the anti-TfR1 antibody is covalently linked to the molecular payload via conjugation to a lysine residue or a cysteine residue of the antibody.

27. A complex comprising an anti-TfR1 antibody covalently linked to an oligonucleotide configured for inducing skipping of exon 55 in a DMD pre-mRNA, wherein the oligonucleotide comprises a region of complementarity to any one of SEQ ID NOs: 160-779.

28. The complex of embodiment 27, wherein the anti-TfR1 antibody is an antibody identified in any one of Tables 2-7.

29. A complex comprising an anti-TfR1 antibody covalently linked to an oligonucleotide configured for inducing skipping of exon 55 in a DMD pre-mRNA, wherein the oligonucleotide comprises a region of complementarity to a splicing feature of the DMD pre-mRNA.

30. An oligonucleotide that targets DMD, wherein the oligonucleotide comprises a region of complementarity to any one of SEQ ID NOs: 160-779.

31. The oligonucleotide of embodiment 30, wherein the region of complementarity comprises at least 15 consecutive nucleosides complementary to any one of SEQ ID NOs: 160-779.

32. The oligonucleotide of embodiment 30 or 31, wherein the oligonucleotide comprises at least 15 consecutive nucleosides of any one of SEQ ID NOs: 780-2019, optionally wherein the oligonucleotide comprises a sequence of any one of SEQ ID NOs: 780-2019, wherein each thymine base (T) may independently and optionally be replaced with a uracil base (U), and each U may independently and optionally be replaced with a T.

33. A method of delivering a molecular payload to a cell, the method comprising contacting the cell with the complex of any one of embodiments 1 to 26.

34. A method of delivering an oligonucleotide to a cell, the method comprising contacting the cell with the complex of any one of embodiments 27 to 29.

35. A method of promoting the expression or activity of a dystrophin protein in a cell, the method comprising contacting the cell with the complex of any one of embodiments 1 to 26 in an amount effective for promoting internalization of the molecular payload to the cell, optionally wherein the cell is a muscle cell.

36. A method of promoting the expression or activity of a dystrophin protein in a cell, the method comprising contacting the cell with the complex of any one of embodiments 27 to 29 in an amount effective for promoting internalization of the oligonucleotide to the cell, optionally wherein the cell is a muscle cell.

37. The method of embodiment 35 or 36, wherein the cell is *in vitro*.

38. The method of embodiment 35 or 36, wherein the cell is in a subject.

39. The method of embodiment 38, wherein the subject is a human.

40. The method of embodiment 39, wherein the subject has a DMD gene that is amenable to skipping of exon 55.

41. The method of any one of embodiments 35 to 40, wherein the dystrophin protein is a truncated dystrophin protein.

42. A method of treating a subject having a mutated DMD allele that is associated with a dystrophinopathy, the method comprising administering to the subject an effective amount of the complex of any one of embodiments 1 to 29.

43. A method of promoting skipping of exon 55 of a DMD pre-mRNA transcript in a cell, the method comprising contacting the cell with an effective amount of the complex of any one of embodiments 1 to 29.

44. A method of treating a subject having a mutated DMD allele that is associated with a dystrophinopathy, the method comprising administering to the subject an effective amount of the complex of any one of embodiments 1 to 29.

EXAMPLES

Example 1. Exon-skipping activity of anti-TfR1 antibody conjugates in Duchenne muscular dystrophy patient myotubes

[000379] In this study, the exon-skipping activities of anti-TfR1 antibody conjugates comprising an anti-TfR1 Fab (3M12 VH4/Vκ3) covalently linked to a DMD exon 51-skipping antisense oligonucleotide (ASO) were evaluated. The DMD exon 51-skipping ASO is a phosphorodiamidate morpholino oligomer (PMO) of 30 nucleotides in length and targets an ESE in DMD exon 51 having the sequence TGGAGGT (SEQ ID NO: 131). Immortalized human myoblasts bearing an exon 52 deletion in the DMD gene were thawed and seeded at a density of 1e6 cell/flask in Promocell Skeletal Cell Growth Media (with 5% FBS and 1x Pen-Strep) and allowed to grow to confluency. Once confluent, cells were trypsinized and pelleted via centrifugation and resuspended in fresh Promocell Skeletal Cell Growth Media. The cell number was counted and cells were seeded into Matrigel-coated 96-well plates at a density of 50,000 cells/well. Cells were allowed to recover for 24 hours. Cells were induced to differentiate into myotubes by aspirating the growth media and replacing with differentiation media with no serum. Cells were then treated with the DMD exon 51-skipping oligonucleotide (not covalently linked to an antibody – "naked") at 10 μM ASO or the anti-TfR1 Fab (3M12 VH4/Vκ3) covalently linked to the DMD exon 51-skipping oligonucleotide at 10 μM ASO equivalent. Cells were incubated with test articles for ten days then total RNA was harvested from the 96 well plates. cDNA synthesis was performed on 75 ng of total RNA, and mutation specific PCRs were performed to evaluate the degree of exon 51 skipping in the cells. Mutation-specific PCR products were run on a 4% agarose gel and visualized using SYBR gold. Densitometry was used to calculate the relative amounts of the skipped and unskipped amplicon and exon skipping was

determined as a ratio of the Exon 51 skipped amplicon divided by the total amount of amplicon present:

$$\%Exon\ Skipping = \frac{Skipped\ Amplicon}{(Skipped\ Amplicon + Unskipped\ Amplicon)} * 100.$$

[000380] The results demonstrate that the conjugate resulted in enhanced exon skipping compared to the naked DMD exon 51-skipping oligonucleotide in patient myotubes (FIG. 1). This indicates that anti-TfR1 Fab 3M12 VH4/Vκ3 enabled cellular internalization of the conjugate into muscle cells resulting in activity of the exon 51-skipping oligonucleotide in the muscle cells. Similarly, an anti-TfR1 antibody (*e.g.*, anti-TfR1 Fab 3M12 VH4/Vκ3) can enable internalization of a conjugate comprising the anti-TfR1 antibody covalently linked to other exon skipping oligonucleotides (*e.g.*, an exon skipping oligonucleotide provided herein, such as an exon 55 skipping oligonucleotide) into muscle cells and facilitate activity of the exon skipping oligonucleotide in the muscle cells.

Example 2. Exon skipping activity of anti-TfR1 Fab-ASO conjugate in vivo in cynomolgus monkeys

[000381] Anti-TfR1 Fab 3M12 VH4/Vκ3 was covalently linked to the DMD exon 51-skipping antisense oligonucleotide (ASO) that was used in Example 1. The exon skipping activity of the conjugate was tested in vivo in healthy non-human primates. Naïve male cynomolgus monkeys (n= 4-5 per group) were administered two doses of vehicle, 30 mg/kg naked ASO (*i.e.*, not covalently linked to an antibody), or 122 mg/kg anti-TfR1 Fab (3M12 VH4/Vκ3) covalently linked to the DMD exon 51-skipping oligonucleotide (30 mg/kg ASO equivalent) via intravenous infusion on days 1 and 8. Animals were sacrificed and tissues harvested either 2 weeks or 4 weeks after the first dose was administered. Total RNA was collected from tissue samples using a Promega Maxwell® RSC instrument and cDNA synthesis was performed using qScript cDNA SuperMix. Assessment of exon 51 skipping was performed using end-point PCR.

[000382] Capillary electrophoresis of the PCR products was used to assess exon skipping, and % exon 51 skipping was calculated using the following formula:

$$\%\ Exon\ Skipping = \frac{Molarity\ of\ Skipped\ Band}{Molarity\ of\ Skipped\ Band + Molarity\ of\ Unskipped\ Band} * 100.$$

Calculated exon 51 skipping results are shown in Table 10.

Table 10. Exon 51 skipping of DMD mRNA in cynomolgus monkey

Time	2 weeks			4 weeks	
Group	**Vehicle**	**Naked ASO[a]**	**Conjugate**	**Naked ASO[a]**	**Conjugate**
Conjugate dose[b]	0	n/a	122	n/a	122
ASO Dose[c]	0	30	30	30	30

Quadriceps [d]	0.00 (0.00)	1.216 (1.083)	4.906 (3.131)	0.840 (1.169)	1.708 (1.395)
Diaphragm [d]	0.00 (0.00)	1.891 (2.911)	7.315 (1.532)	0.717 (1.315)	9.225 (4.696)
Heart [d]	0.00 (0.00)	0.043 (0.096)	3.42 (1.192)	0.00 (0.00)	4.525 (1.400)
Biceps [d]	0.00 (0.00)	0.607 (0.615)	3.129 (0.912)	1.214 (1.441)	4.863 (3.881)
Tibialis anterior [d]	0.00 (0.00)	0.699 (0.997)	1.042 (0.685)	0.384 (0.615)	0.816 (0.915)
Gastrocnemius [d]	0.00 (0.00)	0.388 (0.573)	2.424 (2.329)	0.00 (0.00)	5.393 (2.695)

[a]ASO = antisense oligonucleotide.

[b]Conjugate doses are listed as mg/kg of anti-TfR1 Fab 3M12 VH4/Vκ3-ASO conjugate.

[c]ASO doses are listed as mg/kg ASO or ASO equivalent of the anti-TfR1 Fab 3M12 VH4/Vκ3-ASO dose.

[d]Exon skipping values are mean % exon 51 skipping with standard deviations (n=5) in parentheses.

[000383] Tissue ASO accumulation was also quantified using a hybridization ELISA with a probe complementary to the ASO sequence. A standard curve was generated and ASO levels (in ng/g) were derived from a linear regression of the standard curve. The ASO was distributed to all tissues evaluated at a higher level following the administration of the anti-TfR1 Fab VH4/Vκ3-ASO conjugate as compared to the administration of naked ASO. Intravenous administration of naked ASO resulted in levels of ASO that were close to background levels in all tissues evaluated at 2 and 4 weeks after the first does was administered. Administration of anti-TfR1 Fab VH4/Vκ3-ASO conjugate resulted in distribution of ASO through the tissues evaluated with a rank order of heart>diaphragm>bicep>quadriceps>gastrocnemius>tibialis anterior 2 weeks after first dosing. The duration of tissue concentration was also assessed. Concentrations of the ASO in quadriceps, bicep and diaphragm decreased by less than 50% over the time period evaluated (2 to 4 weeks), while levels of ASO in the heart, tibialis anterior, and gastrocnemius remained virtually unchanged (Table 11). This indicates that anti-TfR1 Fab 3M12 VH4/Vκ3 enabled cellular internalization of the conjugate into muscle cells *in vivo*, resulting in activity of the exon skipping oligonucleotide in the muscle cells. Similarly, an anti-TfR1 antibody (*e.g.*, anti-TfR1 Fab 3M12 VH4/Vκ3) *in vivo* can enable internalization of a conjugate comprising the anti-TfR1 antibody covalently linked to other exon skipping oligonucleotides (*e.g.*, an exon skipping oligonucleotide provided herein, such as an exon 55 skipping oligonucleotide) into muscle cells and facilitate activity of the exon skipping oligonucleotide in the muscle cells.

Table 11. Tissue distribution of DMD exon 51 skipping ASO in cynomolgus monkeys

Time	**2 weeks**			**4 weeks**	
Group	**Vehicle**	**Naked ASO[a]**	**Conjugate**	**Naked ASO[a]**	**Conjugate**
Conjugate Dose[b]	0	n/a	122	n/a	122
ASO Dose[c]	0	30	30	30	30
Quadriceps [d]	0 (59.05)	696.8 (868.15)	2436 (954.0)	197 (134)	682 (281)

Diaphragm [d]	0± (144.3)	580.02 (360.11)	6750 (2256)	60 (120)	3131 (1618)
Heart [d]	0 (396.03)	1449 (1337)	27138 (6315)	943 (1803)	30410 (9247)
Biceps [d]	0 (69.58)	615.63 (335.17)	2840 (980.31)	130 (80)	1326 (623)
Tibialis anterior [d]	0 (76.31)	564.71 (327.88)	1591 (253.50)	169 (110)	1087 (514)
Gastrocnemius [d]	0 (41.15)	705.47 (863.75)	2096 (474.04)	170 (69)	1265 (272)

[a]ASO = Antisense oligonucleotide.

[b]Conjugate doses are listed as mg/kg of anti-TfR1 Fab 3M12 VH4/Vκ3-ASO conjugate.

[c]ASO doses are listed as mg/kg ASO or ASO equivalent of the anti-TfR1 Fab 3M12 VH4/Vκ3-ASO conjugate dose.

[d]ASO values are mean concentrations of ASO in tissue as ng/g with standard deviations (n=5) in parentheses.

Example 3. Exon-skipping activity of anti-TfR1 antibody conjugates in DMD patient myotubes

[000384] In this study, the exon-skipping activities of anti-TfR1 antibody conjugates comprising an anti-TfR1 Fab (3M12 VH4/Vκ3) covalently linked to a DMD exon 55-skipping antisense oligonucleotide (ASO) are evaluated. The DMD exon 55-skipping ASO is a phosphorodiamidate morpholino oligomer (PMO) and targets a DMD exon 55 splicing feature. Immortalized human myoblasts are thawed and seeded at a density of 1e6 cell/flask in Promocell Skeletal Cell Growth Media (with 5% FBS and 1x Pen-Strep) and allowed to grow to confluency. Once confluent, cells are trypsinized and pelleted via centrifugation and resuspended in fresh Promocell Skeletal Cell Growth Media. The cell number is counted and cells are seeded into Matrigel-coated 96-well plates at a density of 50,000 cells/well. Cells are allowed to recover for 24 hours. Cells are induced to differentiate into myotubes by aspirating the growth media and replacing with differentiation media with no serum. Cells are then treated with the DMD exon 55-skipping oligonucleotide (not covalently linked to an antibody – "naked") at 10 μM ASO or the anti-TfR1 Fab (3M12 VH4/Vκ3) covalently linked to the DMD exon 55-skipping oligonucleotide at 10 μM ASO equivalent. Cells are incubated with test articles for ten days then total RNA is harvested from the 96 well plates. cDNA synthesis is performed on 75 ng of total RNA, and mutation specific PCRs are performed to evaluate the degree of exon 55 skipping in the cells. PCR products are measured using capillary electrophoresis with UV detection. Molarity is calculated and relative amounts of the skipped and unskipped amplicon are determined. Exon skipping is determined as a ratio of the Exon 55 skipped amplicon divided by the total amount of amplicon present, according to the following formula:

$$\%Exon\ Skipping = \frac{Skipped\ Amplicon}{(Skipped\ Amplicon + Unskipped\ Amplicon)} * 100$$

[000385] The results demonstrate that the conjugates facilitate enhanced exon skipping compared to the naked DMD exon 55-skipping oligonucleotide in patient myotubes. This indicates that anti-TfR1 Fab 3M12 VH4/Vκ3 enables cellular internalization of the conjugate into muscle cells resulting in activity of the exon 55-skipping oligonucleotide in the muscle cells.

EQUIVALENTS AND TERMINOLOGY

[000386] The disclosure illustratively described herein suitably can be practiced in the absence of any element or elements, limitation or limitations that are not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of", and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the disclosure. Thus, it should be understood that although the present disclosure has been specifically disclosed by preferred embodiments, optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this disclosure.

[000387] In addition, where features or aspects of the disclosure are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the disclosure is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.

[000388] It should be appreciated that, in some embodiments, sequences presented in the sequence listing may be referred to in describing the structure of an oligonucleotide or other nucleic acid. In such embodiments, the actual oligonucleotide or other nucleic acid may have one or more alternative nucleotides or nucleosides (e.g., an RNA counterpart of a DNA nucleoside or a DNA counterpart of an RNA nucleoside) and/or (e.g., and) one or more modified nucleotides/nucleosides and/or (e.g., and) one or more modified internucleoside linkages and/or (e.g., and) one or more other modification compared with the specified sequence while retaining essentially same or similar complementary properties as the specified sequence.

[000389] The use of the terms "a" and "an" and "the" and similar referents in the context of describing the invention (especially in the context of the following claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted

by context. The terms "comprising," "having," "including," and "containing" are to be construed as open-ended terms (*i.e.*, meaning "including, but not limited to,") unless otherwise noted. Recitation of ranges of values herein are merely intended to serve as a shorthand method of referring individually to each separate value falling within the range, unless otherwise indicated herein, and each separate value is incorporated into the specification as if it were individually recited herein. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (*e.g.*, "such as") provided herein, is intended merely to better illuminate the invention and does not pose a limitation on the scope of the invention unless otherwise claimed. No language in the specification should be construed as indicating any non-claimed element as essential to the practice of the invention.

[000390] Embodiments of this invention are described herein. Variations of those embodiments may become apparent to those of ordinary skill in the art upon reading the foregoing description.

[000391] The inventors expect skilled artisans to employ such variations as appropriate, and the inventors intend for the invention to be practiced otherwise than as specifically described herein. Accordingly, this invention includes all modifications and equivalents of the subject matter recited in the claims appended hereto as permitted by applicable law. Moreover, any combination of the above-described elements in all possible variations thereof is encompassed by the invention unless otherwise indicated herein or otherwise clearly contradicted by context. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

CLAIMS

What is claimed is:

1. A complex comprising an anti-transferrin receptor 1 (TfR1) antibody covalently linked to an oligonucleotide configured for inducing skipping of exon 55 in a DMD pre-mRNA, wherein the oligonucleotide comprises a region of complementarity that is complementary with at least 8 consecutive nucleotides of any one of SEQ ID NOs: 160-779.

2. The complex of claim 1, wherein the anti-TfR1 antibody comprises:

(i) a heavy chain complementarity determining region 1 (CDR-H1) of SEQ ID NO: 33, a heavy chain complementarity determining region 2 (CDR-H2) of SEQ ID NO: 34, a heavy chain complementarity determining region 3 (CDR-H3) of SEQ ID NO: 35, a light chain complementarity determining region 1 (CDR-L1) of SEQ ID NO: 36, a light chain complementarity determining region 2 (CDR-L2) of SEQ ID NO: 37, and a light chain complementarity determining region 3 (CDR-L3) of SEQ ID NO: 32;

(ii) a CDR-H1 of SEQ ID NO: 7, a CDR-H2 of SEQ ID NO: 8, a CDR-H3 of SEQ ID NO: 9, a CDR-L1 of SEQ ID NO: 10, a CDR-L2 of SEQ ID NO: 11, and a CDR-L3 of SEQ ID NO: 6;

(iii) a CDR-H1 of SEQ ID NO: 7, a CDR-H2 of SEQ ID NO: 20, a CDR-H3 of SEQ ID NO: 9, a CDR-L1 of SEQ ID NO: 10, a CDR-L2 of SEQ ID NO: 11, and a CDR-L3 of SEQ ID NO: 6;

(iv) a CDR-H1 of SEQ ID NO: 7, a CDR-H2 of SEQ ID NO: 24, a CDR-H3 of SEQ ID NO: 9, a CDR-L1 of SEQ ID NO: 10, a CDR-L2 of SEQ ID NO: 11, and a CDR-L3 of SEQ ID NO: 6;

(v) a CDR-H1 of SEQ ID NO: 51, a CDR-H2 of SEQ ID NO: 52, a CDR-H3 of SEQ ID NO: 53, a CDR-L1 of SEQ ID NO: 54, a CDR-L2 of SEQ ID NO: 55, and a CDR-L3 of SEQ ID NO: 50;

(vi) a CDR-H1 of SEQ ID NO: 64, a CDR-H2 of SEQ ID NO: 52, a CDR-H3 of SEQ ID NO: 53, a CDR-L1 of SEQ ID NO: 54, a CDR-L2 of SEQ ID NO: 55, and a CDR-L3 of SEQ ID NO: 50; or

(vii) a CDR-H1 of SEQ ID NO: 67, a CDR-H2 of SEQ ID NO: 52, a CDR-H3 of SEQ ID NO: 53, a CDR-L1 of SEQ ID NO: 54, a CDR-L2 of SEQ ID NO: 55, and a CDR-L3 of SEQ ID NO: 50.

3. The complex of claim 1 or claim 2, wherein the anti-TfR1 antibody comprises:

(i) a heavy chain variable region (VH) comprising an amino acid sequence at least 85% identical to SEQ ID NO: 76; and/or a light chain variable region (VL) comprising an amino acid sequence at least 85% identical to SEQ ID NO: 75;

(ii) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 69; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 70;

(iii) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 71; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 70;

(iv) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 72; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 70;

(v) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 73; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 74;

(vi) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 73; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 75;

(vii) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 76; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 74;

(viii) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 77; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 78;

(ix) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 79; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 80; or

(x) a VH comprising an amino acid sequence at least 85% identical to SEQ ID NO: 77; and/or a VL comprising an amino acid sequence at least 85% identical to SEQ ID NO: 80.

4. The complex of any one of claims 1 to 3, wherein the anti-TfR1 antibody comprises:

(i) a VH comprising the amino acid sequence of SEQ ID NO: 76 and a VL comprising the amino acid sequence of SEQ ID NO: 75;

(ii) a VH comprising the amino acid sequence of SEQ ID NO: 69 and a VL comprising the amino acid sequence of SEQ ID NO: 70;

(iii) a VH comprising the amino acid sequence of SEQ ID NO: 71and a VL comprising the amino acid sequence of SEQ ID NO: 70;

(iv) a VH comprising the amino acid sequence of SEQ ID NO: 72 and a VL comprising the amino acid sequence of SEQ ID NO: 70;

(v) a VH comprising the amino acid sequence of SEQ ID NO: 73 and a VL comprising the amino acid sequence of SEQ ID NO: 74;

(vi) a VH comprising the amino acid sequence of SEQ ID NO: 73 and a VL comprising the amino acid sequence of SEQ ID NO: 75;

(vii) a VH comprising the amino acid sequence of SEQ ID NO: 76 and a VL comprising the amino acid sequence of SEQ ID NO: 74;

(viii) a VH comprising the amino acid sequence of SEQ ID NO: 77 and a VL comprising the amino acid sequence of SEQ ID NO: 78;

(ix) a VH comprising the amino acid sequence of SEQ ID NO: 79 and a VL comprising the amino acid sequence of SEQ ID NO: 80; or

(x) a VH comprising the amino acid sequence of SEQ ID NO: 77 and a VL comprising the amino acid sequence of SEQ ID NO: 80.

5. The complex of any one of claims 1 to 4, wherein the anti-TfR1 antibody is a Fab fragment, a Fab' fragment, a F(ab')2 fragment, an scFv, an Fv, or a full-length IgG.

6. The complex of claim 5, wherein the anti-TfR1 antibody is a Fab fragment.

7. The complex of claim 6, wherein the anti-TfR1 antibody comprises:

(i) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 101; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 90;

(ii) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 97; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 85;

(iii) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 98; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 85;

(iv) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 99; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 85;

(v) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 100; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 89;

(vi) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 100; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 90;

(vii) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 101; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 89;

(viii) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 102; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 93;

(ix) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 103; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 95; or

(x) a heavy chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 102; and/or a light chain comprising an amino acid sequence at least 85% identical to SEQ ID NO: 95.

8. The complex of claim 6 or claim 7, wherein the anti-TfR1 antibody comprises:

(i) a heavy chain comprising the amino acid sequence of SEQ ID NO: 101; and a light chain comprising the amino acid sequence of SEQ ID NO: 90;

(ii) a heavy chain comprising the amino acid sequence of SEQ ID NO: 97; and a light chain comprising the amino acid sequence of SEQ ID NO: 85;

(iii) a heavy chain comprising the amino acid sequence of SEQ ID NO: 98; and a light chain comprising the amino acid sequence of SEQ ID NO: 85;

(iv) a heavy chain comprising the amino acid sequence of SEQ ID NO: 99; and a light chain comprising the amino acid sequence of SEQ ID NO: 85;

(v) a heavy chain comprising the amino acid sequence of SEQ ID NO: 100; and a light chain comprising the amino acid sequence of SEQ ID NO: 89;

(vi) a heavy chain comprising the amino acid sequence of SEQ ID NO: 100; and a light chain comprising the amino acid sequence of SEQ ID NO: 90;

(vii) a heavy chain comprising the amino acid sequence of SEQ ID NO: 101; and a light chain comprising the amino acid sequence of SEQ ID NO: 89;

(viii) a heavy chain comprising the amino acid sequence of SEQ ID NO: 102; and a light chain comprising the amino acid sequence of SEQ ID NO: 93;

(ix) a heavy chain comprising the amino acid sequence of SEQ ID NO: 103; and a light chain comprising the amino acid sequence of SEQ ID NO: 95; or

(x) a heavy chain comprising the amino acid sequence of SEQ ID NO: 102; and a light chain comprising the amino acid sequence of SEQ ID NO: 95.

9. The complex of any one of claims 1 to 8, wherein the anti-TfR1 antibody does not specifically bind to the transferrin binding site of the transferrin receptor 1 and/or wherein the anti-TfR1 antibody does not inhibit binding of transferrin to the transferrin receptor 1.

10. The complex of any one of claims 1 to 9, wherein the oligonucleotide comprises a region of complementarity to at least 4 consecutive nucleotides of a splicing feature of the DMD pre-mRNA.

11. The complex of claim 10, wherein the splicing feature is an exonic splicing enhancer (ESE) in exon 55 of the DMD pre-mRNA, optionally wherein the ESE comprises a sequence of any one of SEQ ID NOs: 2031-2061.

12. The complex of claim 10, wherein the splicing feature is a branch point, a splice donor site, or a splice acceptor site, optionally wherein the splicing feature is across the junction of exon 54 and intron 54, in intron 54, across the junction of intron 54 and exon 55, across the junction of exon 55 and intron 55, in intron 55, or across the junction of intron 55 and exon 56 of the DMD pre-mRNA, and further optionally wherein the splicing feature comprises a sequence of any one of SEQ ID NOs: 2028-2030, 2062, and 2063.

13. The complex of any one of claims 1 to 9, wherein the oligonucleotide comprises a sequence complementary to any one of SEQ ID NOs: 160-779 or comprises a sequence of any one of SEQ ID NOs: 780-2019, wherein each thymine base (T) may independently and optionally be replaced with a uracil base (U), and each U may independently and optionally be replaced with a T.

14. The complex of any one of claims 1 to 9, wherein the oligonucleotide comprises a sequence of any one of SEQ ID NOs: 1400, 1402-1406, 1408, 1409, 1413, 1418-1420, 1483-1491, 1493, 1495, 1496, 1502-1506, 1508, 1510-1512, 1514, 1522-1524, 1529-1531, 1534, 1535, 1559, 1583, 1587, 1591, 1596, 1597, 1598, 1604, 1606, 1607, 1638, 1641, 1693-1695, 1702, 1703, 1766, 1813, 1988, and 1995, wherein each thymine base (T) may independently and optionally be replaced with a uracil base (U), and each U may independently and optionally be replaced with a T.

15. The complex of any one of claims 1 to 14, wherein the oligonucleotide comprises one or more phosphorodiamidate morpholinos, optionally wherein the oligonucleotide is a phosphorodiamidate morpholino oligomer (PMO).

16. The complex of any one of claims 1 to 15, wherein the anti-TfR1 antibody is covalently linked to the oligonucleotide via a cleavable linker, optionally wherein the cleavable linker comprises a valine-citrulline sequence.

17. The complex of any one of claims 1 to 16, wherein the anti-TfR1 antibody is covalently linked to the oligonucleotide via conjugation to a lysine residue or a cysteine residue of the antibody.

18. An oligonucleotide that targets DMD, wherein the oligonucleotide comprises a region of complementarity to any one of SEQ ID NOs: 160-779, optionally wherein the region of complementarity comprises at least 15 consecutive nucleosides complementary to any one of SEQ ID NOs: 160-779.

19. The oligonucleotide of claim 18, wherein the oligonucleotide comprises at least 15 consecutive nucleosides of any one of SEQ ID NOs: 780-2019, optionally wherein the oligonucleotide comprises a sequence of any one of SEQ ID NOs: 780-2019, wherein each thymine base (T) may independently and optionally be replaced with a uracil base (U), and each U may independently and optionally be replaced with a T.

20. A method of delivering an oligonucleotide to a cell, the method comprising contacting the cell with the complex of any one of claims 1 to 17 or with the oligonucleotide of claim 18 or claim 19.

21. A method of promoting the expression or activity of a dystrophin protein in a cell, the method comprising contacting the cell with the complex of any one of claims 1 to 17 or with the oligonucleotide of claim 18 or claim 19 in an amount effective for promoting internalization of the oligonucleotide to the cell, optionally wherein the cell is a muscle cell.