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

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
06 December 2018 (06.12.2018)

W!P O | PCT

(10) International Publication Number
WO 2018/222926 Al

(51) International Patent Classification:
C12N 9/10 (2006.01) *C07K 14/81* (2006.01)
C07K 14/505 (2006.01)

(21) International Application Number:
PCT/US20 18/035477

(22) International Filing Date:
31 May 2018 (31.05.2018)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/5 13,350 31 May 2017 (31.05.2017) US

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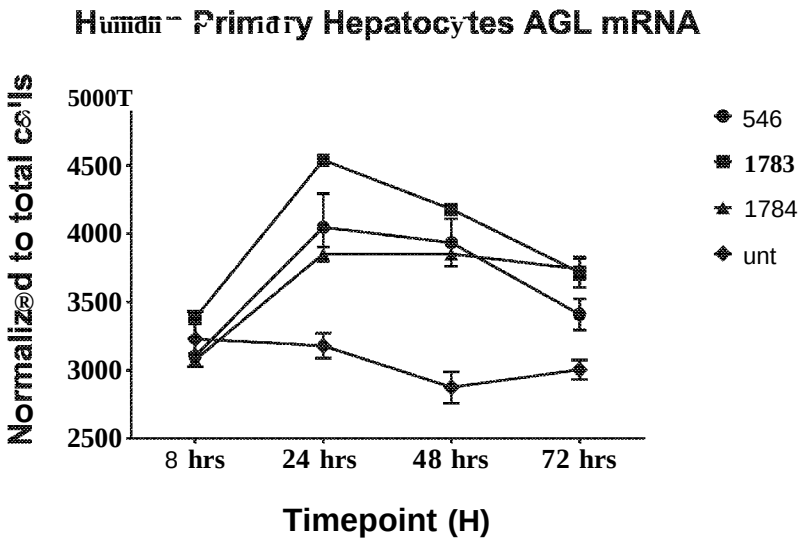
(81) Designated States *(unless otherwise indicated, for every kind of national protection available):* AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME,

(54) Title: THERAPEUTICS FOR GLYCOGEN STORAGE DISEASE TYPE III

FIG. 5



(57) Abstract: This invention provides a range of translatable polynucleotide and oligomer molecules for expressing a human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL), or a fragment thereof having AGL activity. The polynucleotide and oligomer molecules are expressible to provide the human AGL or a fragment thereof having AGL activity. The molecules can be used as active agents to express an active polypeptide or protein in cells or subjects. The agents can be used in methods for ameliorating, preventing, delaying onset, or treating a disease or condition associated with reduced activity of amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL) in a subject.

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[Continued on next page]

MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

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

Declarations under Rule 4.17:

— *as to applicant's entitlement to apply for and be granted a patent (Rule 4.1 7(H))*

Published:

— *with international search report (Art. 21(3))*

— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*

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

THERAPEUTICS FOR GLYCOGEN STORAGE DISEASE TYPE III

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Application Serial No. 62/513,350, filed May 31, 2017, which is herein incorporated by reference in its entirety for all purposes.

TECHNICAL FIELD OF THE INVENTION

[0002] This invention relates to the fields of molecular biology and genetics, as well as to biopharmaceuticals and therapeutics generated from translatable molecules. More particularly, this invention relates to methods, structures and compositions for molecules having the ability to be translated into active polypeptides or proteins, for use *in vivo* and as therapeutics.

DESCRIPTION OF TEXT FILE SUBMITTED ELECTRONICALLY

[0003] The contents of the text file submitted electronically herewith are incorporated herein by reference in their entirety: A computer readable format copy of the Sequence Listing (filename: ULPI_041_01WO_SeqList_ST25.txt, date recorded: May 30, 2018, file size: 226 kilobytes).

BACKGROUND OF THE INVENTION

[0004] Glycogen storage disease type III (also known as GSD III or Cori disease) is a rare (incidence 1:100,000) inborn error of glycogen metabolism caused by the deficiency of a glycogen debranching enzyme known as amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL). This autosomal recessive metabolic disorder is characterized by variable liver, cardiac muscle, and skeletal muscle involvement.

[0005] There are four subtypes GSD III, based on differences in tissue expression of the deficient enzyme, AGL. GSD Ilia accounts for approximately 85% of all GSD III and presents with liver and muscle involvement, resulting from enzyme deficiency in both liver and muscle. GSDIIIb accounts for approximately 15% and generally presents with only liver involvement, resulting from enzyme deficiency in the liver only. Meanwhile, GSDIIIc and GSDIIId are both extremely rate, with GSDIIIc believed to result from a deficiency of glucosidase debranching activity and GSDIIId believed to result from a deficiency of the transferase debranching activity.

[0006] In infancy and early childhood, liver involvement presents as ketotic hypoglycemia, hepatomegaly, hyperlipidemia, and elevated hepatic transaminases. In adolescence and adulthood, liver disease becomes less prominent. Hypertrophic cardiomyopathy develops in the majority of those with GSD Ilia, usually during childhood. Its clinical significance ranges from asymptomatic in the majority to severe cardiac dysfunction, congestive heart failure, and, rarely, sudden death. Skeletal myopathy manifesting as weakness is not usually evident in childhood, but slowly progresses, typically becoming prominent in adults.

[0007] In agreement with the organs affected, enhanced alanine transaminase (ALT), aspartate transaminase (AST), alkaline phosphatase (ALP), and/or creatine phosphokinase (CPK) activities are frequently present in the serum of GSD III patients.

[0008] As noted above, GSD III is caused by a deficiency in AGL. This deficiency is generally attributed to inherited mutation(s) of the AGL gene, which results in partial or total abolishment of AGL enzyme activity in a subject afflicted with GSD III. Molecular analyses of the AGL protein in GSD III patients have been performed in several ethnic populations, and over 100 different AGL mutations have been described. *See* Goldstein *et al.*, 2010, *Genet. Med.* 12: 424-430. *See also* Sentner *et al*, 2013, *JIMD Rep.* 7: 19-26.

[0009] There is presently no effective treatment of GSD III. Attempts have been made to control hypoglycemia with frequent meals high in carbohydrates, often via the use of nocturnal gastric drip feedings or cornstarch supplements. Meanwhile, patients with myopathy have been treated with diets high in protein during the daytime plus overnight enteral infusions. Transient improvement in symptoms has been documented in a few patients but there is no long-term data demonstrating that the high protein diet prevents or treats the progressive myopathy. *See* Chen YT, Burchell A, Glycogen storage disease. In: Scriver CR, Beaudet AL, Sly WS, Valle D, *The metabolic and molecular basis of inherited disease.* New York: McGraw Hill, 1995: 935-65. The progressive myopathy and/or cardiomyopathy is a major cause of morbidity in adults, and patients presenting with progressive liver cirrhosis and hepatic carcinoma have been reported. Thus, there is an urgent need for therapy which can address the underlying cause of this disease, *i.e.*, the deficiency of AGL enzyme activity.

[0010] To date, enzyme replacement has not been explored in diseases in which the defective enzyme is present in the cytosol, such as AGL in GSD III, presumably due to the lack of an efficient and specific cellular uptake mechanism that delivers exogenous enzyme across the plasma membrane into the cytoplasm.

[0011] The present invention addresses the above-mentioned needs by providing molecules, structures, and compositions that have the ability to be translated in the cytoplasm to provide active AGL, which can ameliorate, prevent or treat a disease or condition associated with AGL deficiency, such as GSD III.

SUMMARY OF THE INVENTION

[0012] This invention provides compositions comprising novel molecules having the ability to be translated, which can be used to provide one or more active polypeptides and proteins, or fragments thereof. The invention further provides methods of using these compositions comprising novel molecules for the prevention or treatment of various disorders. More specifically, embodiments of this invention provide compositions comprising translatable molecules to provide active amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL) and methods of using the compositions for the treatment of GSD III.

[0013] The translatable molecules of this invention can have functional cytoplasmic activity for producing AGL polypeptides or proteins. The peptides and proteins may be active for therapeutic modalities.

[0014] The translatable molecules of this invention can have long half-life, particularly in the cytoplasm of a cell. The translatable molecules can be expressible to provide a product that is active for ameliorating, preventing or treating a disease or condition associated with an AGL deficiency.

[0015] This disclosure provides a range of structures for translatable molecules for producing AGL polypeptides or proteins. In some embodiments, the translatable molecules can have an increased ability to be translated and/or an extended half-life over a native mRNA.

[0016] The translatable molecules of this invention can be used in medicines, and for methods and compositions for producing and delivering active polypeptides and proteins. The translatable molecules of this invention can be used to provide polypeptides or proteins *in vitro, ex vivo,* or *in vivo.*

[0017] Embodiments of this disclosure provide a range of novel polynucleotides for expressing a human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL), or a fragment thereof having AGL activity. The polynucleotides can include natural nucleotides and chemically modified nucleotides. The polynucleotides can be expressible to provide a human AGL or a fragment thereof having AGL activity.

[0018] In further aspects, this invention provides a range of novel translatable oligomers comprising one or more unlocked nucleic acid (UNA) monomers for expressing a human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL), or a fragment thereof having AGL activity. A translatable oligomer can contain one or more UNA monomers, along with natural nucleotides and chemically modified nucleotides. A translatable oligomer comprising one or more UNA monomers can be expressible to provide the human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL), or a fragment thereof having AGL activity.

[0019] In certain aspects, the translatable molecules of this invention can provide high-efficiency expression of a polypeptide or protein, or a fragment thereof. The expression can be *in vitro, ex vivo,* or *in vivo.*

[0020] In some embodiments, a molecule of this invention can have increased cytoplasmic half-life over a native, mature mRNA that encodes the same polypeptide or protein. The inventive molecules and compositions can provide increased functional cellular activity with respect to a native, mature mRNA.

[0021] In further aspects, a translatable molecule of this invention can provide increased activity as a drug agent providing a peptide or protein product, as compared to a native, mature mRNA. A translatable molecule of this invention may reduce the dose level required for efficacious therapy.

[0022] Embodiments of this invention include the following.

BRIEF DESCRIPTION OF THE DRAWINGS

[0023] FIG. 1 shows the results of expressing human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL, NM_000028) *in vitro* using translatable molecules of this invention. FIG. 1 shows the relative expression of AGL in AML12 and C2C12 cells normalized to reference molecule 534. The vertical axis reflects the fold-increase relative to the reference, *e.g.,* 10 being a 10-fold increase over the reference. The molecules, including the reference molecule, comprise a tobacco etch virus (TEV) 5' UTR and XenopusXenopus beta-globin (XBG) 3' UTR. The molecules were capped during transcription and synthesized with N^1-methylpseudouridine, so that 100% of uridines were replaced with N'-methylpseudouridine. The translatable molecules encoding AGL were transfected in two cell lines (AML12, C2C12). Cells were lysed and harvested at 6 h post-transfection. Quantitative Western Blot was performed to detect AGL by using an antibody specific for AGL (abl33720, rabbit).

[0024] FIG. 2 shows the results of expressing human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL, NM_000028) *in vitro* using translatable molecules of this invention. FIG. 2 shows the relative expression of AGL in AML12 and C2C12 cells normalized to reference molecule 534. The vertical axis reflects the fold-increase relative to the reference, *e.g.*, 10 being a 10-fold increase over the reference. The molecules, including the reference molecule, comprise a tobacco etch virus (TEV) 5' UTR and Xenopus beta-globin (XBG) 3' UTR. The molecules were capped during transcription and synthesized with N^1-methylpseudouridine, so that 100% of uridines were replaced with N'-methylpseudouridine. The translatable molecules encoding AGL were transfected in two cell lines (AML12, C2C12). Cells were lysed and harvested at 24 h post-transfection. Quantitative Western Blot was performed to detect AGL by using an antibody specific for AGL (abl33720, rabbit).

[0025] FIG. 3 shows the results of expressing human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL, NM_000028) *in vivo* using translatable molecules of this invention. FIG. 3 shows the relative expression of AGL in WT mice for translatable molecules 528 and 534 (reference) at timepoints 24 h and 48 h. The molecules comprise a tobacco etch virus (TEV) 5' UTR and Xenopus beta-globin (XBG) 3' UTR. The molecules were capped during transcription and synthesized with N'-methylpseudouridine, so that 100% of uridines were replaced with N'-methylpseudouridine. The translatable molecules encoding AGL were each prepared in a lipid nanonparticle formulation and intravenously injected into WT mice at 10 mg/kg. Mice livers were harvested at 24 h and 48 h, and Quantitative Western Blot was performed to detect AGL by using an antibody specific for AGL (abl33720, rabbit).

[0026] FIG. 4 shows the results of expressing human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL, NM_000028) *in vivo* using translatable molecules of this invention. FIG. 4 shows the relative liver expression of AGL in WT mice post-dose of translatable molecules 525, 527, 528, 529, and 546, as compared to baseline PBS (100). The synthesized translatable molecules 525, 527, 528, 529, and 546 encoding AGL were prepared in a lipid nanoparticle formulation and injected via IP in WT mice. Dose injected was 10 mpk, and livers were collected at 6 h for further analysis. Quantitative Western Blot was performed to detect AGL by using an antibody specific for AGL (abl 33720, rabbit).

[0027] FIG. 5 shows the result of expressing human AGL from three translatable molecules: 546, 1783, and 1784. Human primary hepatocytes were transfected with codon-optimized mRNA and AGL protein expression was measured by In-Cell Western™ at 6, 24, 48, and 72

hours post-transfection. The expression of the mRNA sequences was compared with an untreated control ("unt").

[0028] FIG. 6 shows expression of human AGL from various mRNA molecules formulated with lipid nanoparticles in wild-type C57BL/6 mice. The protein concentration (ng/mg) of exogenous human AGL expressed from the mRNA molecules in homogenates from liver biopsy samples was determined by a multiple reaction monitoring assay. The translatable molecules shown in the graph as 546.1, 736.1, 738.1, 737.1, 731.1, and 1783.1 are the same as 546, 736, 738, 737, 731, and 1783, respectively, as described in Example 2. Meanwhile, the translatable molecule 546.7 has the same nucleobase sequence as 546, which is described in Example 2, but was synthesized with 5-methoxyuridine in place of uridine instead of N^1-methylpseudouridine, which was used to synthesize translatable molecule 546.

[0029] FIG. 7 shows expression of endogenous mouse AGL in wild-type C57BL/6 mice treated with various mRNA molecules formulated with lipid nanoparticles. The protein concentration (ng/mg) of endogenous mouse AGL expressed in homogenates from liver biopsy samples was determined by a multiple reaction monitoring assay. The translatable molecules shown in the graph as 546.1, 736.1, 738.1, 737.1, 731.1, and 1783.1 are the same as 546, 736, 738, 737, 731, and 1783, respectively, as described in Example 2. Meanwhile, the translatable molecule 546.7 has the same nucleobase sequence as 546, which is described in Example 2, but was synthesized with 5-methoxyuridine in place of uridine instead of N^1-methylpseudouridine, which was used to synthesize translatable molecule 546.

[0030] FIG. 8 shows the histopathology of a liver from an AGL knockout mice treated with vehicle ("VEH"). Marked to severe vacuolation of hepatocytes and moderate to marked increases in glycogen accumulation was observed within hepatocytes treated with vehicle.

[0031] FIG. 9 shows the histopathology of a liver from an AGL knockout mice treated with translatable molecule 546 formulated with ATX2 lipid nanoparticles. Only mild to moderate vacuolation of hepatocytes and only mild to moderate increases in glycogen accumulation within hepatocytes was observed within hepatocytes treated with translatable molecule 546 formulated with ATX2 lipid nanoparticles.

DETAILED DESCRIPTION OF THE INVENTION

[0032] This invention provides a range of novel agents and compositions to be used for therapeutic applications. The molecules and compositions of this invention can be used for

ameliorating, preventing or treating GSD III and/or a disease associated reduced presence or function of amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL) in a subject.

[0033] In some embodiments, this invention encompasses synthetic, purified, translatable polynucleotide molecules for expressing a human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase. The molecules may contain natural and chemically modified nucleotides, and encode the human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL), or a fragment thereof having AGL activity.

[0034] In certain embodiments, this disclosure includes synthetic, purified, translatable oligomer molecules comprising one or more UNA monomers for expressing a human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL), or a fragment thereof having AGL activity. A translatable oligomer may contain one or more UNA monomers, as well as natural and chemically-modified nucleotides. A translatable oligomer comprising one or more UNA monomers can be expressible to provide the human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL), or a fragment thereof having AGL activity.

[0035] As used herein, the term "translatable" may be used interchangeably with the term "expressible" and refers to the ability of polynucleotide, or a portion thereof, to be converted to a polypeptide by a host cell. As is understood in the art, translation is the process in which ribosomes in a cell's cytoplasm create polypeptides. In translation, messenger RNA (mRNA) is decoded by tRNAs in a ribosome complex to produce a specific amino acid chain, or polypeptide. Furthermore, the term "translatable" when used in this specification in reference to an oligomer, means that at least a portion of the oligomer, *e.g.,* the coding region of an oligomer sequence (also known as the coding sequence or CDS), is capable of being converted to a protein or a fragment thereof.

[0036] As used herein, the term "monomer" refers to a single unit, *e.g.* , a single nucleic acid, which may be joined with another molecule of the same or different type to form an oligomer. In some embodiments, a monomer may be an unlocked nucleic acid, *i.e.,* a UNA monomer.

[0037] Meanwhile, the term "oligomer" may be used interchangeably with "polynucleotide" and refers to a molecule comprising at least two monomers and includes oligonucleotides such as DNAs and RNAs. In the case of oligomers containing RNA monomers and/or unlocked nucleic acid (UNA) monomers, the oligomers of the present invention may contain sequences in addition to the coding sequence (CDS). These additional sequences may be untranslated sequences, *i.e.,* sequences which are not converted to protein by a host cell. These untranslated

sequences can include a 5' cap, a 5' untranslated region (5' UTR), a 3' untranslated region (3' UTR), and a tail region, *e.g.,* a polyA tail region. As described in further detail herein, any of these untranslated sequences may contain one or more UNA monomers - these UNA monomers are not capable of being translated by a host cell's machinery. In the context of the present invention, a "translatable oligomer", a "translatable molecule", "translatable polynucleotide", or "translatable compound" refers to a sequence that comprises a region, *e.g.,* the coding region of an RNA *(e.g.,* the coding sequence of human AGL or a codon-optimized version thereof), that is capable of being converted to a protein or a fragment thereof, *e.g.,* the human AGL protein or a fragment thereof.

[0038] As used herein, the term "codon-optimized" means a natural (or purposefully designed variant of a natural) coding sequence which has been redesigned by choosing different codons without altering the encoded protein amino acid sequence increasing the protein expression levels (Gustafsson et al, *Codon bias and heterologous protein expression.* 2004, Trends Biotechnol 22: 346-53). Variables such as high codon adaptation index (CAI), LowU method, mRNA secondary structures, cis-regulatory sequences, GC content and many other similar variables have been shown to somewhat correlate with protein expression levels (Villalobos et al., *Gene Designer: a synthetic biology tool for constructing artificial DNA segments.* 2006, BMC Bioinformatics 7:285). High CAI (codon adaptation index) method picks a most frequently used synonymous codon for an entire protein coding sequence. The most frequently used codon for each amino acid is deduced from 74218 protein-coding genes from a human genome. The LowU method targets only Li-containing codons that can be replaced with a synonymous codon with fewer U moieties. If there are a few choices for the replacement, the more frequently used codon will be selected. The remaining codons in the sequence are not changed by the LowU method. This method may be used in conjunction with the disclosed mRNAs to design coding sequences that are to be synthesized with 5-methoxyuridine.

[0039] As will be appreciated by the skilled artisan equipped with the present disclosure, the translatable molecules of the present invention may be used to ameliorate, prevent, or treat any disease or disorder associated with reduced activity *(e.g.,* resulting from reduced concentration, presence, and/or function) of amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL) in a subject. In some embodiments, the translatable molecules of this invention can be used in methods for ameliorating, preventing or treating one or more of GSD Ilia, GSD Illb, GSDIIIc, and GSDIIId (collectively or individually referred to herein as "GSD III" or "glycogen storage

disease type III"). The disease or disorder to be treated herein *(e.g.,* GSD Ilia, GSD Illb, GSDIIIc, or GSDIIId) may be associated with low blood sugar (hypoglycemia), enlargement of the liver (hepatomegaly), excessive amounts of fat in the blood (hyperlipidemia), elevated blood levels of liver enzymes, chronic liver disease (cirrhosis), liver failure, slow growth, short stature, benign tumors (adenomas), hypertrophic cardiomyopathy, cardiac dysfunction, congestive heart failure, skeletal myopathy, and/or poor muscle tone (hypotonia). In some embodiments, the translatable molecules of the present invention may be used to ameliorate, prevent, or treat any or all of these aforementioned symptoms.

[0040] As is understood by the skilled artisan, GSD III may be referred to by any number of alternative names in the art, including, but not limited to, AGL deficiency, Cori disease, Cori's disease, debrancher deficiency, Forbes disease, glycogen debrancher deficiency, GSD3, or limit dextrinosis (due to the limit dextrin-like structures in the cytosol). Accordingly, GSD III may be used interchangeably with any of these alternative names in the specification, the examples, the drawings, and the claims.

[0041] A translatable molecule of this invention encoding a functional AGL moiety can be delivered to the liver, in particular to hepatocytes, of a patient in need (e.g., a GSD III patient), and can elevate active AGL levels of the patient. The translatable molecule can be used for preventing, treating, ameliorating or reversing any symptoms of GSD III in the patient.

[0042] In further aspects, a translatable molecule of this invention can also be used for reducing the dependence of a GSD III patient on a particular diet to control the disease. For instance, a translatable molecule of this invention can be used to reduce a GSD III patient's dependence on frequent high carbohydrate meals and/or diets abnormally high in protein.

[0043] Embodiments of this invention further encompass processes for making a translatable molecule for expressing a human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL). The processes include transcribing *in vitro* an AGL DNA template in the presence of natural and chemically-modified nucleoside triphosphates to form a product mixture, and purifying the product mixture to isolate the translatable molecule. A translatable molecule may also be made by methods as are known in the art.

[0044] The molecules of this invention can be translatable molecules containing RNA and/or UNA monomers. These translatable molecules can have long half-life, particularly in the cytoplasm. The long duration translatable molecules can be used for ameliorating, preventing, or treating disease or disorder associated with reduced activity (e.g., resulting from reduced

concentration, presence, and/or function) of amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL) in a subject.

[0045] The properties of the translatable molecules of this invention arise according to their molecular structure, and the structure of the molecule in its entirety, as a whole, can provide significant benefits based on those properties. Embodiments of this invention can provide translatable molecules having one or more properties that advantageously provide enhanced protein concentration or increased protein activity. The molecules and compositions of this invention can provide formulations comprising therapeutic agents for ameliorating, preventing, or treating any disease or disorder associated with reduced activity *(e.g.*, resulting from reduced concentration, presence, and/or function) of amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL) in a subject.

[0046] This invention provides a range of translatable molecules that are surprisingly translatable to provide active polypeptide or protein, *in vitro, ex vivo,* and *in vivo.*

[0047] A translatable molecule of this invention is expressible to provide one or more active polypeptides or proteins, or fragments thereof.

[0048] The translatable structures and compositions can have increased translational activity or cytoplasmic half-life. In these embodiments, the translatable structures and compositions can provide increased functional half-life in the cytoplasm of mammalian cells, as compared to a native mRNA.

[0049] As used herein, the term "half-life" is the time required for a quantity such as nucleic acid or protein concentration or activity to fall to half of its value as measured at the beginning of a time period.

[0050] A range of structures for translatable molecules of this invention are provided herein, including oligomers containing one or more UNA monomers. An oligomer containing one or more UNA monomers can incorporate specialized linker groups. The linker groups can be attached in a chain in the translatable molecule. Each linker group can also be attached to a nucleobase.

[0051] In some aspects, a linker group can be a monomer. Monomers can be attached to form a chain molecule. In a chain molecule of this invention, a linker group monomer can be attached at any point in the chain.

[0052] In certain aspects, linker group monomers can be attached in a chain molecule of this invention so that the linker group monomers reside near the ends of the chain, or at any position in the chain.

[0053] In further aspects, the linker groups of a chain molecule can each be attached to a nucleobase. The presence of nucleobases in the chain molecule can provide a sequence of nucleobases in the chain molecule.

[0054] In certain embodiments, this invention provides translatable oligomer molecules having chain structures that incorporate novel combinations of the linker group monomers, along with certain natural nucleotides, or non-natural nucleotides, or modified nucleotides, or chemically modified nucleotides.

[0055] The oligomer molecules of this invention can display a sequence of nucleobases, and can be designed to express a polypeptide or protein, *in vitro, ex vivo,* or *in vivo.* The expressed polypeptide or protein can have activity in various forms, including activity corresponding to a protein expressed from a natural, native or wild type mRNA, or activity corresponding to a negative or dominant negative protein.

[0056] In some aspects, this invention can provide active, translatable oligomer molecules having a base sequence that is identical to at least a fragment of a native nucleic acid molecule of a cell.

[0057] In some embodiments, the cell can be a eukaryotic cell, a mammalian cell, or a human cell.

[0058] This invention provides structures, methods and compositions for translatable oligomeric agents that incorporate the linker group monomers. The oligomeric molecules of this invention can be used as active agents in formulations for therapeutics.

[0059] This invention provides a range of translatable molecules that are useful for providing therapeutic effects because of their ability to be expressed as polypeptide or protein in a cell in a subject.

[0060] In certain embodiments, a translatable molecule can be structured as an oligomer composed of monomers. The oligomeric structures of this invention may contain one or more linker group monomers, along with certain nucleotides.

[0061] In certain embodiments, a translatable molecule may contain a sequence of nucleobases, and can be designed to express a peptide or protein of any isoform, in part by having sufficient homology with a native polynucleotide sequence.

[0062] In some embodiments, a translatable molecule can be from about 200 to about 12,000 monomers in length, or more. In certain embodiments, a translatable molecule can be from 1,000 to 9,000 monomers in length, from 3,000 to 7,000 monomers in length, or from 4,000 to 6,000 monomers in length. In an exemplary embodiment, the translatable molecule is from 4,500 to 5,500 monomers in length. In a further exemplary embodiment, the translatable molecule is about 5,000 monomers in length.

[0063] In some embodiments, a translatable molecule can contain from 1 to about 800 UNA monomers. In certain embodiments, a translatable molecule can contain from 1 to 600 UNA monomers, or 1 to 100 UNA monomers, or 1 to 12 UNA monomers.

[0064] In some embodiments, a translatable molecule can contain from 1 to about 800 locked nucleic acid (LNA) monomers. In certain embodiments, a translatable molecule can contain from 1 to 600 LNA monomers, or 1 to 100 LNA monomers, or 1 to 12 LNA monomers.

[0065] A translatable molecule of this invention may comprise a 5' cap, a 5' untranslated region of monomers, a coding region of monomers, a 3' untranslated region of monomers, and a tail region of monomers.

[0066] A translatable molecule of this invention may comprise a 3' untranslated region of monomers containing one or more UNA monomers.

[0067] A translatable molecule of this invention may comprise a tail region of monomers containing one or more UNA monomers.

[0068] A translatable molecule of this invention may comprise regions of sequences or structures that are operable for translation in a cell, or which have the functionality of regions of an mRNA including, for example, a 5' cap, a 5' untranslated region, a coding region, a 3' untranslated region, and a polyA tail.

[0069] This invention further contemplates methods for delivering one or more vectors comprising one or more translatable molecules to a cell. In further embodiments, the invention also contemplates delivering or one or more translatable molecules to a cell.

[0070] In some embodiments, one or more translatable molecules can be delivered to a cell, *in vitro, ex vivo,* or *in vivo.* Viral and non-viral transfer methods as are known in the art can be

used to introduce translatable molecules in mammalian cells. Translatable molecules can be delivered with a pharmaceutically acceptable vehicle, or for example, with nanoparticles or liposomes.

[0071] In some embodiments, translatable structures and compositions of this invention can reduce the number and frequency of transfections required for cell-fate manipulation in culture as compared to utilizing native compositions.

[0072] In further aspects, this invention provides increased activity for translatable molecules as active agent, as compared to utilizing a native mRNA.

[0073] In some aspects, this invention can provide translatable molecules that may reduce the cellular innate immune response, as compared to that induced by a native nucleic acid, polypeptide or protein.

[0074] This invention can provide synthetic translatable molecules that are refractory to deadenylation as compared to native molecules.

[0075] In certain embodiments, this invention can provide synthetic translatable molecules with increased specific activity and longer functional half-life as compared to native molecules. The synthetic translatable molecules of this invention can provide increased levels of ectopic protein expression. When expressing a translatable molecule using a vector, cellular-delivery can be at increased levels, and cytotoxic innate immune responses can be restrained so that higher levels of ectopic protein expression can be achieved. The translatable molecules of this invention can have increased specific activity and longer functional half-life than native mRNAs.

[0076] In certain aspects, a translatable molecule may have a number of mutations relative to a native mRNA.

[0077] In further embodiments, this invention can provide translatable molecules having cleavable delivery and targeting moieties attached at a 3' end and/or a 5' end.

[0078] In general, the specific activity for a synthetic translatable molecule delivered by transfection can be viewed as the number of molecules of protein expressed per delivered transcript per unit time.

[0079] As used herein, translation efficiency refers to a measure of the production of a protein or polypeptide by translation of a translatable molecule *in vitro* or *in vivo.*

[0080] This invention provides a range of translatable oligomer molecules, which can contain one or more UNA monomers, and a number of nucleic acid monomers, wherein the translatable molecule can be expressible to provide a polypeptide or protein.

[0081] In some embodiments, this invention includes a range of translatable oligomer molecules, which can contain one or more UNA monomers in one or more untranslated regions, and a number of nucleic acid monomers, wherein the translatable molecule can be expressible to provide a polypeptide or protein.

[0082] In some embodiments, this invention includes a range of translatable molecules, which contain one or more UNA monomers in a tail region, and a number of nucleic acid monomers, wherein the translatable molecule can be expressible to provide a polypeptide or protein.

[0083] In some embodiments, a translatable molecule can contain a modified 5' cap.

[0084] In further embodiments, a translatable molecule can contain a translation enhancing 5' untranslated region of monomers.

[0085] In additional embodiments, a translatable molecule can contain a translation enhancing 3' untranslated region of monomers.

[0086] In additional embodiments, a translatable molecule can contain one or more UNA monomers in a 3' untranslated region of monomers.

[0087] In further embodiments, a translatable molecule can contain one or more UNA monomers in a tail region of monomers.

[0088] In further embodiments, a translatable molecule can contain one or more UNA monomers in a polyA tail.

[0089] In some embodiments, a translatable molecule can contain one or more LNA monomers in a 3' untranslated region of monomers or in a tail region of monomers, *e.g.*, in a polyA tail.

[0090] In another aspect, a translatable molecule of this invention can exhibit at least 2-fold, 3-fold, 5-fold, or 10-fold increased translation efficiency *in vivo* as compared to anative mRNA that encodes the same translation product.

[0091] In a further aspect, a translatable molecule can produce at least a 2-fold, 3-fold, 5-fold, or 10-fold increased polypeptide or protein level *in vivo* as compared to a native mRNA that encodes the same polypeptide or protein.

[0092] In certain embodiments, a translatable molecule can provide increased levels of a polypeptide or protein *in vivo* as compared to a native mRNA that encodes the same polypeptide or protein. For example, the level of a polypeptide or protein can be increased by 10%, or 20%, or 30%, or 40%, or 50%, or more.

[0093] In additional embodiments, this invention provides methods for treating a disease or condition in a subject by administering to the subject a composition containing a translatable molecule of the invention.

[0094] A translatable molecule of this invention may be used for ameliorating, preventing or treating a disease or disorder, *e.g.,* a disease or disorder associated with reduced activity (e.g., resulting from reduced concentration, presence, and/or function) of amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL) in a subject. In these embodiments, a composition comprising a translatable molecule of this invention can be administered to regulate, modulate, or increase the concentration or effectiveness of the AGL enzyme in a subject. In some aspects, the enzyme can be an unmodified, natural enzyme for which the patient has an abnormal quantity (e.g., a patient with a mutated version of AGL which partially or totally abolishes AGL activity). In some aspects, the enzyme can be an unmodified, natural AGL enzyme which can be used to treat a patient harboring a mutated version of AGL. In exemplary embodiments, a translatable molecule of this invention may be used for ameliorating, preventing or treating GSD III.

[0095] In some embodiments, a translatable molecule may be delivered to cells or subjects, and translated to increase AGL levels in the cell or subject.

[0096] As used herein, the term "subject" refers to a human or any non-human animal (e.g., mouse, rat, rabbit, dog, cat, cattle, swine, sheep, horse or primate). A human includes pre- and post-natal forms. In many embodiments, a subject is a human being. A subject can be a patient, which refers to a human presenting to a medical provider for diagnosis or treatment of a disease. The term "subject" is used herein interchangeably with "individual" or "patient." A subject can be afflicted with or is susceptible to a disease or disorder but may or may not display symptoms of the disease or disorder.

[0097] In an exemplary embodiment, a subject of the present invention is a subject with reduced activity (e.g., resulting from reduced concentration, presence, and/or function) of amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL). In a further exemplary embodiment, the subject is a human.

[0098] In some embodiments, administering a composition comprising a translatable molecule of the invention can result in increased liver AGL protein levels in a treated subject. In some embodiments, administering a composition comprising a translatable molecule of the invention results in about a 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 95% increase in liver AGL protein levels relative to a baseline AGL protein level in the subject prior to treatment. In an exemplary embodiment, administering a composition comprising a translatable molecule of the invention results in an increase in liver AGL levels relative to baseline liver AGL levels in the subject prior to treatment. In some embodiments, the increase in liver AGL levels can be at least about 5%, 10%, 20%, 30%, 40%, 50%, 100%, 200%, or more.

[0099] In some embodiments, the AGL protein which is expressed from a translatable molecule of the invention is detectable in the liver, serum, plasma, kidney, heart, muscle, brain, cerebrospinal fluid, or lymph nodes. In exemplary embodiments, the AGL protein is expressed in the liver cells, *e.g.,* hepatocytes of a treated subject.

[00100] In some embodiments, administering a composition comprising a translatable molecule of the invention results in the expression of a natural, non-mutated human AGL *(i.e.*, normal or wild-type AGL as opposed to abnormal or mutated AGL) protein level at or above about 10 ng/mg, about 20 ng/mg, about 50 ng/mg, about 100 ng/mg, about 150 ng/mg, about 200 ng/mg, about 250 ng/mg, about 300 ng/mg, about 350 ng/mg, about 400 ng/mg, about 450 ng/mg, about 500 ng/mg, about 600 ng/mg, about 700 ng/mg, about 800 ng/mg, about 900 ng/mg, about 1000 ng/mg, about 1200 ng/mg or about 1500 ng/mg of the total protein in the liver of a treated subject.

[00101] As used herein, the term "about" or "approximately" 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 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).

[00102] In some embodiments, the expression of the natural, non-mutated human AGL protein is detectable 6, 12, 18, 24, 30, 36, 48, 60, and/or 72 hours after administration of a composition comprising a translatable molecule of the invention. In some embodiments, the expression of the natural, non-mutated human AGL protein is detectable 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, and/or 7 days after administration of a composition comprising a translatable molecule of the invention. In some embodiments, the expression of the natural, non-mutated human AGL protein is detectable 1 week, 2 weeks, 3 weeks, and/or 4 weeks after the administration. In some embodiments, the expression of the natural, non-mutated human AGL protein is detectable after administration of a composition comprising a translatable molecule of the invention. In some embodiments, expression of natural, non-mutated human AGL protein is detectable in the liver, *e.g.,* hepatocytes, after administration of a composition comprising a translatable molecule of the invention.

Variant Templates for Making Translatable Molecules

[00103] In various embodiments described herein, the translatable oligomer may comprise a mRNA encoding AGL, wherein the mRNA encoding AGL is codon-optimized. In some embodiments, the AGL is human AGL *(i.e.,* hAGL). In some embodiments, the human AGL comprises an amino acid sequence of SEQ ID NO: 2. In some embodiments, the human AGL consists of an amino acid sequence of SEQ ID NO: 2.

[00104] In some embodiments, a variant DNA template may be utilized to make a translatable molecule capable of encoding AGL. A variant DNA template of this disclosure may exhibit advantages in processes for making a translatable molecule, and the efficiency of the translatable molecule. Variation of the template can be utilized to enhance incorporation of modified nucleotides or monomers in a translatable molecule of this invention. In certain aspects, variation of the template can be utilized to enhance the structural features of the translatable molecule. The enhanced structural features of the translatable molecule can provide unexpectedly advantageous properties, including translation efficiency to provide a polypeptide or protein product.

[00105] In some aspects of this invention, variation of the template may include reducing the occurrence or frequency of appearance of certain nucleotides in the template strand. Reducing the occurrence of a certain nucleotide can alter the structures and processes of this

disclosure to provide non-native forms, which achieve surprisingly improved properties of a translatable RNA product encoding AGL.

[00106] Aspects of this invention may require a variant DNA template in processes for making a translatable molecule. A DNA molecule can have a non-coding template strand of nucleotides that can be transcribed to provide a target translatable molecule encoding AGL.

[00107] A target translatable molecule can be any RNA, whether native or modified, synthetic or derived from a natural source.

[00108] In some embodiments, a variant DNA template can be used for which an open reading frame of the template strand is transformed to an alternative form, while preserving codon assignment.

[00109] In certain embodiments, a DNA template can be used for which alternative nucleotides are used based on alternative codon optimization and/or sequence degeneracy.

[00110] In additional embodiments, a DNA template may have certain nucleotides replaced with alternative nucleotides, while preserving codon assignment.

[00111] Embodiments of this invention advantageously utilize alternative codons in a DNA template of this invention to be used in processes for making a translatable molecule encoding AGL. The variations that can be achieved in a DNA template of this invention can be far greater in scope than for cells and organisms, which may require preferred codons in many processes. In this invention, a wide range of alternative codons and positions can be used in a DNA template for transcribing a translatable molecule.

[00112] In further aspects of this invention, variation of the template may include reducing the occurrence or frequency of appearance of certain nucleotides in the template strand. For example, the occurrence of a nucleotide in a template may be reduced to a level below 25% of nucleotides in the template. In further examples, the occurrence of a nucleotide in a template may be reduced to a level below 20% of nucleotides in the template. In some examples, the occurrence of a nucleotide in a template may be reduced to a level below 16% of nucleotides in the template. In certain examples, the occurrence of a nucleotide in a template may be reduced to a level below 12% of nucleotides in the template.

Human AGL

[00113] The human AGL gene encodes a 1532 amino acid protein with a molecular mass of approximately 174.8 kDa. AGL is a multifunctional enzyme acting as a 1,4-alpha-D-glucan:l,4-alpha-D-glucan-4-alpha-D-glycosyltransferase and an amylo-l,6-glucosidase in glycogen degradation. As noted above, genetic deficiency of normal AGL activity causes glycogen storage disease III.

[00114] The consensus human AGL coding sequence has an RNA sequence of 4,599 nucleobases, shown in SEQ ID NO: 1.

[00115] The consensus human AGL coding sequence - found at NCBI Accession No. NP_000019.2 - translates into SEQ ID NO: 2.

[00116] In some embodiments, a translatable molecule can be made and used for expressing human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (hAGL) with advantageously increased efficiency of translation, as compared to a native mRNA of hAGL. The translatable molecule expressing hAGL may exhibit activity suitable for use in methods for ameliorating, preventing or treating disease. In some embodiments, the translatable molecule may comprise one or more UNA monomers.

[00117] In some embodiments, a translatable molecule may include a 5' cap, a 5' UTR, a translation initiation sequence, ***e.g.***, a Kozak sequence, a human AGL CDS, a 3'UTR, and/or a tail region. In an exemplary embodiment, a translatable molecule may include a 5' cap (m7GpppGm), a 5' UTR of tobacco etch virus (TEV), a Kozak sequence, a human AGL CDS, a 3' UTR of Xenopus beta-globin, and a tail region. In further exemplary embodiments, the human AGL CDS may comprise a codon-optimized sequence of SEQ ID NOs: 7-32 or SEQ ID NOs: 41-45, described in further detail below. In any of these and other embodiments described herein, the translatable molecule may comprise one or more UNA monomers. In any of these and other embodiments described herein, the translatable molecule may comprise one or more LNA monomers.

[00118] The translation efficiency of the molecule can be increased as compared to a native mRNA of AGL. In particular, after 48 hours, the translation efficiency of the molecule may be more than doubled as compared to the native mRNA of AGL.

[00119] In some embodiments, a suitable mRNA sequence for the present invention comprises an mRNA sequence encoding the human AGL protein. The sequence of the naturally occurring human AGL protein is shown in SEQ ID NO: 2.

[00120] In some embodiments, a suitable mRNA sequence may be an mRNA sequence that encodes a homolog or variant of human AGL. As used herein, a homolog or a variant of human AGL protein may be a modified human AGL protein containing one or more amino acid substitutions, deletions, and/or insertions as compared to a wild-type or naturally-occurring human AGL protein while retaining substantial AGL protein activity. In some embodiments, an mRNA suitable for the present invention encodes a protein substantially identical to human AGL protein. In some embodiments, an mRNA suitable for the present invention encodes an amino acid sequence at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to SEQ ID NO: 2. In some embodiments, an mRNA suitable for the present invention encodes a fragment or a portion of human AGL protein.

[00121] In some embodiments, an mRNA suitable for the present invention encodes a fragment or a portion of human AGL protein, wherein the fragment or portion of the protein still maintains AGL activity similar to that of the wild-type protein.

[00122] In some embodiments, an mRNA suitable for the present invention comprises a sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to SEQ ID NOs: 7-32 or SEQ ID NOs: 41-45.

[00123] In some embodiments, a translatable oligomeric molecule of the present invention comprises a coding sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to SEQ ID NOs: 7-32 or SEQ ID NOs: 41-45. In some embodiments, a translatable oligomeric molecule comprising a coding sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to SEQ ID NOs: 7-32 or SEQ ID NOs: 41-45 further comprises one or more sequences selected from a 5' cap, a 5' UTR, a translation initiation sequence, a 3' UTR, and a tail region.

[00124] In some embodiments, a translatable oligomeric molecule of the present invention comprises a coding sequence that is less than 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the wild-type human AGL coding sequence over the full length human AGL coding sequence of SEQ ID NO: 1, and expresses a functional human AGL protein. In an exemplary embodiment, a translatable oligomeric molecule of the present invention comprises a coding sequence that is less than 80% identical to the wild-type human AGL coding sequence over the full length human AGL coding sequence of SEQ ID NO: 1, and expresses a functional human AGL protein. In another exemplary embodiment, a

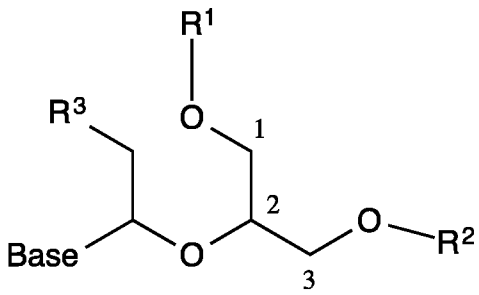
translatable oligomeric molecule of the present invention comprises a coding sequence that is less than 80% identical to the wild-type human AGL coding sequence over the full length human AGL coding sequence of SEQ ID NO: 1, and expresses a functional human AGL protein, wherein the coding sequence is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to a sequence selected from SEQ ID NOs: 7-32 or SEQ ID NOs: 41-45. In yet another exemplary embodiment, a translatable oligomeric molecule of the present invention comprises a coding sequence that is less than 80% identical to the wild-type human AGL coding sequence over the full length human AGL coding sequence of SEQ ID NO: 1, and expresses a functional human AGL protein, wherein the coding sequence is at least 95% identical to a sequence selected from SEQ ID NOs: 7-32 or SEQ ID NOs: 41-45. In yet another exemplary embodiment, a translatable oligomeric molecule of the present invention comprises a coding sequence that is less than 80% identical to the wild-type human AGL coding sequence over the full length human AGL coding sequence of SEQ ID NO: 1, and expresses a functional human AGL protein, wherein the coding sequence is at least 95% identical to a sequence selected from SEQ ID NO: 19, SEQ ID NO: 31, or SEQ ID NO: 45. Accordingly, in some embodiments, the present application provides a polynucleotide comprising of or consisting of a nucleobase sequence that is less than 80% identical to the wild-type human AGL coding sequence over the full length human AGL coding sequence of SEQ ID NO: 1, and wherein the human AGL coding sequence is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to a sequence selected from SEQ ID NOs: 7-32 or SEQ ID NOs: 41-45. In an exemplary embodiment, the present application provides a polynucleotide comprising of or consisting of a nucleobase sequence that is less than 80% identical to the wild-type human AGL coding sequence over the full length human AGL coding sequence of SEQ ID NO: 1, and wherein the human AGL coding sequence is at least 95% identical to a sequence selected from SEQ ID NO: 19, SEQ ID NO: 31, or SEQ ID NO: 45. In a specific embodiment, the present application provides a polynucleotide comprising of a nucleobase sequence that is less than 80% identical to the wild-type human AGL coding sequence over the full length human AGL coding sequence of SEQ ID NO: 1, and wherein the human AGL coding sequence is at least 95% identical to SEQ ID NO: 19. In another specific embodiment, the present application provides a polynucleotide comprising of a nucleobase sequence that is less than 80% identical to the wild-type human AGL coding sequence over the full length human AGL coding sequence of SEQ ID NO: 1, and wherein the human AGL coding sequence is at least 95% identical to SEQ ID NO: 31. In another specific embodiment, the present application provides a polynucleotide comprising of a nucleobase

sequence that is less than 80% identical to the wild-type human AGL coding sequence over the full length human AGL coding sequence of SEQ ID NO: 1, and wherein the human AGL coding sequence is at least 95% identical to SEQ ID NO: 45.

[00125] In some embodiments, a translatable oligomeric molecule of the invention encodes a fusion protein comprising a full length, fragment or portion of a AGL protein fused to another sequence *(e.g.* , an N or C terminal fusion). In some embodiments, the N or C terminal sequence is a signal sequence or a cellular targeting sequence.

UNA Monomers and Oligomers

[00126] In some embodiments, linker group monomers can be unlocked nucleomonomers (UNA monomers), which are small organic molecules based on a propane-1,2,3-tri-yl-trisoxy structure as shown below:

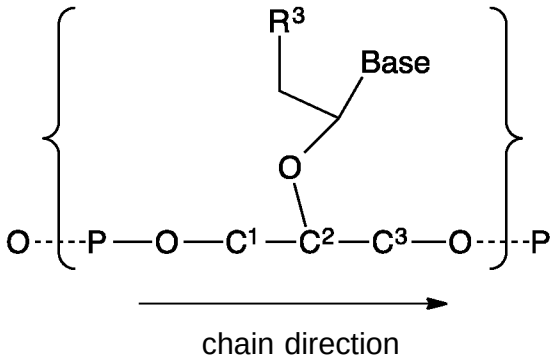


UNA MONOMER

where R^1 and R^2 are H, and R^1 and R^2 can be phosphodiester linkages, Base can be a nucleobase, and R^3 is a functional group described below.

[00127] In another view, the UNA monomer main atoms can be drawn in IUPAC notation as follows:

UNA monomer unit



where the direction of progress of the oligomer chain is from the 1-end to the 3-end of the propane residue.

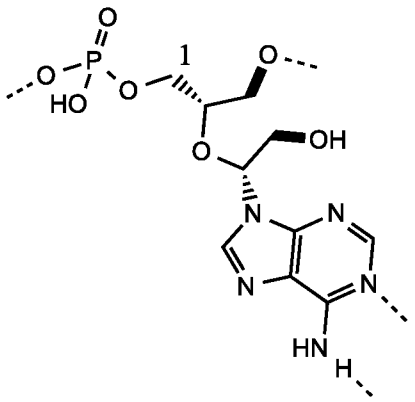
[00128] Examples of a nucleobase include uracil, thymine, cytosine, 5-methylcytosine, adenine, guanine, inosine, and natural and non-natural nucleobase analogues.

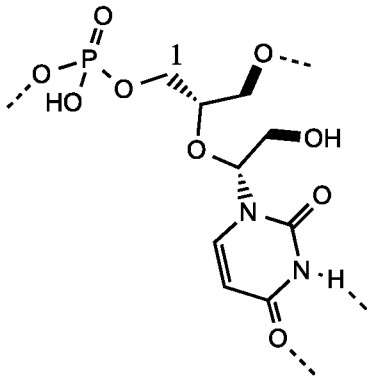
[00129] Examples of a nucleobase include pseudouracil, 1-methylpseudouracil (ηιΙΨ), ***i.e.,*** N^methylpseudouracil, and 5-methoxyuracil.

[00130] In general, a UNA monomer, which is not a nucleotide, can be an internal linker monomer in an oligomer. An internal UNA monomer in an oligomer is flanked by other monomers on both sides.

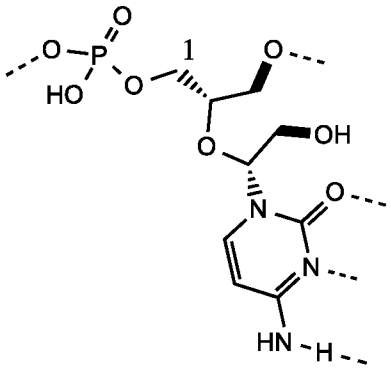
[00131] A UNA monomer can participate in base pairing when the oligomer forms a complex or duplex, for example, and there are other monomers with nucleobases in the complex or duplex.

[00132] Examples of UNA monomer as internal monomers flanked at both the propane-1-yl position and the propane-3-yl position, where **R^3** is **-OH,** are shown below.

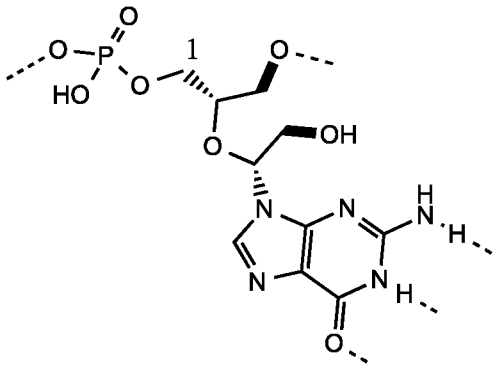




UNA-A



UNA-U

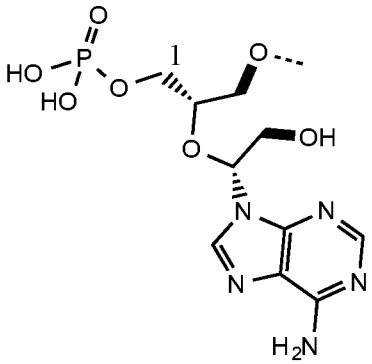


UNA-C

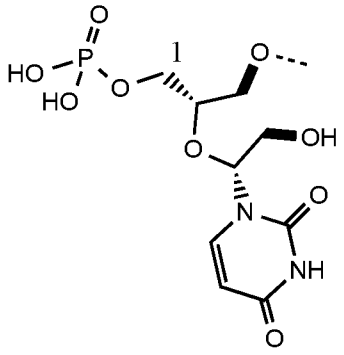
UNA-G

[00133] A UNA monomer can be a terminal monomer of an oligomer, where the UNA monomer is attached to only one monomer at either the propane-1-yl position or the propane-3-yl position. Because the UNA monomers are flexible organic structures, unlike nucleotides, the terminal UNA monomer can be a flexible terminator for the oligomer.

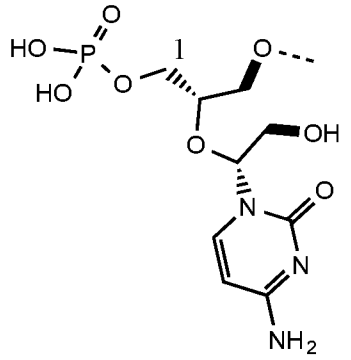
[00134] Examples of a UNA monomer as a terminal monomer attached at the propane-3-yl position are shown below.



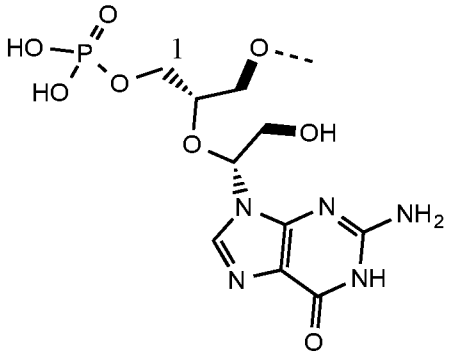
terminal UNA-A



terminal UNA-U

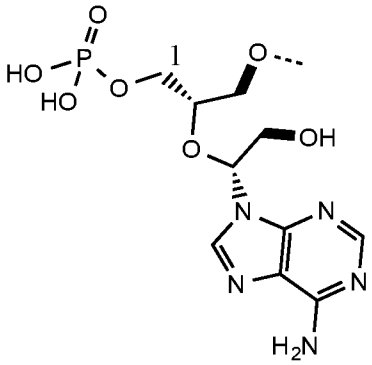


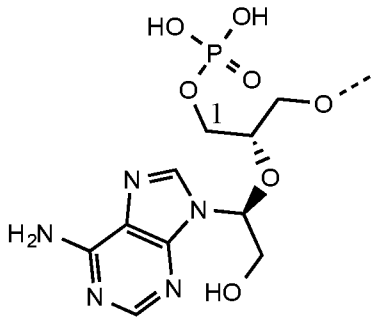
terminal UNA-C



terminal UNA-G

[00135] Because a UNA monomer can be a flexible molecule, a UNA monomer as a terminal monomer can assume widely differing conformations. An example of an energy minimized UNA monomer conformation as a terminal monomer attached at the propane-3-yl position is shown below.





UNA-A terminal forms: the dashed bond shows the propane-3-yl attachment

[00136] Among other things, the structure of the UNA monomer allows it to be attached to naturally-occurring nucleotides.

[00137] A UNA oligomer can be a chain composed of UNA monomers, as well as various nucleotides that may be based on naturally-occurring nucleosides.

[00138] In some embodiments, the functional group R^3 of a UNA monomer can be —OR^4, —SR^4, —NR^4_2, —NH(C=0)R^4, morpholino, morpholin-l-yl, piperazin-l-yl, or 4-alkanoyl-piperazin-l-yl, where R^4 is the same or different for each occurrence, and can be H, alkyl, a cholesterol, a lipid molecule, a polyamine, an amino acid, or a polypeptide.

[00139] The UNA monomers are organic molecules. UNA monomers are not nucleic acid monomers or nucleotides, nor are they naturally-occurring nucleosides or modified naturally-occurring nucleosides.

[00140] A UNA oligomer of this invention is a synthetic chain molecule.

[00141] In some embodiments, as shown above, a UNA monomer can be UNA-A (designated Ã), UNA-U (designated Ũ), UNA-C (designated Č), and UNA-G (designated Ğ).

[00142] Designations that may be used herein include mA, mG, mC, and mU, which refer to the 2'**-0** -Methyl modified ribonucleotides.

[00143] Designations that may be used herein include dT, which refers to a 2'-deoxy T nucleotide.

[00144] As used herein, in the context of oligomer sequences, the symbol N can represent any natural nucleotide monomer, or any modified nucleotide monomer.

[00145] As used herein, in the context of oligomer sequences, the symbol Q represents a non-natural, modified, or chemically-modified nucleotide monomer.

[00146] As used herein, in the context of oligomer sequences, the symbol X may be used to represent a UNA monomer.

Modified and Chemically-Modified Nucleotides

[00147] In the examples of modified or chemically-modified nucleotides herein, an alkyl, cycloalkyl, or phenyl substituent may be unsubstituted, or further substituted with one or more alkyl, halo, haloalkyl, amino, or nitro substituents.

[00148] Examples of nucleic acid monomers include non-natural, modified, and chemically-modified nucleotides, including any such nucleotides known in the art.

[00149] Examples of modified or chemically-modified nucleotides include 5-hydroxycytidines, 5-alkylcytidines, 5-hydroxyalkylcytidines, 5-carboxycytidines, 5-formylcytidines, 5-alkoxycytidines, 5-alkynylcytidines, 5-halocytidines, 2-thiocytidines, N^4-alkylcytidines, N^4-aminocytidines, N^4-acetylcytidines, and N^4,N^4-dialkylcytidines.

[00150] Examples of modified or chemically-modified nucleotides include 5-hydroxycytidine, 5-methylcytidine, 5-hydroxymethylcytidine, 5-carboxycytidine, 5-formylcytidine, 5-methoxycytidine, 5-propynylcytidine, 5-bromocytidine, 5-iodocytidine, 2-

thiocytidine; N^4-methylcytidine, N^4-aminocytidine, N^4-acetylcytidine, and N^4,N^4-dimethylcytidine.

[00151] Examples of modified or chemically-modified nucleotides include 5-hydroxyuridines, 5-alkyluridines, 5-hydroxyalkyluridines, 5-carboxyuridines, 5-carboxyalkylesteruridines, 5-formyluridines, 5-alkoxyuridines, 5-alkynyluridines, 5-halouridines, 2-thiouridines, and 6-alkyluridines.

[00152] Examples of modified or chemically-modified nucleotides include 5-hydroxyuridine, 5-methyluridine, 5-hydroxymethyluridine, 5-carboxyuridine, 5-carboxymethylesteruridine, 5-formyluridine, 5-methoxyuridine, 5-propynyluridine, 5-bromouridine, 5-fluorouridine, 5-iodouridine, 2-thiouridine, and 6-methyluridine.

[00153] Examples of modified or chemically-modified nucleotides include 5-methoxycarbonylmethy1-2-thiouridine, 5-methylaminomethy1-2-thiouridine, 5-carbamoylmethyluridine, 5-carbamoylmethy1-2'-**O**-methyluridine, l-methyl-3-(3-amino-3-carboxypropy)pseudouridine, 5-methylaminomethyl-2-selenouridine, 5-carboxymethyluridine, 5-methyldihydrouridine, 5-taurinomethyluridine, 5-taurinomethyl-2-thiouridine, 5-(isopentenylaminomethyl)uridine, 2'-**0** -methylpseudouridine, 2-thio-2'**0**-methyluridine, and 3,2'-**0** -dimethyluridine.

[00154] Examples of modified or chemically-modified nucleotides include N^6-methyladenosine, 2-aminoadenosine, 3-methyladenosine, 8-azaadenosine, 7-deazaadenosine, 8-oxoadenosine, 8-bromoadenosine, 2-methylthio-N^6-methyladenosine, N^6-isopentenyladenosine, 2-methylthio-N^6-isopentenyladenosine, N^6-(cis-hydroxyisopentenyl)adenosine, 2-methylthio-N^6-(cis-hydroxyisopentenyl)adenosine, N^6-glycinylcarbamoyladenosine, N6-threonylcarbamoyl-adenosine, N^6-methyl-N^6-threonylcarbamoyl-adenosine, 2-methylthio-N^6-threonylcarbamoyl-adenosine, N^6,N^6-dimethyladenosine, N6-hydroxynorvalylcarbamoyladenosine, 2-methylthio-N^6-hydroxynorvalylcarbamoyl-adenosine, N^6-acetyl-adenosine, 7-methyl-adenine, 2-methylthio-adenine, 2-methoxy-adenine, alpha-thio-adenosine, 2'-**0** -methyl-adenosine, N^6,2'-**0** -dimethyl-adenosine, N^6,N^6,2'-**0** -trimethyl-adenosine, l,2 '-**0** -dimethyl-adenosine, **2'-0**-ribosyladenosine, 2-amino-N^6-methyl-purine, 1-thio-adenosine, 2'-F-ara-adenosine, 2'-F-adenosine, 2'-**OH**-ara-adenosine, and N^6-(19-amino-pentaoxanonadecyl)-adenosine.

[00155] Examples of modified or chemically-modified nucleotides include N^1-alkylguanosines, N^2-alkylguanosines, thienoguanosines, 7-deazaguanosines, 8-oxoguanosines, 8-bromoguanosines, 0^6-alkylguanosines, xanthosines, inosines, and N'-alkylinosines.

[00156] Examples of modified or chemically-modified nucleotides include N^1-methylguanosine, N^2-methylguanosine, thienoguanosine, 7-deazaguanosine, 8-oxoguanosine, 8-bromoguanosine, 0^6-methylguanosine, xanthosine, inosine, and N'-methylinosine.

[00157] Examples of modified or chemically-modified nucleotides include pseudouridines. Examples of pseudouridines include N'-alkylpseudouridines, N^1-cycloalkylpseudouridines, N^hydroxypseudouridines, N^hydroxyalkylpseudouridines, N^1-phenylpseudouridines, N'-phenylalkylpseudouridines, N'-aminoalkylpseudouridines, N^3-alkylpseudouridines, N^6-alkylpseudouridines, N^6-alkoxypseudouridines, N^6-hydroxypseudouridines, N^6-hydroxyalkylpseudouridines, N^6-morpholinopseudouridines, N^6-phenylpseudouridines, and N^6-halopseudouridines. Examples of pseudouridines include N^1-alkyl-N^6-alkylpseudouridines, N^1-alkyl-N^6-alkoxypseudouridines, N'-alkyl-N^6-hydroxypseudouridines, N^1-alkyl-N^6-hydroxyalkylpseudouridines, N'-alkyl-N^6-morpholinopseudouridines, N^1-alkyl-N^6-phenylpseudouridines, and N'-alkyl-N^6-halopseudouri dines. In these examples, the alkyl, cycloalkyl, and phenyl substituents may be unsubstituted, or further substituted with alkyl, halo, haloalkyl, amino, or nitro substituents.

[00158] Examples of pseudouridines include N'-methylpseudouridine, N^1-ethylpseudouridine, N'-propylpseudouridine, N'-cyclopropylpseudouridine, N^1-phenylpseudouridine, N'-aminomethylpseudouridine, N^3-methylpseudouridine, N^1-hydroxypseudouridine, and N^hydroxymethylpseudouridine.

[00159] Examples of nucleic acid monomers include modified and chemically-modified nucleotides, including any such nucleotides known in the art.

[00160] Examples of modified and chemically-modified nucleotide monomers include any such nucleotides known in the art, for example, 2'-0-methyl ribonucleotides, 2'-0-methyl purine nucleotides, 2'-deoxy-2'-fluoro ribonucleotides, 2'-deoxy-2'-fluoro pyrimidine nucleotides, 2'-deoxy ribonucleotides, 2'-deoxy purine nucleotides, universal base nucleotides, 5-C-methyl-nucleotides, and inverted deoxyabasic monomer residues.

[00161] Examples of modified and chemically-modified nucleotide monomers include 3'-end stabilized nucleotides, 3'-glyceryl nucleotides, 3'-inverted abasic nucleotides, and 3'-inverted thymidine.

[00162] Examples of modified and chemically-modified nucleotide monomers include locked nucleic acid nucleotides (LNA), 2'-**0**,4'-C-methylene-(D-ribofuranosyl) nucleotides, 2'-methoxyethoxy (MOE) nucleotides, 2'-methyl-thio-ethyl, 2'-deoxy-2'-fluoro nucleotides, and 2'-**0**-methyl nucleotides. In an exemplary embodiment, the modified monomer is a locked nucleic acid nucleotide (LNA).

[00163] Examples of modified and chemically-modified nucleotide monomers include 2',4'-constrained 2'-**0**-methoxyethyl (cMOE) and 2'-**0**-Ethyl (cEt) modified DNAs.

[00164] Examples of modified and chemically-modified nucleotide monomers include 2'-amino nucleotides, 2'-**0**-amino nucleotides, 2'-C-allyl nucleotides, and 2'-**0**-allyl nucleotides.

[00165] Examples of modified and chemically-modified nucleotide monomers include N^6-methyladenosine nucleotides.

[00166] Examples of modified and chemically-modified nucleotide monomers include nucleotide monomers with modified bases 5-(3-amino)propyluridine, 5-(2-mercapto)ethyluridine, 5-bromouridine; 8-bromoguanosine, or 7-deazaadenosine.

[00167] Examples of modified and chemically-modified nucleotide monomers include 2'-**0**-aminopropyl substituted nucleotides.

[00168] Examples of modified and chemically-modified nucleotide monomers include replacing the 2'-OH group of a nucleotide with a 2'-R, a 2'-OR, a 2'-halogen, a 2'-SR, or a 2'-amino, where R can be H, alkyl, alkenyl, or alkynyl.

[00169] Some examples of modified nucleotides are given in Saenger, Principles of Nucleic Acid Structure, Springer-Verlag, 1984.

[00170] Example of base modifications described above can be combined with additional modifications of nucleoside or nucleotide structure, including sugar modifications and linkage modifications.

[00171] Certain modified or chemically-modified nucleotide monomers may be found in nature.

Translatable Molecules Containing One or More UNA Monomers

[00172] Aspects of this invention provide structures and compositions for translatable molecules that are oligomeric compounds containing one or more UNA monomers. The translatable oligomers can be active agents for pharmaceutical compositions. In some embodiments, the translatable oligomers encode human AGL or a variant thereof.

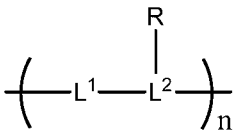
[00173] An oligomeric, translatable molecule of this invention may contain one or more UNA monomers. Oligomeric molecules of this invention can be used as active agents in formulations for supplying peptide and protein therapeutics. In some embodiments, the translatable oligomers encode human AGL or a variant thereof.

[00174] In some embodiments, this invention provides oligomeric, translatable compounds having a structure that incorporates novel combinations of UNA monomers with certain natural nucleotides, non-natural nucleotides, modified nucleotides, or chemically-modified nucleotides.

[00175] Translatable oligomeric compounds of this invention can have a length of from about 200 to about 12,000 bases in length. Translatable oligomeric compounds of this invention can have a length of about 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, or about 9000 bases. In some embodiments, translatable oligomeric compounds of this invention can have a length of about 4000, 4100, 4200, 4300, 4400, 4500, 4600, 4700, 4800, 4900, 5000, 5100, 5200, 5300, 5400, or about 5500 bases. In an exemplary embodiment, the translatable oligomeric compound of the invention has a length of about 5000 bases.

[00176] In further aspects, the oligomeric, translatable compounds of this invention which comprise one or more UNA monomers can be pharmacologically active molecules. A translatable oligomeric molecule can be used as an active pharmaceutical ingredient for generating a peptide or protein active agent *in vitro, in vivo,* or *ex vivo.* In an exemplary embodiment, the translatable oligomeric compound of this invention encodes human AGL or a variant thereof.

[00177] A translatable oligomeric molecule of this invention can have the structure of Formula I:



Formula I

wherein L^1 is a linkage, n is from 200 to 12,000, and for each occurrence L^2 is a UNA linker group having the formula $-C^1-C^2-C^3-$, where R is attached to C^2 and has the formula $-OCH(CH_2R^3)R^5$, where R^3 is $—OR^4$, $—SR^4$, $—NR^4_2$, $—NH(C=0)R^4$, morpholino, morpholin-1-yl, piperazin-l-yl, or 4-alkanoyl-piperazin-l -yl, where R^4 is the same or different for each occurrence and is H, alkyl, a cholesterol, a lipid molecule, a polyamine, an amino acid, or a polypeptide, and where R^5 is a nucleobase, or $L^2(R)$ is a sugar such as a ribose and R is a nucleobase, or L^2 is a modified sugar such as a modified ribose and R is a nucleobase. In certain embodiments, a nucleobase can be a modified nucleobase. L^1 can be a phosphodiester linkage.

[00178] The base sequence of a translatable oligomeric molecule can be any sequence of nucleobases.

[00179] In some aspects, a translatable oligomeric molecule of this invention can have any number of phosphorothioate intermonomer linkages in any intermonomer location.

[00180] In some embodiments, any one or more of the intermonomer linkages of a translatable oligomeric molecule can be a phosphodiester, a phosphorothioate including dithioates, a chiral phosphorothioate, and other chemically modified forms.

[00181] When a translatable oligomeric molecule terminates in a UNA monomer, the terminal position has a 1-end, or the terminal position has a 3-end, according to the positional numbering shown above.

Enhanced Translation

[00182] A translatable molecule of this invention can incorporate a region that enhances the translational efficiency of the molecule.

[00183] In general, translational enhancer regions as known in the art can be incorporated into the structure of a translatable molecule to increase peptide or protein yields.

[00184] A translatable molecule containing a translation enhancer region can provide increased production of peptide or protein.

[00185] In some embodiments, a translation enhancer region can comprise, or be located in a 5' or 3' untranslated region of a translatable molecule.

[00186] Examples of translation enhancer regions include naturally-occurring enhancer regions from TEV 5'UTR and Xenopus beta-globin 3'UTR.

Molecular Structures and Sequences

[00187] A translatable molecule can be designed to express a target peptide or protein. In some embodiments, the target peptide or protein can be associated with a condition or disease in a subject.

[00188] In some aspects, the base sequence of a translatable molecule can include a portion that is identical to at least an effective portion or domain of a base sequence of an mRNA, where an effective portion is sufficient to impart a therapeutic activity to a translation product of the translatable molecule.

[00189] In some aspects, this invention provides active translatable molecules having a base sequence identical to at least a fragment of a native nucleic acid molecule of a cell.

[00190] In certain embodiments, the base sequence of a translatable molecule can include a portion that is identical to a base sequence of an mRNA, except for one or more base mutations. The number of mutations for the translatable molecule should not exceed an amount that would produce a translation product of the translatable molecule having substantially less activity than the mRNA.

[00191] The oligomeric, translatable UNA molecules of this invention can display a sequence of nucleobases, and can be designed to express a peptide or protein, in vitro, ex vivo, or in vivo. The expressed peptide or protein can have activity in various forms, including activity corresponding to protein expressed from a native or natural mRNA.

[00192] In some embodiments, a translatable molecule of this invention may have a chain length of about 400 to 15,000 monomers, where any monomer that is not a UNA monomer can be an N or Q monomer.

Molecular Cay Structure

[00193] A translatable molecule of this invention may have a 5'-end capped with various groups and their analogues as are known in the art. In an exemplary embodiment, the 5' cap may be a m7GpppGm cap. In further embodiments, the 5' cap may be selected from m7GpppA, m7GpppC; unmethylated cap analogs **(e.g.**, GpppG); dimethylated cap analog **(e.g.**, m2,7GpppG), a trimethylated cap analog **(e.g.**, m2,2,7GpppG), dimethylated symmetrical cap analogs **(e**.g., m7Gpppm7G), or anti reverse cap analogs **(e**.g., ARCA; m7, 2'0meGpppG, m72'dGpppG, m7,3'OmeGpppG, m7,3'dGpppG and their tetraphosphate derivatives) *(see, e.g.*, Jemielity, J. et al, RNA 9: 1108-1122 (2003). In other embodiments, the 5' cap may be an ARCA cap (3'-OMe-m7G(5')pppG). The 5' cap may be an mCAP (m7G(5')ppp(5')G, N^7-Methyl-Guanosine-5'-Triphosphate-5'-Guanosine). The 5' cap may be resistant to hydrolysis.

[00194] Some examples of 5' cap structures are given in WO2015/051169A2, WO/2015/061491, and US Patent Nos. 8,093,367 and 8,304,529.

Tail Region

[00195] In some embodiments, the translatable oligomer encoding AGL comprises a tail region, which can serve to protect the mRNA from exonuclease degradation. In some embodiments, the tail region can be a polyA tail.

[00196] PolyA tails can be added using a variety of methods known in the art, **e**.g., using poly A polymerase to add tails to synthetic or *in vitro* transcribed RNA. Other methods include the use of a transcription vector to encode poly A tails or the use of a ligase **(e**.g., via splint ligation using a T4 RNA ligase and/or T4 DNA ligase), wherein polyA may be ligated to the 3' end of a sense RNA. In some embodiments, a combination of any of the above methods is utilized.

[00197] In some embodiments, a translatable oligomer comprises a 3' polyA tail structure. In some embodiments, the length of the polyA tail can be at least about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 200, or 300 nucleotides. In some embodiments, a 3' polyA tail contains about 5 to 300 adenosine nucleotides **(e**.g., about 30 to 250 adenosine nucleotides, about 60 to 220 adenosine nucleotides, about 80 to 200 adenosine nucleotides, about 90 to about 150 adenosine nucleotides, or about 100 to about 120 adenosine nucleotides). In an

exemplary embodiment, the 3' polyA tail is about 100 nucleotides in length. In another exemplary embodiment, the 3' polyA tail is about 115 nucleotides in length. In another exemplary embodiment, the 3' polyA tail is about 250 nucleotides in length.

[00198] In some embodiments, the 3' polyA tail comprises one or more UNA monomers. In some embodiments, the 3' polyA tail contains 2, 3, 4, 5, 10, 15, 20, or more UNA monomers. In an exemplary embodiment, the 3' polyA tail contains 2 UNA monomers. In a further exemplary embodiment, the 3' polyA tail contains 2 UNA monomers which are found consecutively, *i.e.,* contiguous to each other in the 3' polyA tail.

[00199] In an exemplary embodiment, the 3' polyA tail comprises or consists of a sequence shown in SEQ ID NO: 6. In another exemplary embodiment, the 3' polyA tail comprises or consists of a sequence shown in SEQ ID NO: 38. In yet another exemplary embodiment, the 3' polyA tail comprises or consists of a sequence shown in SEQ ID NO: 39.

[00200] In some embodiments, the translatable oligomer comprises a 3' polyC tail structure. In some embodiments, the length of the polyC tail can be at least about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 200, or 300 nucleotides. In some embodiments, a 3' polyC tail contains about 5 to 300 cytosine nucleotides (e.g., about 30 to 250 cytosine nucleotides, about 60 to 220 cytosine nucleotides, about 80 to about 200 cytosine nucleotides, about 90 to 150 cytosine nucleotides, or about 100 to about 120 cytosine nucleotides). In an exemplary embodiment, the 3' polyC tail is about 100 nucleotides in length. In another exemplary embodiment, the 3' polyC tail is about 115 nucleotides in length. The polyC tail may be added to the polyA tail or may substitute the polyA tail. The polyC tail may be added to the 5' end of the polyA tail or the 3' end of the polyA tail.

[00201] In some embodiments, the length of the poly A and/or poly C tail is adjusted to control the stability of a modified translatable oligomeric molecule of the invention and, thus, the transcription of protein. For example, since the length of the polyA tail can influence the half-life of a translatable molecule, the length of the polyA tail can be adjusted to modify the level of resistance of the mRNA to nucleases and thereby control the time course of polynucleotide expression and/or polypeptide production in a target cell.

5' and 3' Untranslated Regions (UTRs)

[00202] In some embodiments, the translatable oligomer encoding AGL may comprise a 5' untranslated region and/or a 3' untranslated region. As is understood in the art, the 5'

and/or 3' UTR may affect an mRNA's stability or efficiency of translation. In an exemplary embodiment, the translatable oligomer comprises a 5' UTR and a 3' UTR.

[00203] In some embodiments, the translatable oligomer may comprise a 5' UTR that is at least about 25, 50, 75, 100, 125, 150, 175, 200, 300, 400, or 500 nucleotides. In some embodiments, a 5' UTR contains about 50 to 300 nucleotides (e.g., about 75 to 250 nucleotides, about 100 to 200 nucleotides, about 120 to 150 nucleotides, or about 135 nucleotides). In an exemplary embodiment, the 5' UTR is about 135 nucleotides in length.

[00204] In some embodiments, the 5' UTR is derived from an mRNA molecule known in the art to be relatively stable (e.g., histone, tubulin, globin, GAPDH, actin, or citric acid cycle enzymes) to increase the stability of the translatable oligomer. In other embodiments, a 5' UTR sequence may include a partial sequence of a CMV immediate-early 1 (IE1) gene. Examples of 5' UTR sequences may be found in US Patent No. 9,149,506. In some embodiments, the 5' UTR comprises a sequence selected from the 5' UTRs of human IL-6, alanine aminotransferase 1, human apolipoprotein E, human fibrinogen alpha chain, human transthyretin, human haptoglobin, human alpha-1-antichymotrypsin, human antithrombin, human alpha-1-antitrypsin, human albumin, human beta globin, human complement C3, human complement C5, SynK, AT1G58420, mouse beta globin, mouse albumin, and a tobacco etch virus, or fragments of any of the foregoing. In an exemplary embodiment, the 5' UTR is derived from a tobacco etch virus (TEV). In a further exemplary embodiment, the 5' UTR comprises or consists of a sequence set forth in SEQ ID NO: 3. In yet another exemplary embodiment, the 5' UTR is a fragment of a sequence set forth in SEQ ID NO: 3, such as a fragment of at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, or 125 contiguous nucleotides of SEQ ID NO: 3.

[00205] In some embodiments, the translatable oligomeric molecule comprises an intemal ribosome entry site (IRES). As is understood in the art, an IRES is an RNA element that allows for translation initiation in an end-independent manner. In exemplary embodiments, the IRES is in the 5' UTR. In other embodiments, the IRES may be outside the 5' UTR.

[00206] In some embodiments, the translatable oligomer may comprise a 3' UTR that is at least about 25, 50, 75, 100, 125, 150, 175, 200, 300, 400, or 500 nucleotides. In some embodiments, a 3' UTR contains about 50 to 300 nucleotides (e.g., about 75 to 250 nucleotides,

about 100 to 200 nucleotides, about 140 to 175 nucleotides, or about 160 nucleotides). In an exemplary embodiment, the 3' UTR is about 160 nucleotides in length.

[00207] In some embodiments, the 3' UTR comprises one or more UNA monomers. In some embodiments, the 3' UTR contains 2, 3, 4, 5, 10, 15, 20, or more UNA monomers.

[00208] Examples of 3' UTR sequences may be found in US Patent No. 9,149,506. In some embodiments, the 3' UTR comprises a sequence selected from the 3' UTRs of alanine aminotransferase 1, human apolipoprotein E, human fibrinogen alpha chain, human haptoglobin, human antithrombin, human alpha globin, human betaglobin, human complement C3, human growth factor, human hepcidin, MALAT-1, mouse beta globin, mouse albumin, and Xenopus beta globin, or fragments of any of the foregoing In an exemplary embodiment, the 3' UTR is derived from Xenopus beta globin. In another exemplary embodiment, the 3' UTR is derived from Xenopus beta globin and contains one or more UNA monomers. In a further exemplary embodiment, the 3' UTR comprises or consists of a sequence set forth in SEQ ID NOs: 5 and 33-37. In yet another exemplary embodiment, the 3' UTR is a fragment of a sequence set forth in SEQ ID NOs: 5 and 33-37, such as a fragment of at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 contiguous nucleotides of SEQ ID NO: 5 and 33-37.

[00209] In certain exemplary embodiments, the translatable oligomer encoding AGL comprises a 5' UTR sequence of SEQ ID NO: 3 and a 3' UTR sequence selected from SEQ ID NOs: 5 and 33-37. In some embodiments, the translatable oligomer encoding AGL further comprises a polyA tail shown in SEQ ID NO: 6, SEQ ID NO: 38, or SEQ ID NO: 39. In some embodiments, the mRNA coding sequence of AGL comprises a sequence selected from SEQ ID NOs: 7-32 or SEQ ID NOs: 41-45.

Triple Stop Codon

[00210] In some embodiments, the translatable oligomer encoding AGL may comprise a sequence immediately downstream of the CDS that creates a triple stop codon. The triple stop codon may be incorporated to enhance the efficiency of translation. In some embodiments, the transatable oligomer may comprise the sequence AUAAGUGAA (SEQ ID NO: 40) immediately downstream of a PAH CDS described herein, as exemplified in SEQ ID NOs: 7-32 or SEQ ID NOs: 41-45.

Translation Initiation Sites

[00211] In some embodiments, the translatable oligomer encoding AGL may comprise a translation initiation site. Such sequences are known in the art and include the Kozak sequence. See, for example, Kozak, Marilyn (1988) Mol. and Cell Biol, 8:2737-2744; Kozak, Marilyn (1991) J. Biol. Chem, 266:19867-19870; Kozak, Marilyn (1990) Proc Natl. Acad. Sci. USA, 87:8301-8305; and Kozak, Marilyn (1989) J. Cell Biol, 108:229-241; and the references cited therein. As is understood in the art, a Kozak sequence is a short consensus sequence centered around the translational initiation site of eukaryotic mRNAs that allows for efficient initiation of translation of the mRNA. The ribosomal translation machinery recognizes the AUG initiation codon in the context of the Kozak sequence.

[00212] In some embodiments, the translation initiation site, *e.g.,* a Kozak sequence, is inserted upstream of the coding sequence for AGL. In some embodiments, the translation initiation site is inserted downstream of a 5' UTR. In certain exemplary embodiments, the translation initiation site is inserted upstream of the coding sequence for AGL and downstream of a 5' UTR.

[00213] As is understood in the art, the length of the Kozak sequence may vary. Generally, increasing the length of the leader sequence enhances translation.

[00214] In some embodiments, the translatable oligomer encoding AGL comprises a Kozak sequence having the sequence of SEQ ID NO: 4. In certain exemplary embodiments, the translatable oligomer encoding AGL comprises a Kozak sequence having the sequence of SEQ ID NO: 4, wherein the Kozak sequence is immediately downstream of a 5' UTR and immediately upstream of the coding sequence for AGL.

Synthesis Methods

[00215] In various aspects, this invention provides methods for synthesis of translatable messenger molecules.

[00216] Translatable molecules of this invention can be synthesized and isolated using methods disclosed herein, as well as any pertinent techniques known in the art.

[00217] Some methods for preparing nucleic acids are given in, for example, Merino, Chemical Synthesis of Nucleoside Analogues, (2013); Gait, Oligonucleotide synthesis: a

practical approach (1984); Herdewijn, Oligonucleotide Synthesis, Methods in Molecular Biology, Vol. 288 (2005).

[00218] In some embodiments, a translatable molecule can be made by *in vitro* transcription (IVT) reaction. A mix of nucleoside triphosphates (NTP) can be polymerized using T7 reagents, for example, to yield RNA from a DNA template. The DNA template can be degraded with RNase-free DNase, and the RNA column-separated.

[00219] In some embodiments, a ligase can be used to link a synthetic oligomer to the 3' end of an RNA molecule or an RNA transcript to form a translatable molecule. The synthetic oligomer that is ligated to the 3' end can provide the functionality of a polyA tail, and advantageously provide resistance to its removal by 3'-exoribonucleases. The ligated product translatable molecule can have increased specific activity and provide increased levels of ectopic protein expression.

[00220] In certain embodiments, the ligated product of the translatable molecules of this invention can be made with an RNA transcript that has native specificity. The ligated product can be a synthetic molecule that retains the structure of the RNA transcript at the 5' end to ensure compatibility with the native specificity.

[00221] In further embodiments, the ligated product of the translatable molecules of this invention can be made with an exogenous RNA transcript or non-natural RNA. The ligated product can be a synthetic molecule that retains the structure of the RNA.

[00222] Without wishing to be bound by theory, the canonical mRNA degradation pathway in cells includes the steps: (i) the polyA tail is gradually cut back to a stub by 3' exonucleases, shutting down the looping interaction required for efficient translation and leaving the cap open to attack; (ii) decapping complexes remove the 5' cap; (iii) the unprotected and translationally incompetent residuum of the transcript is degraded by 5' and 3' exonuclease activity.

[00223] Embodiments of this invention involve new translatable structures which can have increased translational activity over a native transcript. Among other things, translatable molecules herein may prevent exonucleases from trimming back the polyA tail in the process of de-adenylation.

[00224] Embodiments of this invention provide structures, compositions and methods for translatable molecules. Embodiments of this invention can provide translatable molecules containing one or more UNA monomers and having increased functional half-life.

[00225] It has been found that ligation of a synthetic oligomer to the 3' end of an mRNA transcript can surprisingly be accomplished with high conversion of the mRNA transcript to the ligation product.

[00226] As used herein, the terms polyA tail and polyA oligomer refer to an oligomer of monomers, wherein the monomers can include nucleotides based on adenine, UNA monomers, naturally-occurring nucleotides, modified nucleotides, or nucleotide analogues.

[00227] Oligomers for ligation to the 3' end of an RNA may be from 2 to 120 monomers in length, or from 3 to 120 monomers in length, or from 4 to 120 monomers in length, or from 5 to 120 monomers in length, or longer. In an exemplary embodiment, the oligomer for ligation is about 30 monomers in length.

Lipid-Based Formulations

[00228] Lipid-based formulations have been increasingly recognized as one of the most promising delivery systems for RNA due to their biocompatibility and their ease of large-scale production. Cationic lipids have been widely studied as synthetic materials for delivery of RNA. After mixing together, nucleic acids are condensed by cationic lipids to form lipid/nucleic acid complexes known as lipoplexes. These lipid complexes are able to protect genetic material from the action of nucleases and to deliver it into cells by interacting with the negatively charged cell membrane. Lipoplexes can be prepared by directly mixing positively charged lipids at physiological pH with negatively charged nucleic acids.

[00229] Conventional liposomes consist of a lipid bilayer that can be composed of cationic, anionic, or neutral (phospho)lipids and cholesterol, which encloses an aqueous core. Both the lipid bilayer and the aqueous space can incorporate hydrophobic or hydrophilic compounds, respectively. Liposome characteristics and behaviour in vivo can be modified by addition of a hydrophilic polymer coating, e.g. polyethylene glycol (PEG), to the liposome surface to confer steric stabilization. Furthermore, liposomes can be used for specific targeting by attaching ligands (e.g., antibodies, peptides, and carbohydrates) to its surface or to the terminal end of the attached PEG chains (Front Pharmacol. 2015 Dec 1;6:286).

[00230] Liposomes are colloidal lipid-based and surfactant-based delivery systems composed of a phospholipid bilayer surrounding an aqueous compartment. They may present as spherical vesicles and can range in size from 20 nm to a few microns. Cationic lipid-based liposomes are able to complex with negatively charged nucleic acids via electrostatic

interactions, resulting in complexes that offer biocompatibility, low toxicity, and the possibility of the large-scale production required for in vivo clinical applications. Liposomes can fuse with the plasma membrane for uptake; once inside the cell, the liposomes are processed via the endocytic pathway and the genetic material is then released from the endosome/carrier into the cytoplasm. Liposomes have long been perceived as drug delivery vehicles because of their superior biocompatibility, given that liposomes are basically analogs of biological membranes, and can be prepared from both natural and synthetic phospholipids (Int J Nanomedicine. 2014; 9: 1833-1 843).

[00231] Cationic liposomes have been traditionally the most commonly used non-viral delivery systems for oligonucleotides, including plasmid DNA, antisense oligos, and siRNA/small hairpin R A-shRNA). Cationic lipids, such as DOTAP, (l ,2-dioleoyl-3-trimethylammonium-propane) and DOTMA (N-[l-(2,3-dioleoyloxy)propyl]-N,N,N-trimethyl-ammonium methyl sulfate) can form complexes or lipoplexes with negatively charged nucleic acids to form nanoparticles by electrostatic interaction, providing high in vitro transfection efficiency . Furthermore, neutral lipid-based nanoliposomes for RNA delivery as e.g. neutral l,2-dioleoyl-sn-glycero-3- phosphatidylcholine (DOPC)-based nanoliposomes were developed. (Adv Drug Deliv Rev. 2014 Feb; 66: 110-1 16.)

According to some embodiments, the expressible polynucleotides and heterologous mRNA constructs described herein are lipid formulated. The lipid formulation is preferably selected from, but not limited to, liposomes, lipoplexes, copolymers, such as PLGA, and lipid nanoparticles. In one preferred embodiment, a lipid nanoparticle (LNP) comprises:

(a) a nucleic acid,

(b) a cationic lipid,

(c) an aggregation reducing agent (such as polyethylene glycol (PEG) lipid or PEG-modified lipid),

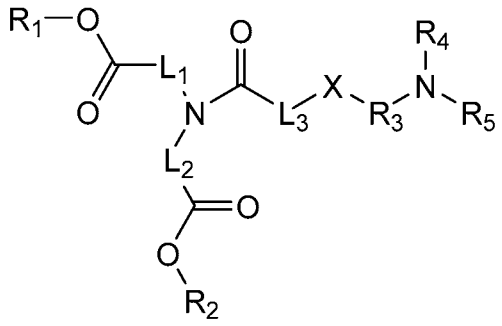
(d) optionally a non-cationic lipid (such as a neutral lipid), and

(e) optionally, a sterol.

[00232] In one embodiment, the lipid nanoparticle formulation consists of (i) at least one cationic lipid; (ii) a neutral lipid; (iii) a sterol, e.g. , cholesterol; and (iv) a PEG-lipid, in a molar ratio of about 20-60% cationic lipid: 5-25% neutral lipid: 25-55% sterol; 0.5-1 5% PEG-lipid.

Thiocarbamate and Carbamate-Containing Lipid Formulations

[00233] Some examples of lipids and lipid compositions for delivery of an active molecule of this invention are given in WO/2015/074085 and USSN 15/387,067, each of which is hereby incorporated by reference in its entirety. In certain embodiments, the lipid is a compound of the following formula:



wherein

R_1 and R_2 both consist of a linear alkyl consisting of 1 to 14 carbons, or an alkenyl or alkynyl consisting of 2 to 14 carbons;

L_1 and L_2 both consist of a linear alkylene or alkenylene consisting of 5 to 18 carbons, or forming a heterocycle with N;

X is S;

L_3 consists of a bond or a linear alkylene consisting of 1 to 6 carbons, or forming a heterocycle with N;

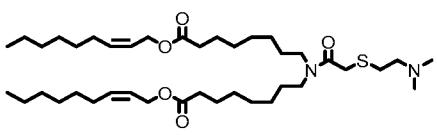
R_3 consists of a linear or branched alkylene consisting of 1 to 6 carbons; and

R_4 and R_5 are the same or different, each consisting of a hydrogen or a linear or branched alkyl consisting of 1 to 6 carbons;

or a pharmaceutically acceptable salt thereof.

[00234] The lipid formuation may contain one or more ionizable cationic lipids selected from among the following:

ATX-001



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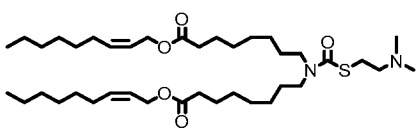
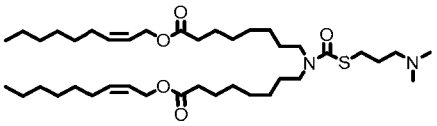
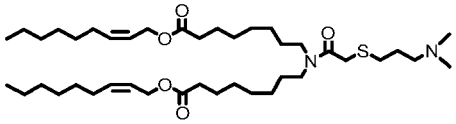
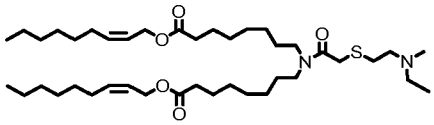
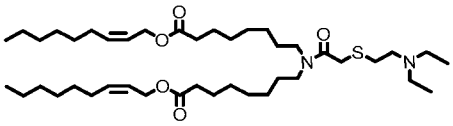
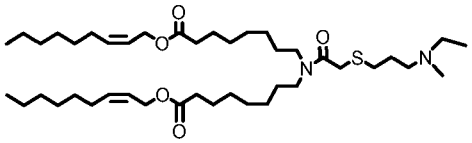


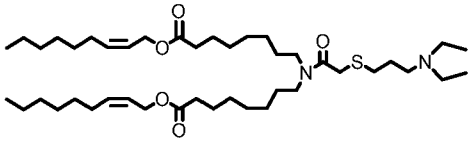
ATX-003 

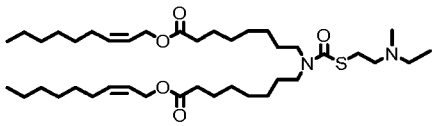
ATX-004 

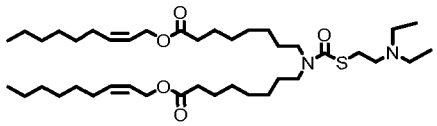
ATX-005 

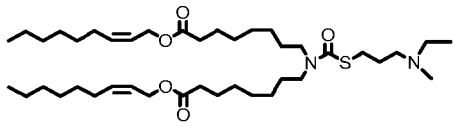
ATX-006 

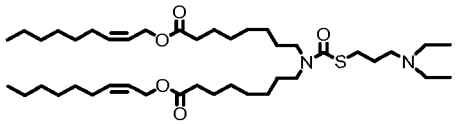
ATX-007 

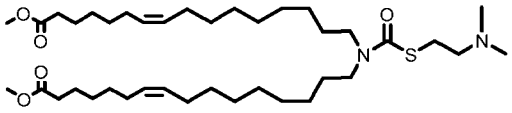
ATX-008 

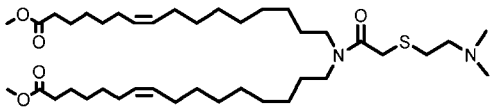
ATX-009 

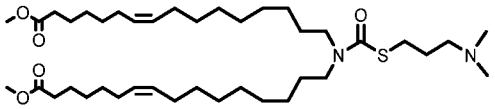
ATX-010 

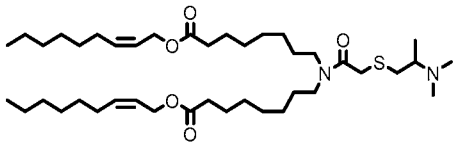
ATX-011 

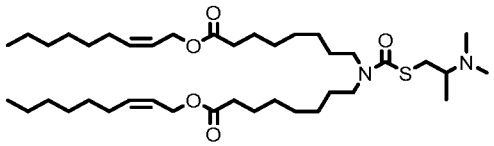
ATX-012 

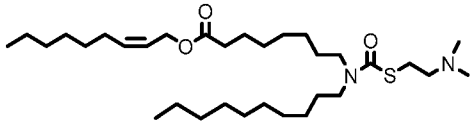
ATX-013 

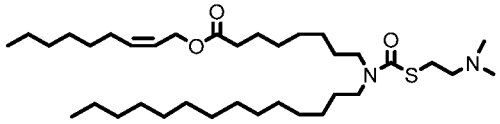
ATX-014 

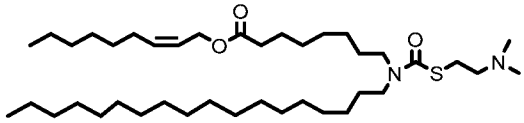
ATX-015 

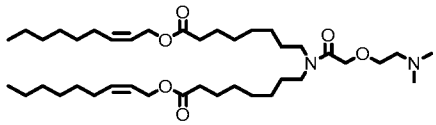
ATX-016 

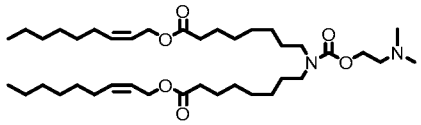
ATX-017 

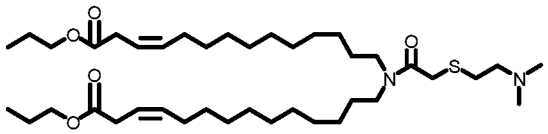
ATX-018 

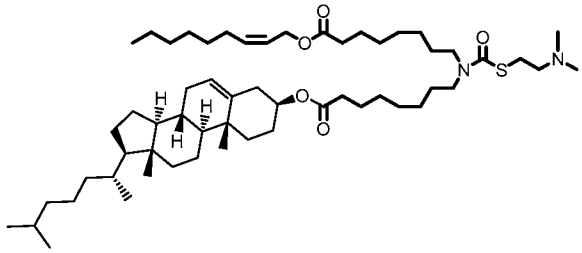
ATX-019 

ATX-020 

ATX-021 

ATX-022 

ATX-023 

ATX-024 

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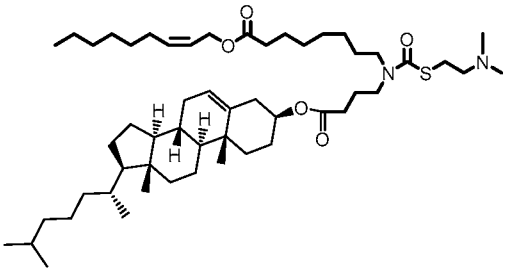

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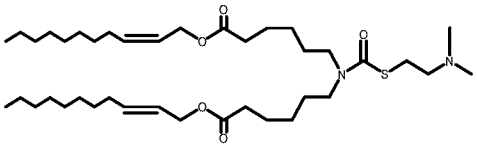

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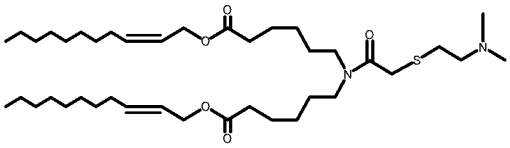

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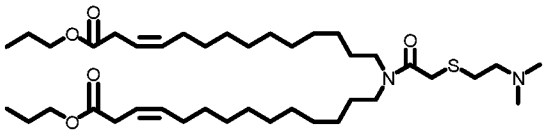

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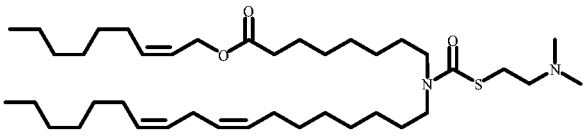

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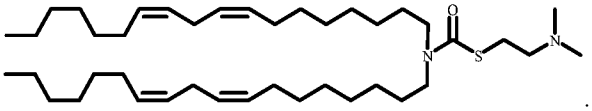

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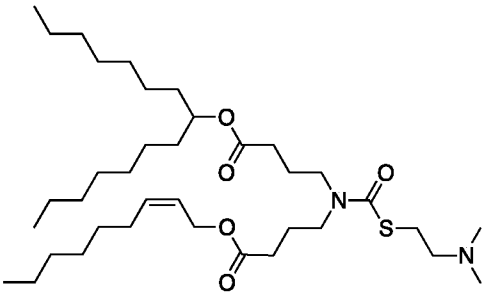

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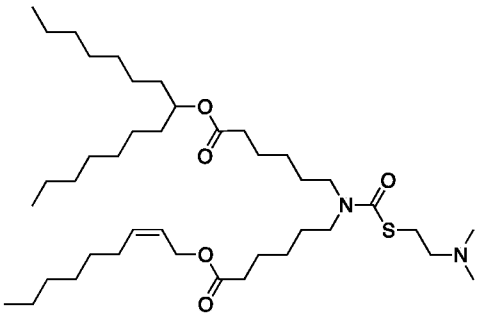

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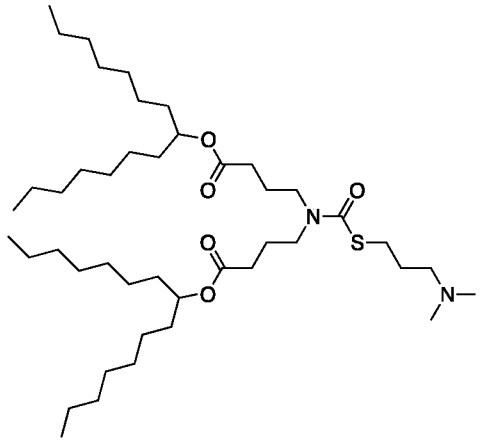


Cationic Lipids

[00235] The lipid nanoparticle preferably includes a cationic lipid suitable for forming a lipid nanoparticle. Preferably, the cationic lipid carries a net positive charge at about physiological pH.

[00236] The cationic lipid may be, for example, N,N-dioleyl-N,N-dimethylammonium chloride (DODAC), N,N-distearyl-N,N-dimethylammonium bromide (DDAB), 1,2-dioleoyltrimethylammoniumpropane chloride (DOTAP) (also known as N-(2,3-dioleoyloxy)propyl)-N,N,N-trimethylammonium chloride and l,2-Dioleyloxy-3-trimethylaminopropane chloride salt), N-(l-(2,3-dioleyloxy)propyl)-N,N,N-trimethylammonium chloride (DOTMA), N,N-dimethyl-2,3-dioleyloxy)propylamine (DODMA), l,2-DiLinoleyloxy-N,N-dimethylaminopropane (DLinDMA), 1,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLenDMA), l,2-di-y-linolenyloxy-N,N-dimethylaminopropane (y-DLenDMA), l,2-Dilinoleylcarbamoyloxy-3-dimethylaminopropane (DLin-C-DAP), 1,2-Dilinoleyoxy-3-(dimethylamino)acetoxypropane (DLin-DAC), l,2-Dilinoleyoxy-3-morpholinopropane (DLin-MA), l,2-Dilinoleoyl-3-dimethylaminopropane (DLinDAP), 1,2-Dilinoleylthio-3-dimethylaminopropane (DLin-S- DMA), l-Linoleoyl-2-linoleyloxy-3-dimethylaminopropane (DLin-2-DMAP), l,2-Dilinoleyloxy-3-trimethylaminopropane chloride salt (DLin-TMA.CI), l,2-Dilinoleoyl-3-trimethylaminopropane chloride salt (DLin-TAP.CI), l,2-Dilinoleyloxy-3-(N-methylpiperazino)propane (DLin-MPZ), or 3-(N,N-Dilinoleylamino)-l,2-propanediol (DLinAP), 3-(N,N-Dioleylamino)-l,2-propanedio (DOAP), l,2-Dilinoleyloxo-3-(2-N,N- dimethylamino)ethoxy propane (DLin-EG-DM A), 2,2-Dilinoleyl-4-dimethylaminomethyl-[l,3]-dioxolane (DLin-K-DMA) or analogs thereof, (3aR,5s,6aS)-N,N-dimethyl-2,2-di((9Z,12Z)-octadeca-9,12-dienyl)tetrahydro-3aH-

cyclopenta[d][l,3]dioxol-5-amine, (6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,31-tetraen-19-yl4-(dimethylamino)butanoate (MC3), l,l'-(2-(4-(2-((2-(bis(2-hydroxydodecyl)amino)ethyl)(2-hydroxydodecyl)amino)ethyl)piperazin-l-yl)ethylazanediyl)didodecan-2-ol (CI 2-200), 2,2-dilinoleyl-4-(2-dimethylaminoethyl)-[l,3]-dioxolane (DLin-K-C2-DMA), 2,2-dilinoleyl-4-dimethylaminomethyl-[l,3]-dioxolane (DLin-K-DMA), (6Z,9Z,28Z,3 lZ)-heptatriaconta-6,9,28 31-tetraen-19-yl 4-(dimethylamino) butanoate (DLin-M-C3-DMA), 3-((6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,3 l-tetraen-19-yloxy)-N,N-dimethylpropan-l-amine (MC3 Ether), 4-((6Z,9Z,28Z,31 Z)-heptatriaconta-6,9,28,31-tetraen-19-yloxy)-N,N-dimethylbutan-l-amine (MC4 Ether), or any combination of any of the foregoing. Other cationic lipids include, but are not limited to, N,N-distearyl-N,N-dimethylammonium bromide (DDAB), 3P-(N-(N',N'-dimethylaminoethane)- carbamoyl)cholesterol (DC-Choi), N-(l-(2,3-dioleyloxy)propyl)-N-2-(sperrninecarboxamido)ethyl)-N,N-dimethylammonium trifluoracetate (DOSPA), dioctadecylamidoglycyl carboxyspermine (DOGS), l,2-dileoyl-sn-3-phosphoethanolamine (DOPE), l,2-dioleoyl-3-dimethylammonium propane (DODAP), N-(l,2-dimyristyloxyprop-3-yl)-N,N-dimethyl-N-hydroxyethyl ammonium bromide (DMRIE), and 2,2-Dilinoleyl-4-dimethylaminoethyl-[l,3]-dioxolane (XTC). Additionally, commercial preparations of cationic lipids can be used, such as, e.g., LIPOFECTIN (including DOTMA and DOPE, available from GIBCO/BRL), and Lipofectamine (comprising DOSPA and DOPE, available from GIBCO/BRL).

[00237] Other suitable cationic lipids are disclosed in International Publication Nos. WO 09/086558, WO 09/127060, WO 10/048536, WO 10/054406, WO 10/088537, WO 10/129709, and WO 2011/153493; U.S. Patent Publication Nos. 2011/0256175, 2012/0128760, and 2012/0027803; U.S. Patent Nos. 8,158,601; and Love et al, PNAS, 107(5), 1864-69, 2010. Other suitable amino lipids include those having alternative fatty acid groups and other dialkylamino groups, including those, in which the alkyl substituents are different (e.g., N-ethyl- N-methylamino-, and N-propyl-N-ethylamino-). In general, amino lipids having less saturated acyl chains are more easily sized, particularly when the complexes must be sized below about 0.3 microns, for purposes of filter sterilization. Amino lipids containing unsaturated fatty acids with carbon chain lengths in the range of C14 to C22 may be used. Other scaffolds can also be used to separate the amino group and the fatty acid or fatty alkyl portion of the amino lipid.

[00238] In a further preferred embodiment, the LNP comprises the cationic lipid with formula (III) according to the patent application PCT/EP2017/064066. In this context, the disclosure of PCT/EP2017/064066 is also incorporated herein by reference.

[00239] In certain embodiments, amino or cationic lipids of the invention have at least one protonatable or deprotonatable group, such that the lipid is positively charged at a pH at or below physiological pH (e.g. pH 7.4), and neutral at a second pH, preferably at or above physiological pH. It will, of course, be understood that the addition or removal of protons as a function of pH is an equilibrium process, and that the reference to a charged or a neutral lipid refers to the nature of the predominant species and does not require that all of the lipid be present in the charged or neutral form. Lipids that have more than one protonatable or deprotonatable group, or which are zwitterionic, are not excluded from use in the invention. In certain embodiments, the protonatable lipids have a pKa of the protonatable group in the range of about 4 to about 11, e.g., a pKa of about 5 to about 7.

[00240] The cationic lipid can comprise from about 20 mol % to about 70 or 75 mol % or from about 45 to about 65 mol % or about 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, or about 70 mol % of the total lipid present in the particle. In another embodiment, the lipid nanoparticles include from about 25% to about 75% on a molar basis of cationic lipid, e.g., from about 20 to about 70%, from about 35 to about 65%, from about 45 to about 65%, about 60%, about 57.5%, about 57. 1%, about 50% or about 40% on a molar basis (based upon 100% total moles of lipid in the lipid nanoparticle). In one embodiment, the ratio of cationic lipid to nucleic acid is from about 3 to about 15, such as from about 5 to about 13 or from about 7 to about 11.

Pharmaceutical Compositions

[00241] In some aspects, this invention provides pharmaceutical compositions containing a translatable compound and a pharmaceutically acceptable carrier.

[00242] A pharmaceutical composition can be capable of local or systemic administration. In some aspects, a pharmaceutical composition can be capable of any modality of administration. In certain aspects, the administration can be by any route, including intravenous, subcutaneous, pulmonary, intramuscular, intraperitoneal, dermal, oral, inhalation or nasal administration.

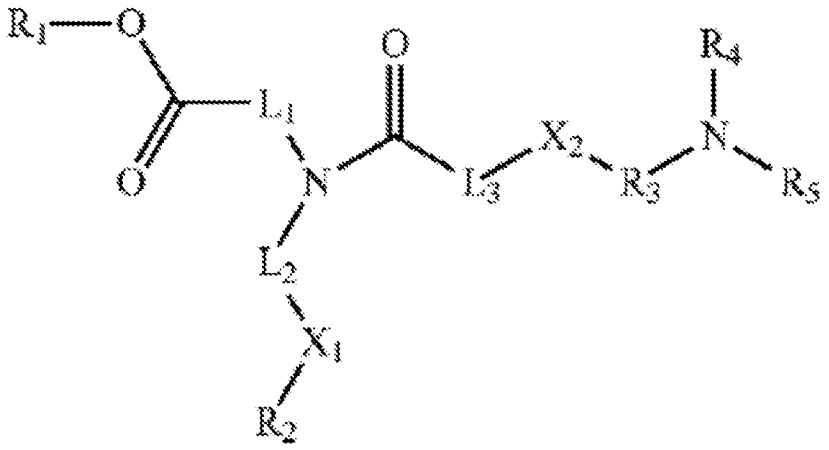
[00243] Embodiments of this invention include pharmaceutical compositions containing a translatable compound in a lipid formulation.

[00244] In some embodiments, a pharmaceutical composition may comprise one or more lipids selected from cationic lipids, anionic lipids, sterols, pegylated lipids, and any combination of the foregoing. In some embodiments, the pharmaceutical composition containing a translatable compound comprises a cationic lipid, a phospholipid, cholesterol, and a pegylated lipid.

[00245] In certain embodiments, a pharmaceutical composition can be substantially free of liposomes.

[00246] In further embodiments, a pharmaceutical composition can include nanoparticles.

[00247] Some examples of lipids and lipid compositions for delivery of an active molecule of this invention are given in WO/2015/074085, which is hereby incorporated by reference in its entirety. In certain embodiments, the lipid is a cationic lipid. In some embodiment, the cationic lipid comprises a compound of formula II:



Formula II,

in which Ri and R2 are the same or different, each a linear or branched alkyl, alkenyl, or alkynyl, Li and L2 are the same or different, each a linear alkyl having at least five carbon atoms, or form a heterocycle with the N, Xi is a bond, or is --CO--O-- whereby L2-CO--O--R2 is formed X2 is S or O, L3 is a bond or a lower alkyl, R3 is a lower alkyl, R4 and R5 are the same or different, each a lower alkyl. What is also described herein is the compound of formula II, in which L3 is absent, Ri and R2 each consists of at least seven carbon atoms, R3 is ethylene or n-propylene, R4 and R5 are methyl or ethyl, and Li and L2 each consists of a linear alkyl having at least five carbon atoms. What is also described herein is the compound of formula II, in

which L_3 is absent, R_1 and R_2 each consists of at least seven carbon atoms, R_3 is ethylene or n-propylene, R_4 and R_5 are methyl or ethyl, and L_1 and L_2 each consists of a linear alkyl having at least five carbon atoms. What is also described herein is the compound of formula II, in which L_3 is absent, R_1 and R_2 each consists of an alkenyl of at least nine carbon atoms, R_3 is ethylene or n-propylene, R_4 and R_5 are methyl or ethyl, and L_1 and L_2 each consists of a linear alkyl having at least five carbon atoms. What is also described herein is the compound of formula II, in which L_3 is methylene, R_1 and R_2 each consists of at least seven carbon atoms, R_3 is ethylene or n-propylene, R_4 and R_5 are methyl or ethyl, and L_1 and L_2 each consists of a linear alkyl having at least five carbon atoms. What is also described herein is the compound of formula II, in which L_3 is methylene, R_1 and R_2 each consists of at least nine carbon atoms, R_3 is ethylene or n-propylene, R_4 and R_5 are each methyl, L_1 and L_2 each consists of a linear alkyl having at least seven carbon atoms. What is also described herein is the compound of formula II, in which L_3 is methylene, R_1 consists of an alkenyl having at least nine carbon atoms and R_2 consists of an alkenyl having at least seven carbon atoms, R_3 is n-propylene, R_4 and R_5 are each methyl, L_1 and L_2 each consists of a linear alkyl having at least seven carbon atoms. What is also described herein is the compound of formula II, in which L_3 is methylene, R_1 and R_2 each consists of an alkenyl having at least nine carbon atoms, R_3 is ethylene, R_4 and R_5 are each methyl, L_1 and L_2 each consists of a linear alkyl having at least seven carbon atoms.

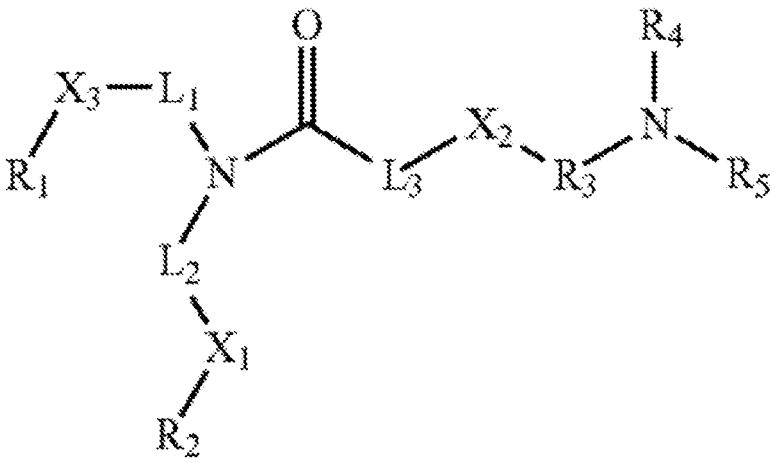
[00248] In exemplary embodiments, the cationic lipid comprises a compound of selected from the group consisting of ATX-001, ATX-002, ATX-003, ATX-004, ATX-005, ATX-006, ATX-007, ATX-008, ATX-009, ATX-010, ATX-011, ATX-012, ATX-013, ATX-014, ATX-015, ATX-016, ATX-017, ATX-018, ATX-019, ATX-020, ATX-021, ATX-022, ATX-023, ATX-024, ATX-025, ATX-026, ATX-027, ATX-028, ATX-029, ATX-030, ATX-031, ATX-032, ATX-081, ATX-095, and ATX-126, or a pharmaceutically acceptable salt thereof.

[00249] In certain exemplary embodiments, the cationic lipid comprises ATX-002, ATX-081, ATX-095, or ATX-126.

[00250] In some embodiments, the cationic lipid or a pharmaceutically acceptable salt thereof, may be presented in a lipid composition, comprising a nanoparticle or a bilayer of lipid molecules. The lipid bilayer preferably further comprises a neutral lipid or a polymer. The lipid composition preferably comprises a liquid medium. The composition preferably further encapsulates a translatable compound of the present invention. The lipid composition

preferably further comprises a translatable compound of the present invention and a neutral lipid or a polymer. The lipid composition preferably encapsulates the translatable compound.

[00251] In further embodiments, the cationic lipid comprises a compound of formula III:



Formula III,

wherein R_i and R_2 are the same or different, each a linear or branched alkyl consisting of 1 to 9 carbons, an alkenyl or alkynyl consisting of 2 to 11 carbons, or cholesteryl, L_i and L_2 are the same or different, each a linear alkylene or alkenylene consisting of 5 to 18 carbons, X_i is ~ CO--O-- whereby -L2-CO--O--R2 is formed, X_2 is S or O, X_3 is -CO--O-- whereby -L1-CO--0~Ri is formed, L_3 is a bond, R_3 is a linear or branched alkylene consisting of 1 to 6 carbons, and R_4 and R_5 are the same or different, each hydrogen or a linear or branched alkyl consisting of 1 to 6 carbons; or a pharmaceutically acceptable salt thereof. In one embodiment, X_2 is S. In another embodiment, R_3 is selected from ethylene, n-propylene, or isobutylene. In yet another embodiment, R_4 and R_5 are separately methyl, ethyl, or isopropyl. In yet another embodiment, L_i and L_2 are the same. In yet another embodiment, L_i and L_2 differ. In yet another embodiment, L_i or L_2 consists of a linear alkylene having seven carbons. In yet another embodiment, L_i or L_2 consists of a linear alkylene having nine carbons. In yet another embodiment, R_i and R_2 are the same. In yet another embodiment, R_i and R_2 differ. In yet another embodiment, R_i and R_2 each consists of an alkenyl. In yet another embodiment, R_i and R_2 each consists of an alkyl. In yet another embodiment, the alkenyl consists of a single double bond. In yet another embodiment, R_i or R_2 consists of nine carbons. In yet another embodiment, R_i or R_2 consists of eleven carbons. In yet another embodiment, R_i or R_2 consists of seven carbons. In yet another embodiment, L_3 is a bond, R_3 is ethylene, X_2 is S, and R_4 and

R^5 are each methyl. In yet another embodiment, L^3 is a bond, R^3 is n-propylene, X^2 is S, R^4 and R^5 are each methyl. In yet another embodiment, L^3 is a bond, R^3 is ethylene, X^2 is S, and R^4 and R^5 are each ethyl.

[00252] As would be appreciated by the skilled artisan, the compounds of formulas II and III form salts that are also within the scope of this disclosure. Reference to a compound of formulas II and III herein is understood to include reference to salts thereof, unless otherwise indicated. The term "salt(s)", as employed herein, denotes acidic salts formed with inorganic and/or organic acids, as well as basic salts formed with inorganic and/or organic bases. In addition, when a compound of formula II or III contains both a basic moiety, such as, but not limited to, a pyridine or imidazole, and an acidic moiety, such as, but not limited to, a carboxylic acid, zwitterions ("inner salts") may be formed and are included within the term "salt(s)" as used herein. The salts can be pharmaceutically acceptable (i.e., non-toxic, physiologically acceptable) salts, although other salts are also useful. Salts of the compounds of the formula II or III may be formed, for example, by reacting a compound of formula II or III with an amount of acid or base, such as an equivalent amount, in a medium such as one in which the salt precipitates or in an aqueous medium followed by lyophilization.

[00253] Exemplary acid addition salts include acetates, adipates, alginates, ascorbates, aspartates, benzoates, benzenesulfonates, bisulfates, borates, butyrates, citrates, camphorates, camphorsulfonates, cyclopentanepropionates, digluconates, dodecylsulfates, ethanesulfonates, fumarates, glucoheptanoates, glycerophosphates, hemisulfates, heptanoates, hexanoates, hydrochlorides, hydrobromides, hydroiodides, 2-hydroxyethanesulfonates, lactates, maleates, methanesulfonates, 2-napthalenesulfonates, nicotinates, nitrates, oxalates, pectinates, persulfates, 3-phenylpropionates, phosphates, picrates, pivalates, propionates, salicylates, succinates, sulfates, sulfonates (such as those mentioned herein), tartarates, thiocyanates, toluenesulfonates (also known as tosylates) undecanoates, and the like. Additionally, acids which are generally considered suitable for the formation of pharmaceutically useful salts from basic pharmaceutical compounds are discussed, for example, by S. Berge et al, J. Pharmaceutical Sciences (1977) 66(1)1-19; P. Gould, International J. Pharmaceutics (1986) 33 201-217; Anderson et al, The Practice of Medicinal Chemistry (1996), Academic Press, New York; and in The Orange Book (Food & Drug Administration, Washington, D.C. on their website). These disclosures are incorporated by reference herein.

[00254] Exemplary basic salts include ammonium salts, alkali metal salts such as sodium, lithium, and potassium salts, alkaline earth metal salts such as calcium and magnesium

salts, salts with organic bases (for example, organic amines) such as benzathines, dicyclohexylamines, hydrabamines (formed with **N,N**-bis(dehydroabietyl)ethylenediamine), **N**-methyl-D-glucamines, **N**-methyl-D-glucamides, t-butyl amines, and salts with amino acids such as arginine, lysine, and the like. Basic nitrogen-containing groups may be quarternized with agents such as lower alkyl halides (e.g., methyl, ethyl, propyl, and butyl chlorides, bromides, and iodides), dialkyl sulfates (e g, dimethyl, diethyl, dibutyl, and diamyl sulfates), long chain halides (e.g., decyl, lauryl, myristyl, and stearyl chlorides, bromides, and iodides), arylalkyl halides (e.g., benzyl and phenethyl bromides), and others.

[00255] All such acid and base salts are intended to be pharmaceutically acceptable salts within the scope of the disclosure and all acid and base salts are considered equivalent to the free forms of the corresponding compounds for purposes of the disclosure. Compounds of formula II or III can exist in unsolvated and solvated forms, including hydrated forms. In general, the solvated forms, with pharmaceutically acceptable solvents such as water, ethanol, and the like, are equivalent to the unsolvated forms for the purposes of this disclosure. Compounds of formula II or III and salts, solvates thereof, may exist in their tautomeric form (for example, as an amide or imino ether). All such tautomeric forms are contemplated herein as part of the present disclosure.

[00256] The cationic lipid compounds described herein may be combined with a translatable compound of the invention to form microparticles, nanoparticles, liposomes, or micelles. The translatable compound of the invention to be delivered by the particles, liposomes, or micelles may be in the form of a gas, liquid, or solid. The cationic lipid compound and the translatable compound may be combined with other cationic lipid compounds, polymers (synthetic or natural), surfactants, cholesterol, carbohydrates, proteins, lipids, etc. to form the particles. These particles may then optionally be combined with a pharmaceutical excipient to form a pharmaceutical composition.

[00257] In certain embodiments, the cationic lipid compounds are relatively non-cytotoxic. The cationic lipid compounds may be biocompatible and biodegradable. The cationic lipid may have a pKa in the range of approximately 5.5 to approximately 7.5, more preferably between approximately 6.0 and approximately 7.0. It may be designed to have a

desired pKa between approximately 3.0 and approximately 9.0, or between approximately 5.0 and approximately 8.0.

[00258] A composition containing a cationic lipid compound may be 30-70% cationic lipid compound, 0-60% cholesterol, 0-30% phospholipid and 1-10% polyethylene glycol (PEG). Preferably, the composition is 30-40% cationic lipid compound, 40-50% cholesterol, and 10-20% PEG. In other preferred embodiments, the composition is 50-75% cationic lipid compound, 20-40% cholesterol, and 5 to 10% phospholipid, and 1-10% PEG. The composition may contain 60-70% cationic lipid compound, 25-35% cholesterol, and 5-10% PEG. The composition may contain up to 90% cationic lipid compound and 2 to 15% helper lipid. The formulation may be a lipid particle formulation, for example containing 8-30% compound, 5-30% helper lipid, and 0-20% cholesterol; 4-25% cationic lipid, 4-25% helper lipid, 2 to 25% cholesterol, 10 to 35% cholesterol-PEG, and 5% cholesterol-amine; or 2-30% cationic lipid, 2-30% helper lipid, 1 to 15% cholesterol, 2 to 35% cholesterol-PEG, and 1-20% cholesterol-amine; or up to 90% cationic lipid and 2-10% helper lipids, or even 100% cationic lipid.

[00259] In some embodiments, the one or more cholesterol-based lipids are selected from cholesterol, PEGylated cholesterol and DC-Choi (N,N-dimethyl-N-ethylcarboxamidocholesterol), and l,4-bis(3-N-oleylamino-propyl)piperazine. In an exemplary embodiment, the cholesterol-based lipid is cholesterol.

[00260] In some embodiments, the one or more pegylated lipids, *i.e.,* PEG-modified lipids. In some embodiments, the one or more PEG-modified lipids comprise a poly(ethylene) glycol chain of up to 5 kDa in length covalently attached to a lipid with alkyl chain(s) of C_6-C20 length. In some embodiments, a PEG-modified lipid is a derivatized ceramide such as N-Octanoyl-Sphingosine-l-[Succinyl(Methoxy Polyethylene Glycol)-2000]. In some embodiments, a PEG-modified or PEGylated lipid is PEGylated cholesterol or Dimyristoylglycerol (DMG)-PEG-2K. In an exemplary embodiment, the PEG-modified lipid is PEGylated cholesterol.

[00261] In additional embodiments, a pharmaceutical composition can contain an oligomeric compound within a viral or bacterial vector.

[00262] A pharmaceutical composition of this disclosure may include carriers, diluents or excipients as are known in the art. Examples of pharmaceutical compositions and methods are described, for example, in Remington's Pharmaceutical Sciences, Mack Publishing Co.

(A.R. Gennaro ed. 1985), and Remington, The Science and Practice of Pharmacy, 21st Edition (2005).

[00263] Examples of excipients for a pharmaceutical composition include antioxidants, suspending agents, dispersing agents, preservatives, buffering agents, tonicity agents, and surfactants.

[00264] An effective dose of an agent or pharmaceutical formulation of this invention can be an amount that is sufficient to cause translation of a translatable molecule in a cell.

[00265] A therapeutically effective dose can be an amount of an agent or formulation that is sufficient to cause a therapeutic effect. A therapeutically effective dose can be administered in one or more separate administrations, and by different routes. As will be appreciated in the art, a therapeutically effective dose or a therapeutically effective amount is largely determined based on the total amount of the therapeutic agent contained in the pharmaceutical compositions of the present invention. Generally, a therapeutically effective amount is sufficient to achieve a meaningful benefit to the subject **(e**.**g**., treating, modulating, curing, preventing and/or ameliorating GSD III). For example, a therapeutically effective amount may be an amount sufficient to achieve a desired therapeutic and/or prophylactic effect. Generally, the amount of a therapeutic agent **(e**.**g**., a translatable oligomer encoding AGL) administered to a subject in need thereof will depend upon the characteristics of the subject. Such characteristics include the condition, disease severity, general health, age, sex and body weight of the subject. One of ordinary skill in the art will be readily able to determine appropriate dosages depending on these and other related factors. In addition, both objective and subjective assays may optionally be employed to identify optimal dosage ranges.

[00266] Methods provided herein contemplate single as well as multiple administrations of a therapeutically effective amount of the translatable compound **(e**.**g**., a translatable oligomer encoding AGL) described herein. Pharmaceutical compositions comprising a translatable compound encoding AGL can be administered at regular intervals, depending on the nature, severity and extent of the subject's condition **(e**.g., the severity of a subject's GSD III disease state and the associated symptoms of GSD III, and/or the subject's AGL activity levels). In some embodiments, a therapeutically effective amount of the translatable compound **(e**.g., a translatable oligomer encoding AGL) of the present invention may be administered periodically at regular intervals **(e**.g., once every year, once every six months, once every four months, once every three months, once every two months, once a month), biweekly, weekly,

daily, twice a day, three times a day, four times a day, five times a day, six times a day, or continuously.

[00267] In some embodiments, the pharmaceutical compositions of the present invention are formulated such that they are suitable for extended-release of the translatable compound encoding AGL contained therein. Such extended-release compositions may be conveniently administered to a subject at extended dosing intervals. For instance, in one embodiment, the pharmaceutical compositions of the present invention are administered to a subject twice a day, daily or every other day. In some embodiments, the pharmaceutical compositions of the present invention are administered to a subject twice a week, once a week, every 10 days, every two weeks, every 28 days, every month, every six weeks, every eight weeks, every other month, every three months, every four months, every six months, every nine months or once a year. Also contemplated herein are pharmaceutical compositions which are formulated for depot administration *(e.g.* , subcutaneously, intramuscularly) to either deliver or release a translatable compound encoding AGL over extended periods of time. Preferably, the extended-release means employed are combined with modifications made to the translatable compound encoding AGL to enhance stability.

[00268] In some embodiments, a therapeutically effective dose, upon administration, can result in serum or plasma levels of AGL of 1-1000 pg/ml, or 1-1000 ng/ml, or 1-1000 μg/ml, or more.

[00269] In some embodiments, administering a therapeutically effective dose of a composition comprising a translatable molecule of the invention can result in increased liver AGL protein levels in a treated subject. In some embodiments, administering a composition comprising a translatable molecule of the invention results in a 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 95% increase in liver AGL protein levels relative to a baseline AGL protein level in the subject prior to treatment. In certain embodiments, administering a therapeutically effective dose of a composition comprising a translatable molecule of the invention will result an increase in liver AGL levels relative to baseline liver AGL levels in the subject prior to treatment. In some embodiments, the increase in liver AGL levels relative to baseline liver AGL levels will be at least 5%, 10%, 20%, 30%, 40%, 50%, 100%, 200%, or more.

[00270] In some embodiments, a therapeutically effective dose, when administered regularly, results in increased expression of AGL in the liver as compared to baseline levels

prior to treatment. In some embodiments, administering a therapeutically effective dose of a composition comprising a translatable molecule of the invention results in the expression of a AGL protein level at or above about 10 ng/mg, about 20 ng/mg, about 50 ng/mg, about 100 ng/mg, about 150 ng/mg, about 200 ng/mg, about 250 ng/mg, about 300 ng/mg, about 350 ng/mg, about 400 ng/mg, about 450 ng/mg, about 500 ng/mg, about 600 ng/mg, about 700 ng/mg, about 800 ng/mg, about 900 ng/mg, about 1000 ng/mg, about 1200 ng/mg or about 1500 ng/mg of the total protein in the liver of a treated subject.

[00271] In some embodiments, administering a therapeutically effective dose of a composition comprising a translatable oligomer encoding AGL will result in reduced levels of one or more of markers selected from alanine transaminase (ALT), aspartate transaminase (AST), alkaline phosphatase (ALP), creatine phosphokinase (CPK), glycogen, and limit dextrin *(i.e.,* a low-molecular carbohydrate produced by the hydrolysis of glycogen).

[00272] In some emobdiments, a therapeutically effective dose, when administered regularly, results in a reduction of ALT, AST, ALP, and/or CPK levels in a biological sample. In some embodiments, administering a therapeutically effective dose of a composition comprising a translatable molecule of this invention results in a reduction of ALT, AST, ALP, and/or CPK levels in a biological sample *(e.g.* , a plasma or serum sample) by at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, or at least about 95% as compared to baseline ALT, AST, ALP, and/or CPK levels before treatment. In some embodiments, the biological sample is selected from plasma, serum, whole blood, urine, or cerebrospinal fluid.

[00273] In certain exemplary embodiments, a therapeutically effective dose, when administered regularly, results in a reduction of ALT levels, *e.g.,* as measured in units of ALT activity/liter (U/l), in a serum or plasma sample. In some embodiments, administering a therapeutically effective dose of a composition comprising a translatable molecule of this invention results in a reduction of ALT levels in a biological sample *(e.g.,* a plasma or serum sample) by at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, or at least about 95% as compared to baseline ALT levels before treatment. In an exemplary

embodiment, administering a therapeutically effective dose of a composition comprising a translatable molecule of this invention results in a reduction of ALT levels in a biological sample (e.g., a plasma or serum sample) by at least about 50% as compared to baseline ALT levels before treatment. In a further exemplary embodiment, ALT levels are measured after fasting, *e.g.*, after 6, 8, 10, 12, 18, or 24 hours of fasting.

[00274] In other exemplary embodiments, a therapeutically effective dose, when administered regularly, results in a reduction of AST levels, *e.g.*, as measured in units of AST activity/liter (U/l), in a serum or plasma sample. In some embodiments, administering a therapeutically effective dose of a composition comprising a translatable molecule of this invention results in a reduction of AST levels in a biological sample *(e.g.*, a plasma or serum sample) by at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, or at least about 95% as compared to baseline AST levels before treatment. In an exemplary embodiment, administering a therapeutically effective dose of a composition comprising a translatable molecule of this invention results in a reduction of AST levels in a biological sample *(e.g.*, a plasma or serum sample) by at least about 50% as compared to baseline AST levels before treatment. In a further exemplary embodiment, AST levels are measured after fasting, *e.g.*, after 6, 8, 10, 12, 18, or 24 hours of fasting.

[00275] Measurements of ALT, AST, ALP, and/or CPK levels can be made using any method known in the art, *e.g.*, using a Fuji Dri-Chem Clinical Chemistry Analyzer FDC 3500 as described in Liu *et al.*, 2014, *Mol Genet and Metabolism* 111: 467-76.

[00276] In other exemplary embodiments, a therapeutically effective dose, when administered regularly, results in a reduction of glycogen levels in a biological sample. In some embodiments, administering a therapeutically effective dose of a composition comprising a translatable molecule of this invention results in a reduction of glycogen accumulation in a biological sample *(e.g.*, a liver sample) by at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, or at least about 95% as compared to baseline glycogen levels before treatment. In some embodiments, the biological sample is a portion of an organ selected from

liver, heart, diaphragm, quadriceps, and gastrocnemius. In an exemplary embodiment, the biological sample is a liver section, *e.g.*, a section of hepatocytes.

[00277] In other exemplary embodiments, a therapeutically effective dose, when administered regularly, results in a reduction of limit dextrin levels in a biological sample. In some embodiments, administering a therapeutically effective dose of a composition comprising a translatable molecule of this invention results in a reduction of limit dextrin accumulation in a biological sample *(e.g.*, a liver sample) by at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, or at least about 95% as compared to baseline limit dextrin levels before treatment. In some embodiments, the biological sample is a portion of an organ selected from liver, heart, diaphragm, quadriceps, and gastrocnemius. In an exemplary embodiment, the biological sample is a liver section, *e.g.*, a section of hepatocytes. In a further exemplary embodiment, a therapeutically effective dose, when administered regularly, results in at least a 50%, 60%, 70%, or 80% reduction of limit dextrin levels in a liver sample as compared to baseline limit dextrin levels before treatment.

[00278] In further embodiments, a therapeutically effective dose, when administered regularly, delays the onset of liver fibrosis in a treated subject. In some embodiments, a therapeutically effective dose, when administered regularly, slows the development of liver fibrosis or reduces the amount of liver fibrosis in a subject afflicted with GSD III.

[00279] A therapeutically effective dose of an active agent *(e.g.*, a translatable oligomer encoding AGL) *in vivo* can be a dose of about 0.001 to about 500 mg/kg body weight. For instance, the therapeutically effective dose may be about 0.001-0.01 mg/kg body weight, or 0.01-0.1 mg/kg, or 0.1-1 mg/kg, or 1-10 mg/kg, or 10-100 mg/kg. In some embodiments, a translatable oligomer encoding AGL is provided at a dose ranging from about 0.1 to about 10 mg/kg body weight, *e.g.*, from about 0.5 to about 5 mg/kg, from about 1 to about 4.5 mg/kg, or from about 2 to about 4 mg/kg.

[00280] A therapeutically effective dose of an active agent *(e.g.*, a translatable oligomer encoding AGL) *in vivo* can be a dose of at least about 0.001 mg/kg body weight, or at least about 0.01 mg/kg, or at least about 0.1 mg/kg, or at least about 1 mg/kg, or at least about 2 mg/kg, or at least about 3 mg/kg, or at least about 4 mg/kg, or at least about 5 mg/kg, at least

about 10 mg/kg, at least about 20 mg/kg, at least about 50 mg/kg, or more. In some embodiments, a translatable oligomer encoding AGL is provided at a dose of about 0.1 mg/kg, about 0.5 mg/kg, about 1 mg/kg, about 1.5 mg/kg, about 2 mg/kg, about 2.5 mg/kg, about 3 mg/kg, about 3.5 mg/kg, about 4 mg/kg, about 5 mg/kg, or about 6, 7, 8, 9, 10, 15, 20, 25, 50, 75, or 100 mg/kg.

[00281] Nucleobase sequences shown herein are from left to right, 5' to 3', unless stated otherwise.

Transfections

[00282] In some experiments, translatable messenger molecules were transfected into Hepal-6 or AML12 cells in 96 well plates. The MessengerMAX transfection reagent (Thermo Fisher Scientific) was used by manufacture instruction for all transfections. Other suitable cell lines include HEK293 and Hep3B cells.

[00283] An example transfection protocol in vitro was as follows:

[00284] Plate hepatocyte Hepal-6 cells 5000 cells per well in 96 well plate at least 8 hours before transfection.

[00285] Replace 90 μL DMEM medium containing 10% FBS and Non-essential amino acid) adding 90 μL into each well of 96 well plate immediately before beginning the transfection experiment.

[00286] Prepare MessengerMAX transfection reagent (Thermo Fisher Scientific) translatable molecule complex according to manufacturer's instruction.

[00287] Transfer 10 μL of the complex into a well containing the cells in the 96-well plate.

[00288] Collect the medium after desired time points and add 100 μL fresh medium into each well. Medium will be kept at -80˚C until an ELISA assay for AGL is performed using the standard manufacturer protocol.

[00289] An example of a transfection protocol *in vivo* was as follows:

[00290] The translatable molecule is formulated with nanoparticles.

[00291] Inject the nanoparticle-formulated translatable molecule (1 mg/kg) into BL57BL/c mice (4-6 week-old) via standard i.v. injection in the lateral tail vein.

[00292] Collect approximately 50 μL of blood in a Heparin-coated microcentrifuge tube at a suitable time post-injection.

[00293] Centrifuge at 3,000 X g for 10 minutes at 4°C.

[00294] Transfer the supernatant (plasma) into a fresh microcentrifuge tube. Plasma will be kept at -80°C until an ELISA assay for AGL is performed using the standard manufacturer protocol.

Nanoyarticle Formulations

[00295] Lipid nanoparticles can be prepared containing an mRNA, using appropriate volumes of lipids in an ethanol/aqueous buffer containing the mRNA. A Nanossemblr microfluidic device can be used for this purpose, followed by downstream processing. For example, to prepare nanoparticles, a desired amount of targeted mRNA can be dissolved into 5 mM Citric Acid buffer (pH 3.5). The lipids can be dissolved at the adequate molar ratio, in ethanol. The molar percentage ratio for the constituent lipids can be, for example, 50% ionizable lipid, 7% DSPC (l,2-distearoyl-sn-glycero-3-phosphocholine; Avanti Polar Lipids), 40% cholesterol (Avanti Polar Lipids), and 3% DMG-PEG (1,2-Dimyristoyl-sn-glycerol, methoxypoly ethylene glycol, PEG chain molecular weight: 2000; NOF America Corporation). Next, the lipid and mRNA solutions can be combined in the microfluidic device (Precision NanoSystems) at a flow ratio of 1:3 (ethanol: aqueous phase). The total combined flow rate can be 12 mL/min. Lipid nanoparticles can be formed and subsequently purified by overnight dialysis using a phosphate buffer in a dialysis device (Float-a-lyzer, Spectrum Labs), followed by concentration using Amicon Ultra-15 centrifugal filters (Merck Millipore). The particle size can be determined by dynamic light scattering (ZEN3600, Malvern Instruments). An "encapsulation" efficiency can be calculated by determining the un-encapsulated mRNA content measured by the fluorescence upon the addition of RiboGreen (Molecular Probes) to the LNP slurry (Fi); then, the value was compared to the total mRNA content that is obtained upon lysis of the LNPs by 1% Triton X-100 (Ft), where percentage of "encapsulation" = (Ft - Fi)/Ft × 100. Encapsulation can refer to inclusion of the mRNA in the nanoparticle, regardless of form.

In-Cell Western

[00296] 96-well collagen plates were used to seed the cells at the appropriate density in DMEM/FBS culture media. At the optimal confluence, cells were transfected with the targeted mRNAs diluted in the transfection reagent mix (MessengerMax and Opti-MEM). Cells were placed in the C02 incubator and let them grow. At the desire timepoint, media was removed and cells were fixed in 4% fresh PFA for 20min. After that, fixative was removed and cells were permeabilized in TBST for 5 minutes several times. When permeabilization washes are complete, cells were incubated with the blocking buffer for 45 min. Primary antibody was then added and incubated for 1h at room temperature. Following that, cells were washed several times in TBST, and then incubated for 1h with the secondary antibody diluted in blocking buffer and containing the CellTag 700 stain. To finalize, cells were washed several times in TBST followed by a last wash in TBS. Then, plate was imaged using the Licor detection system and data was normalized to the total number of cells labeled by the CellTag 700.

Generating Tail PCR Products

[00297] Plasmid DNA (10 ng) containing each mRNA expression construct can be used to generate the poly A tail 120 PCR products in a 50 µï PCR reaction with 2X KAPA HiFi PCR mix (KR0370) as per the manufacturer's instructions. The product can be then checked on a 2% gel from Thermo Fisher Scientific and approximately quantified based on the intensity of the low molecular weight ladder (Thermo Fisher Scientific, 10068-013), and cleaned with the Qiagen PCR purification kit and resuspended in 50ul water.

In vitro Transcription (IVT) for Synthesis

[00298] The following protocol is for a 200 µï IVT reaction using NEB HiScribe T7 RNA polymerase reagents, which should yield about 1 mg of RNA. 2.5X NTP mix was prepared as required by thawing individual lOOmM NTP stocks (ATP, GTP, CTP, and UTP nucleotides, or chemically modified counterparts) and pooling them together. For the IVT reaction, about 2-4 µg of the template was used for a 200 µï reaction. The 10X IVT reaction buffer, the 2.5X dNTP mix, the template DNA and the T7 RNA polymerase are mixed well by pipetting and incubated at 37°C for 4 hours. To degrade the DNA template, the IVT reaction

is diluted with 700ul of nuclease-free water and then 10X DNase I buffer and 20ul of the RNase-free DNase I are added to the IVT mix and incubated at 37°C for 15 minutes. The diluted (to 1 ml) and DNase treated reaction is then purified by a Qiagen RNeasy Maxi columns as per the manufacturer's instructions with a final elution in RNase-free water. The purified RNA is then quantified by UV absorbance where the A260/A280 should be about 1.8-2.2, depending on the resuspension buffer used.

Enzymatic Capping of IVT RNA

[00299] For enzymatic capping, a 50X scaled-up version of NEB's one-step capping and 2'**0** -methylation reaction can be used, that is suitable for treating up to lmg of IVT transcripts. A 10 μg RNA in a 20 μΐ reaction is recommended, based on the assumption that transcript length would be as short as 100 nt. However, a higher substrate-to-reaction volume is acceptable for transcripts, which can be generally longer (about 300-600 nt) in length. Before initiating the capping reaction, the RNA is denatured at 65°C for 5 minutes and then snap chilled to relieve any secondary conformations. For the total 1 ml capping reaction, 1 mg denatured RNA in 700 μΐ of nuclease-free water is used along with 100 μΐ (10X) capping buffer, 50 μΐ (10 mM) GTP, 50 μΐ (4 mM) SAM, 50 μΐ of (10 U/μI) Vaccinia capping enzyme and 50 μΐ of mRNA cap 2'**-0** -methyltransferase at (50 U/μI) are combined and incubated at 37°C for 1 hour. The resulting capped mRNA is eluted using RNase free water, re-purified on an RNeasy column, quantified by nanodrop. The mRNA is also visualized on the gel by running 500 ng of the purified product per lane in a denaturing gel after denaturation and snap-chill to remove secondary structures.

EXAMPLES

[00300] **Example 1: Reference translatable molecule 534.**

[00301] In this example, a reference translatable molecule 534 was made and used for expressing human WT amylo-alpha-1 , 6-glucosidase, 4-alpha-glucanotransferase (AGL). The translatable molecule comprised a 5' cap (7mGpppG), a 5' UTR of TEV, a Kozak sequence, a WT AGL CDS (SEQ ID NO: 1), a 3'UTR of Xenopus beta-globin, and a Poly(A) tail region consisting of 114 As ***(i.e.,*** "Poly(A) 114 tail region"). The reference translatable molecule further comprised the sequence of SEQ ID NO: 40 immediately downstream of the AGL CDS.

This reference translatable molecule was synthesized with N^methylpseudouridine in place of uridine.

[00302] Details of the structure of this reference translatable molecule are as follows: Tobacco Etch Virus (TEV) 5' UTR of SEQ ID NO: 3, a Kozak Sequence of SEQ ID NO: 4, a Xenopus beta-globin (XBG) 3' UTR of SEQ ID NO: 5, and a Poly(A) 114 Tail of SEQ ID NO: 6.

[00303] Translatable molecules in the examples below can be synthesized with the 5' cap being a m7GpppGm cap. The translatable molecules in the examples below can contain a 5'-UTR *(e.g.,* a 5' UTR of TEV (SEQ ID NO: 3)), a translation initiation sequence *(e.g.,* a Kozak sequence of SEQ ID NO: 4), a sequence of SEQ ID NO: 40, a 3' UTR *(e.g.,* a 3' UTR of Xenopus beta-globin (SEQ ID NO: 5)), and a poly(A) tail *(e.g.,* a polyA tail of SEQ ID NO: 6, SEQ ID NO: 38, or SEQ ID NO: 39).

[00304] **Example 2: Translatable molecules encoding** AGL.

[00305] In this example, translatable molecules 522-533, 546, 730-740, and 1783-1784 were made and used for expressing human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL) with advantageously increased efficiency of translation. These translatable molecules expressing human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL) exhibited activity suitable for use in methods for ameliorating or treating GSD III. These translatable molecules comprised a 5' cap (7mGpppG), a 5' UTR of TEV, a Kozak sequence, an AGL CDS, and a 3'UTR of Xenopus beta-globin. Translatable molecules 522-533, 546, and 1783-1784 further comprise a Poly(A) 114 tail region. Translatable molecule 730 further comprises a Poly(A) 100 tail region, while translatable molecules 731-740 further comprise a Poly(A) 110 tail region. Translatable molecules 522-533, 546, 730-740, and 1783-1784 further comprise the sequence of SEQ ID NO: 40 immediately downstream of the AGL CDS. Two additional translatable molecules - 2258 and 2259 - were developed that are identical to 546 and 1783, respectively, except that they contain a Poly(A) 100 tail region as opposed to a Poly(A) 114 tail region. The coding sequence of 1783 and 2259 may optionally be modified to contain 12 nucleotide differences, as reflected in SEQ ID NO: 45. The translatable molecules described in this example were synthesized with N^methylpseudouridine in place of uridine

[00306] The AGL CDS in each of the translatable molecules is comprised of the following sequences:

Molecule	AGL CDS
522	SEQ ID NO: 7
523	SEQ ID NO: 8
524	SEQ ID NO: 9
525	SEQ ID NO: 10
526	SEQ ID NO: 11
527	SEQ ID NO: 12
528	SEQ ID NO: 13
529	SEQ ID NO: 14
530	SEQ ID NO: 15
531	SEQ ID NO: 16
532	SEQ ID NO: 17
533	SEQ ID NO: 18
546 & 2258	SEQ ID NO: 19
730	SEQ ID NO: 20
731	SEQ ID NO: 21
732	SEQ ID NO: 22
733	SEQ ID NO: 23
734	SEQ ID NO: 24
735	SEQ ID NO: 25
736	SEQ ID NO: 26
737	SEQ ID NO: 27
738	SEQ ID NO: 28
739	SEQ ID NO: 29
740	SEQ ID NO: 30
1783 & 2259	SEQ ID NO: 31
1784	SEQ ID NO: 32

[00307] The translatable molecules of this example were translated in AML12 and C2C12 cells to produce human AGL.

[00308] **Example 3: Translation enhancer based on Xenopus beta-globin 3'UTR.**

[00309] In this example, the structures of 3' UTR sequences for use in enhancing translational efficiency of a translatable molecule are shown.

[00310] The base sequences shown in SEQ ID NOs: 33-37 are the portion of the translatable molecule that may correspond in functionality to the 3'-UTR of Xenopus beta-globin. The complete translatable molecule comprises a 5' cap (m7GpppGm), 5'-UTR, and coding region (CDS) upstream of the sequence below, and a polyA tail downstream of the sequence below, each of which corresponds to the structure of a native human mRNA. As shown above, a Kozak sequence may optionally be used. Thus, a translatable molecule incorporating the fragment below can have enhanced translational efficiency. The Xenopus beta-globin gene sequence is shown in accession no. NM_00 1096347.1

[00311] Example 4: AGL Expression in Human Primary Hepatocytes

[00312] In this example, human primary hepatocytes were transfected with codon-optimized mRNA molecules 546, 1783, and 1784. AGL protein expression was measured by In-Cell Western™ at 6, 24, 48, and 72 hours post-transfection. The expression of the mRNA sequences as compared with an untreated control ("unt") is shown in FIG. 5.

[00313] Example 5: In vivo Analysis of AGL Protein Expression in Wild-Type Mice

[00314] In this example, wild-type C57BL/6 mice were injected with human AGL mRNA formulated with lipid nanoparticles. Mice were sacrificed 6 hours post-injection. Liver biopsy samples were taken from mice, and human and mouse AGL protein expression in liver homogenates was analyzed. FIG 6. shows ectopic expression of human AGL protein from various mRNA molecules. FIG 7. shows mouse AGL protein levels, indicating similar levels of endogenous expression of mouse AGL protein across the treated mice. Translatable molecule 546.7 - as shown in FIGs. 6 and 7 - has an identical nucleobase sequence to translatable molecule 546, but was synthesized with 5-methoxyuridine in place of uridine instead of N^methylpseudouridine.

[00315] Example 6; mRNA Treatment Reduces Glycogen Accumulation in GSD3 Mice

[00316] In this example, AGL knockout mice were treated with vehicle or translatable molecule 546 formulated with ATX2 lipid nanoparticles. Livers from knockout mice treated with vehicle ("VEH") showed marked to severe vacuolation of hepatocytes and moderate to marked increases in glycogen accumulation within hepatocytes (FIG. 8). In contrast, livers from knockout mice treated with translatable molecule 546 formulated with ATX2 lipid nanoparticles had only mild to moderate vacuolation of hepatocytes and only mild to moderate increases in glycogen accumulation within hepatocytes (FIG. 9). Based upon the histopathology results shown in this example, there appears to be a reduction in the severity of hepatocellular vacuolization and glycogen accumulation in livers from knockout mice treated with mRNA compared with KO mice treated with vehicle.

[00317] Example 7: Additional Translatable Molecules Expressing AGL

[00318] Four additional translatable molecules - 1970, 1987, SD1, and SD2 - were designed with additionally modified codon-optimized human AGL coding sequences shown in SEQ ID NOs: 41, 42, 43, and 44, respectively. Translatable molecules 1970, 1987, SD1, and SD2 further comprise a 5' cap (7mGpppG), a 5' UTR of TEV, a Kozak sequence, a sequence

of SEQ ID NO: 40 immediately downstream of the coding sequence, a 3' UTR of Xenopus beta-globin, and a Poly(A) tail region *(e.g.,* a poly(A) 100, 110, or 114 tail region). These translatable molecules may optionally be synthesized with either N^methylpseudouridine or 5-methoxyuridine in place of uridine.

[00319] All publications, patents and literature specifically mentioned herein are incorporated by reference for all purposes.

[00320] It is understood that this invention is not limited to the particular methodology, protocols, materials, and reagents described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention, which will be encompassed by the appended claims.

[00321] It must be noted that as used herein and in the appended claims, the singular forms "a", "an", and "the" include plural reference unless the context clearly dictates otherwise. As well, the terms "a" (or "an"), "one or more" and "at least one" can be used interchangeably herein. It is also to be noted that the terms "comprises," "comprising", "containing," "including", and "having" can be used interchangeably.

[00322] Without further elaboration, it is believed that one skilled in the art can, based on the above description, utilize the present invention to its fullest extent. The following specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

[00323] All of the features disclosed in this specification may be combined in any combination. Each feature disclosed in this specification may be replaced by an alternative feature serving the same, equivalent, or similar purpose.

WHAT IS CLAIMED IS:

1. A polynucleotide for expressing a human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL), or a fragment thereof, wherein the polynucleotide comprises natural and chemically-modified nucleotides and is expressible to provide the human AGL or a fragment thereof having AGL activity.

2. The polynucleotide of claim 1, wherein the polynucleotide is codon-optimized as compared to human AGL wild type mRNA.

3. The polynucleotide of claim 1, wherein the chemically-modified nucleotides are selected from

5-hydroxycytidine, 5-methylcytidine, 5-hydroxymethylcytidine, 5-carboxycytidine, 5-formylcytidine, 5-methoxycytidine, 5-propynylcytidine, 2-thiocytidine;

5-hydroxyuridine, 5-methyluridine, 5,6-dihydro-5-methyluridine, 2'-0-methyluridine, 2'-0-methy 1-5 -methyluridine, 2'-fluoro-2'-deoxyuridine, 2'-amino-2'-deoxyuridine, 2'-azido-2'-deoxyuridine, 4-thiouridine, 5-hydroxymethyluridine, 5-carboxyuridine, 5-carboxymethylesteruridine, 5-formyluridine, 5-methoxyuridine, 5-propynyluridine, 5-bromouridine, 5-iodouridine, 5-fluorouridine;

pseudouridine, 2'-0-methyl-pseudouridine, N^hydroxypseudouridine, N^1-methylpseudouridine, 2'-0-methyl-N^1-methylpseudouridine, N^ethylpseudouridine, N^1-hydroxymethylpseudouridine, and Arauridine;

N^6-methyladenosine, 2-aminoadenosine, 3-methyladenosine, 7-deazaadenosine, 8-oxoadenosine, inosine;

thienoguanosine, 7-deazaguanosine, 8-oxoguanosine, and 6-O-methylguanine.

4. The polynucleotide of claim 1, wherein the chemically-modified nucleotides are N^1-methylpseudouridines.

5. The polynucleotide of claim 1, wherein the chemically-modified nucleotides are 5-methoxyuridines.

6. The polynucleotide of claim 1, wherein the chemically-modified nucleotides are a combination of pseudouridines and N^methylpseudouridines.

7. The polynucleotide of claim 1, wherein the chemically-modified nucleotides are a combination of 5-methylcytidines and N^methylpseudouridines.

8. The polynucleotide of claim 1, wherein the chemically-modified nucleotides are a combination of 5-methoxyuridines andN^methylpseudouridines.

9. The polynucleotide of claim 1, wherein the chemically-modified nucleotides are a combination of 5-methoxyuridines, 5-methylcytidines and N^methylpseudouridines.

10. The polynucleotide of any one of the preceding claims, wherein the translation efficiency of the polynucleotide is increased at least 50% as compared to human AGL wild type mRNA.

11. The polynucleotide of any one of the preceding claims, wherein the translation efficiency of the polynucleotide is increased at least three-fold as compared to human AGL wild type mRNA.

12. The polynucleotide of any one of the preceding claims, wherein the polynucleotide comprises from 200 to 12,000 nucleotides.

13. The polynucleotide of any one of the preceding claims, wherein chemically-modified nucleotides comprise 1-99% of the nucleotides.

14. The polynucleotide of any one of the preceding claims, wherein chemically-modified nucleotides comprise 50-99% of the nucleotides.

15. The polynucleotide of claim 1, wherein the polynucleotide comprises a 5' cap, a 5' untranslated region, a coding region, a 3' untranslated region, and a tail region.

16. The polynucleotide of claim 1, wherein the polynucleotide comprises a translation enhancer.

17. The polynucleotide of claim 1, wherein the polynucleotide is translatable in a mammalian cell to express the human AGL or a fragment thereof having AGL activity.

18. The polynucleotide of claim 1, wherein the polynucleotide is translatable in a subject *in vivo* to express the human AGL or a fragment thereof having AGL activity.

19. The polynucleotide of claim 1, wherein a translation product of the polynucleotide is an active human AGL or a fragment thereof having AGL activity.

20. The polynucleotide of claim 1, wherein the polynucleotide has reduced immunogenicity as compared to a human AGL wild type mRNA.

21. The polynucleotide of claim 1, wherein the polynucleotide comprises a nucleobase sequence selected from SEQ **ID** NOs: 7-32 or SEQ **ID** NOs: 41-45.

22. A translatable oligomer for expressing a human amylo-alpha-1 , 6-glucosidase, 4-alpha-glucanotransferase (AGL), or a fragment thereof, wherein the oligomer comprises natural and chemically-modified nucleotides, one or more UNA monomers, and is expressible to provide the human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL) or a fragment thereof having AGL activity.

23. The oligomer of claim 22, wherein the oligomer is codon optimized as compared to human AGL wild type mRNA.

24. The oligomer of claim 22, wherein the translation efficiency of the oligomer is increased at least 50% as compared to human AGL wild type mRNA.

25. The oligomer of claim 22, wherein the translation efficiency of the oligomer is increased at least three-fold as compared to human AGL wild type mRNA.

26. The oligomer of claim 22, wherein the chemically-modified nucleotides are selected from

5-hydroxycytidine, 5-methylcytidine, 5-hydroxymethylcytidine, 5-carboxycytidine, 5-formylcytidine, 5-methoxycytidine, 5-propynylcytidine, 2-thiocytidine;

5-hydroxyuridine, 5-methyluridine, 5-hydroxymethyluridine, 5-carboxyuridine, 5-carboxymethylesteruridine, 5-formyluridine, 5-methoxyuridine, 5-propynyluridine, 5-bromouridine, 5-fluorouridine, 5-iodouridine, 5,6-dihydro-5-methyluridine, **2'-0-**methyluridine, 2'**-0** -methyl-5-methyluridine, 2'-fluoro-2'-deoxyuridine, 2'-amino-2'-deoxyuridine, 2'-azido-2'-deoxyuridine;

pseudouridine, 2'**-0** -methyl-pseudouridine, N^hydroxypseudouridine, N^1-methylpseudouridine, N^hydroxymethylpseudouridine, 2'**-0** -methyl-N^1-methylpseudouridine, N^ethylpseudouridine, Arauridine;

N^6-methyladenosine, 2-aminoadenosine, 3-methyladenosine, 7-deazaadenosine, 8-oxoadenosine, inosine;

thienoguanosine, 7-deazaguanosine, 8-oxoguanosine, and 6-O-methylguanine.

27. The oligomer of any one of claims 22-26, wherein the chemically-modified nucleotides comprise 1-99% of the nucleotides.

28. The oligomer of any one of claims 22-27, wherein the oligomer comprises a 5' cap, a 5' untranslated region, a coding region, a 3' untranslated region, and a tail region.

29. The oligomer of claim 22, wherein the oligomer comprises a translation enhancer.

30. The oligomer of claim 22, wherein the oligomer is translatable in a mammalian cell to express the human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL) or a fragment thereof having AGL activity.

31. The oligomer of claim 22, wherein a translation product of the oligomer is an active human amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase or a fragment thereof having AGL activity.

32. The oligomer of claim 22, wherein the oligomer has reduced immunogenicity as compared to a human AGL wild type mRNA.

33. The oligomer of any one of claims 22-32, wherein the oligomer comprises a nucleobase sequence selected from SEQ ID NOs: 7-32 or SEQ ID NOs: 41-45.

34. A polynucleotide comprising a nucleobase sequence that is at least 90% identical to a nucleobase sequence selected from SEQ ID NOs: 7-32 or SEQ ID NOs: 41-45.

35. The polynucleotide of claim 34, wherein the polynucleotide comprises a nucleobase sequence that is at least 95% identical to a nucleobase sequence selected from SEQ ID NOs: 7-32 or SEQ ID NOs: 41-45.

36. The polynucleotide of claim 34, wherein the polynucleotide comprises a nucleobase sequence that is at least 99% identical to a nucleobase sequence selected from SEQ ID NOs: 7-32 or SEQ ID NOs: 41-45.

37. The polynucleotide of claim 34, wherein the polynucleotide comprises a nucleobase selected from SEQ ID NOs: 7-32 or SEQ ID NOs: 41-45.

38. A composition comprising one or more polynucleotides of any of claims 1-21 or claims 34-37, and a pharmaceutically acceptable carrier.

39. A composition comprising one or more oligomers of any of claims 22-33 and a pharmaceutically acceptable carrier.

40. A composition comprising one or more polynucleotides of any of claims 1-21 or claims 34-37, and one or more oligomers of any of claims 22-33 and a pharmaceutically acceptable carrier.

41. The composition of any one of claims 38 to 40, wherein the carrier comprises a transfection reagent, a nanoparticle, or a liposome.

42. A composition of any of claims 38 to 40 for use in medical therapy.

43. A composition of any of claims 38 to 40 for use in the treatment of the human or animal body.

44. The use of a composition of any of claims 38 to 40 for preparing or manufacturing a medicament for ameliorating, preventing, delaying onset, or treating a disease or disorder associated with reduced activity of amylo-alpha-1 , 6-glucosidase, 4-alpha-glucanotransferase (AGL) in a subject need thereof.

45. The use of claim 44, wherein the disease is glycogen storage disease type III.

46. The use of claim 45, wherein the glycogen storage disease type III is selected from glycogen storage disease type Ilia, glycogen storage disease type Illb, glycogen storage disease type IIIc, and glycogen storage disease type Hid.

47. A method for ameliorating, preventing, delaying onset, or treating a disease or disorder associated with reduced activity of amylo-alpha-1 , 6-glucosidase, 4-alpha-glucanotransferase (AGL) in a subject need thereof, the method comprising administering to the subject a composition of any of claims 38-40.

48. The method of claim 47, wherein the disease is glycogen storage disease type III.

49. The method of claim 48, wherein the glycogen storage disease type III is selected from glycogen storage disease type Ilia, glycogen storage disease type Illb, glycogen storage disease type IIIc, and glycogen storage disease type Hid.

50. The method of any of claims 47-49, wherein the administration is intravenous, subcutaneous, pulmonary, intramuscular, intraperitoneal, dermal, oral, nasal, or inhalation.

51. The method of any of claims 47-50, wherein the administration is once daily, weekly, biweekly, or monthly.

52. The method of any of claims 47-51, wherein the administration comprises an effective dose of from 0.01 to 10 mg/kg.

53. The method of any of claims 47-52, wherein the administration increases expression of AGL in the liver, serum, plasma, kidney, heart, muscle, brain, cerebrospinal fluid, or lymph nodes of the subject.

54. The method of claim 47, wherein after administration the level of AGL in the liver of the subject is from 10 to 1500 ng/mg of total liver protein.

55. The method of claim 47, wherein after administration the level of AGL in the liver of the subject is from 20 to 150 ng/mg of total liver protein.

56. A kit for expressing a human AGL *in vivo*, the kit comprising a 0.1 to 500 mg dose of one or more polynucleotides of any of claims 1-21 or claims 34-37, or one or more oligomers of any of claims 22-33 and a device for administering the dose.

57. The kit of claim 56, wherein the device is an injection needle, an intravenous needle, or an inhalation device.

58. A polynucleotide comprising a nucleobase sequence that is less than 80% identical to the wild-type human AGL coding sequence over the full length human AGL coding sequence of SEQ ID NO: 1, and wherein the human AGL coding sequence is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to a sequence selected from SEQ ID NOs: 7-32 or SEQ ID NOs: 41-45.

59. A polynucleotide consisting of a nucleobase sequence that is less than 80% identical to the wild-type human AGL coding sequence over the full length human AGL coding sequence

of SEQ ID NO: 1, and wherein the human AGL coding sequence is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to a sequence selected from SEQ ID NOs: 7-32 or SEQ ID NOs: 41-45.

60. A polynucleotide comprising a nucleobase sequence that is less than 80% identical to the wild-type human AGL coding sequence over the full length human AGL coding sequence of SEQ ID NO: 1, and wherein the human AGL coding sequence is at least 95% identical to SEQ ID NO: 19.

61. A polynucleotide comprising a nucleobase sequence that is less than 80% identical to the wild-type human AGL coding sequence over the full length human AGL coding sequence of SEQ ID NO: 1, and wherein the human AGL coding sequence is at least 95% identical to SEQ ID NO: 31.

62. A polynucleotide comprising a nucleobase sequence that is less than 80% identical to the wild-type human AGL coding sequence over the full length human AGL coding sequence of SEQ ID NO: 1, and wherein the human AGL coding sequence is at least 95% identical to SEQ ID NO: 45.

63. A polynucleotide comprising a nucleobase sequence of SEQ ID NO: 19.

64. A polynucleotide comprising a nucleobase sequence of SEQ ID NO: 31.

65. A polynucleotide comprising a nucleobase sequence of SEQ ID NO: 45.

FIG. 1

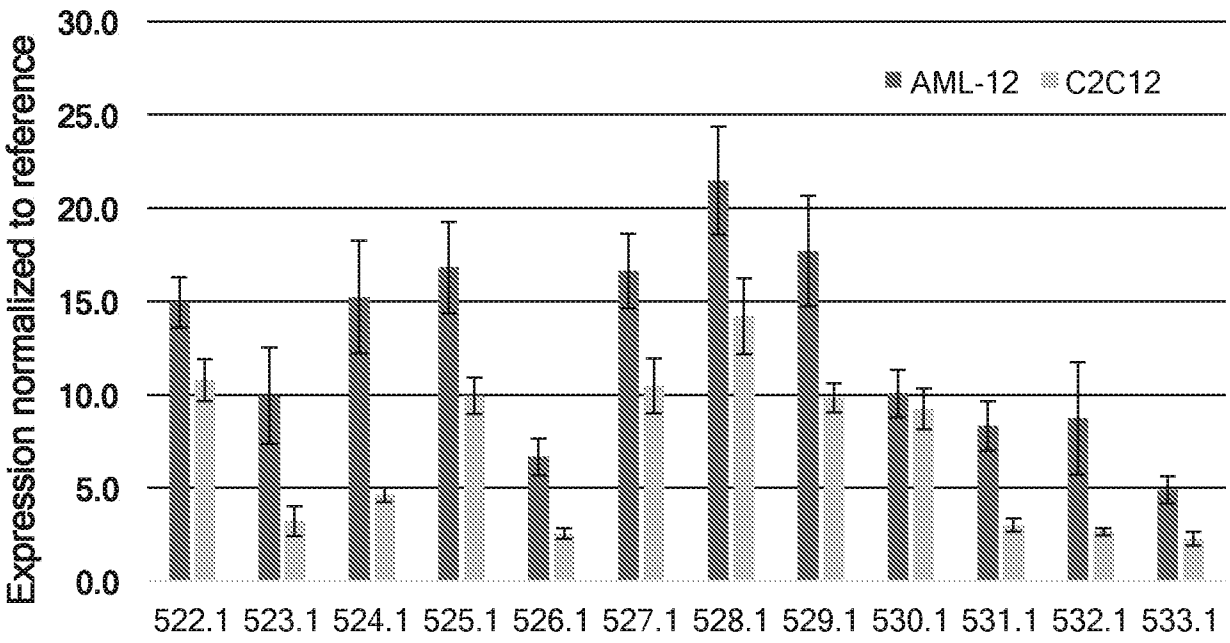

Expression normalized to reference
30.0
25.0
20.0
15.0
10.0
5.0
0.0
AML-12
C2C12
522.1
523.1
524.1
525.1
526.1
527.1
528.1
529.1
530.1
531.1
532.1
533.1

FIG. 2

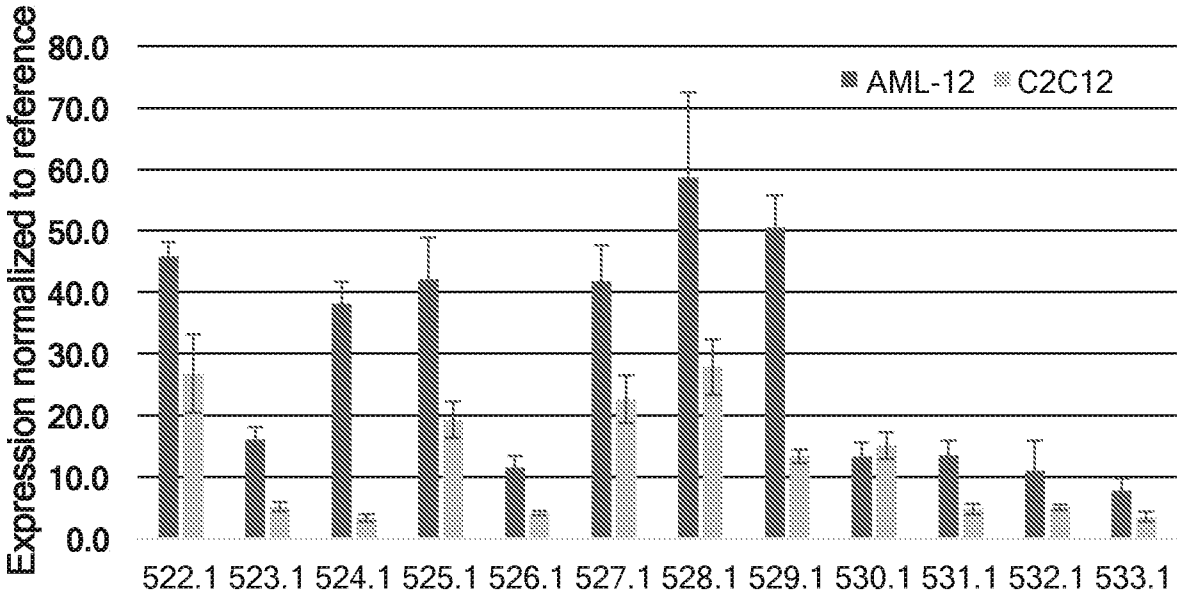

Expression normalized to reference
80.0
70.0
60.0
50.0
40.0
30.0
20.0
10.0
0.0
AML-12
C2C12
522.1
523.1
524.1
525.1
526.1
527.1
528.1
529.1
530.1
531.1
532.1
533.1

Fig. 3 AGL expression in WT mice

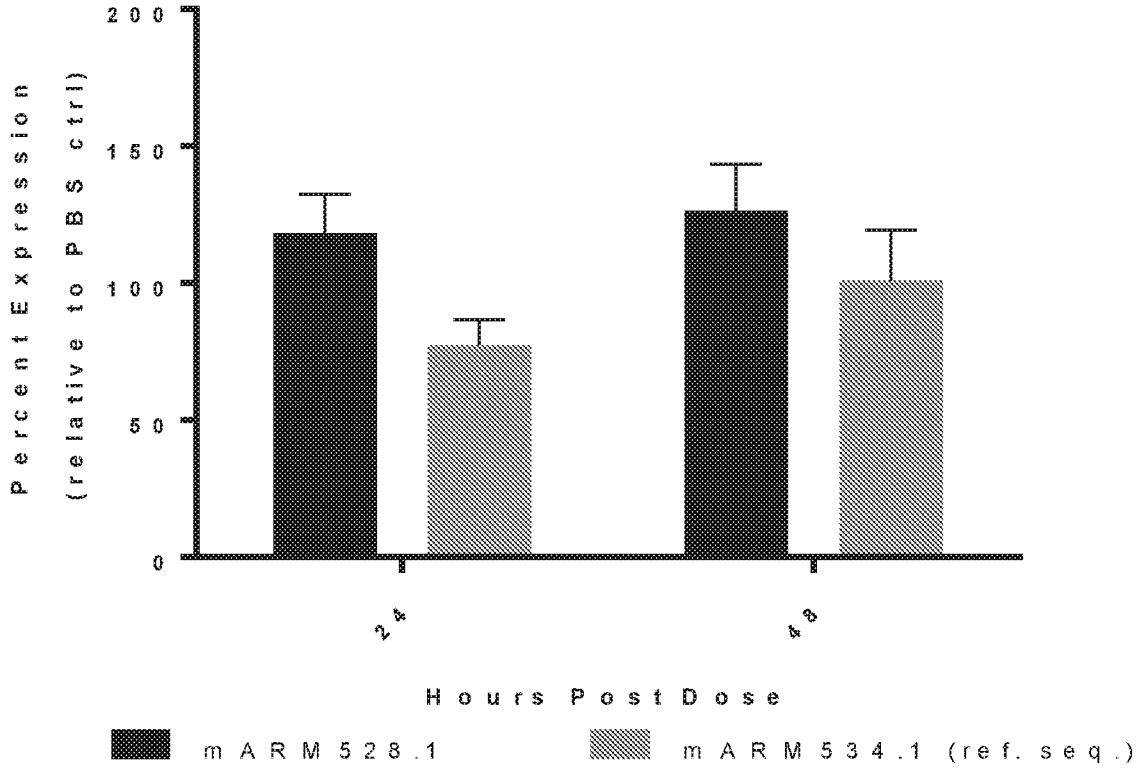


Fig. 4 AGL expression in WT mouse liver

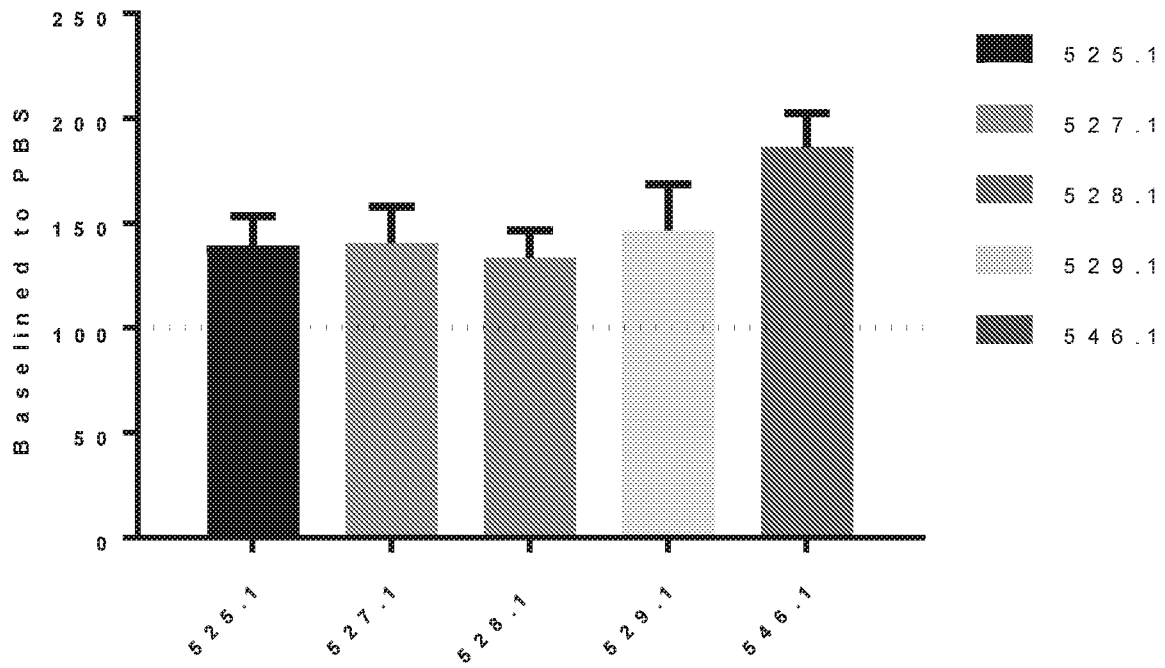


FIG. 5

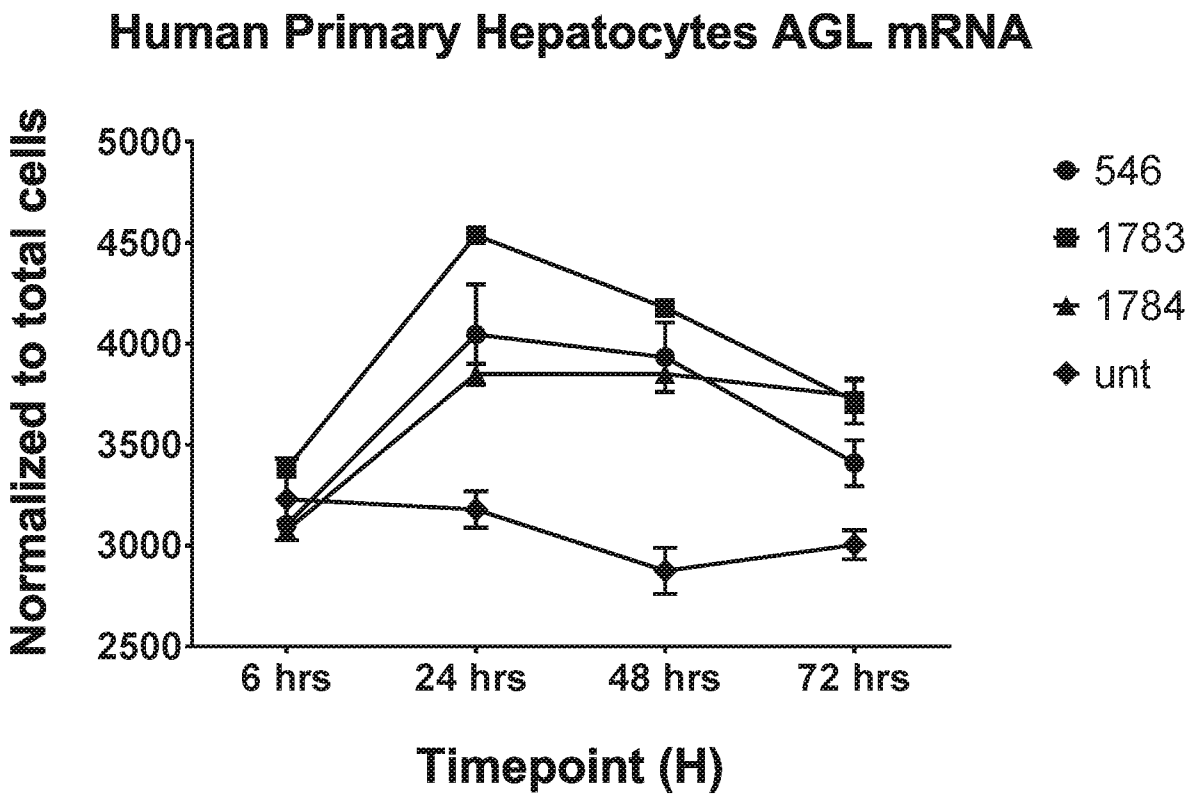

Human Primary Hepatocytes AGL mRNA
Normalized to total cells
5000
4500
4000
3500
3000
2500
6 hrs
24 hrs
48 hrs
72 hrs
Timepoint (H)
546
1783
1784
unt

FIG. 6

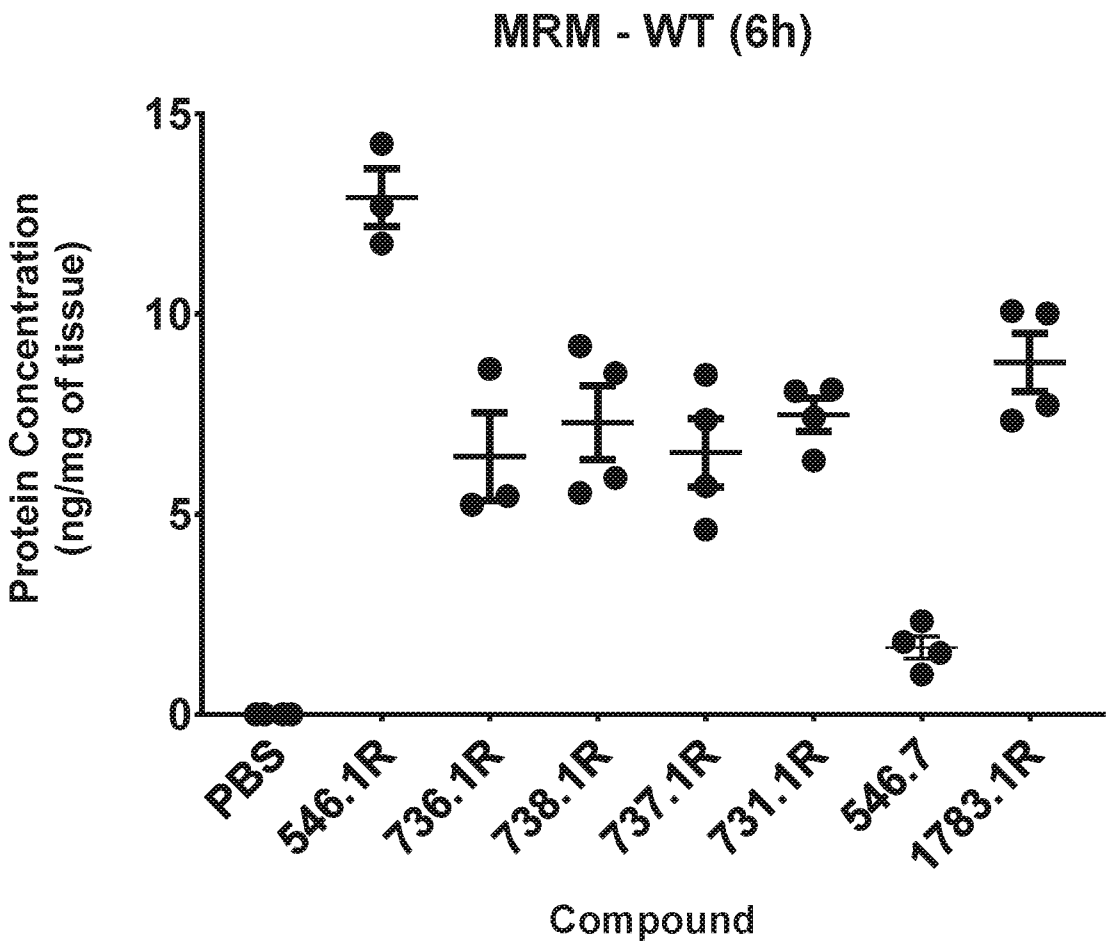

MRM - WT (6h)
Protein Concentration (ng/mg of tissue)
15
10
5
0
PBS
546.1R
736.1R
738.1R
737.1R
731.1R
546.7
1783.1R
Compound

FIG. 7

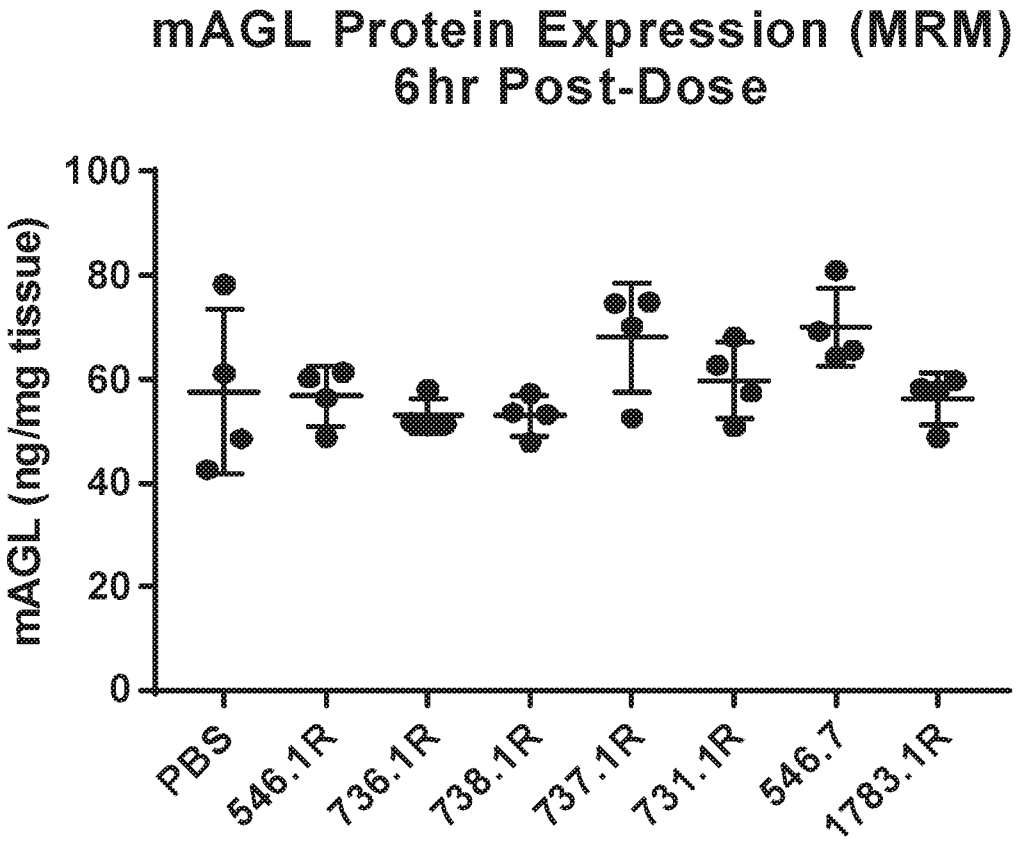

mAGL Protein Expression (MRM)
6hr Post-Dose
mAGL (ng/mg tissue)
100
80
60
40
20
0
PBS
546.1R
736.1R
738.1R
737.1R
731.1R
546.7
1783.1R

FIG. 8

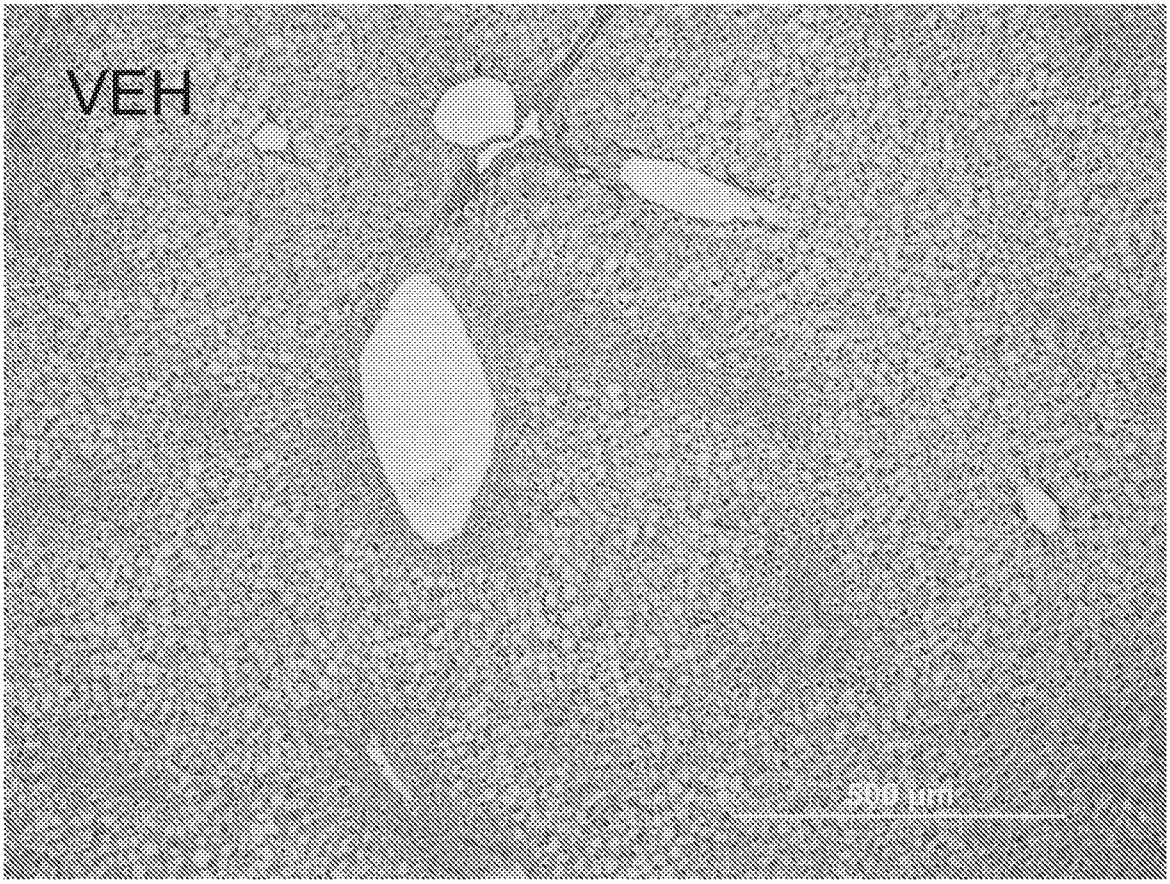
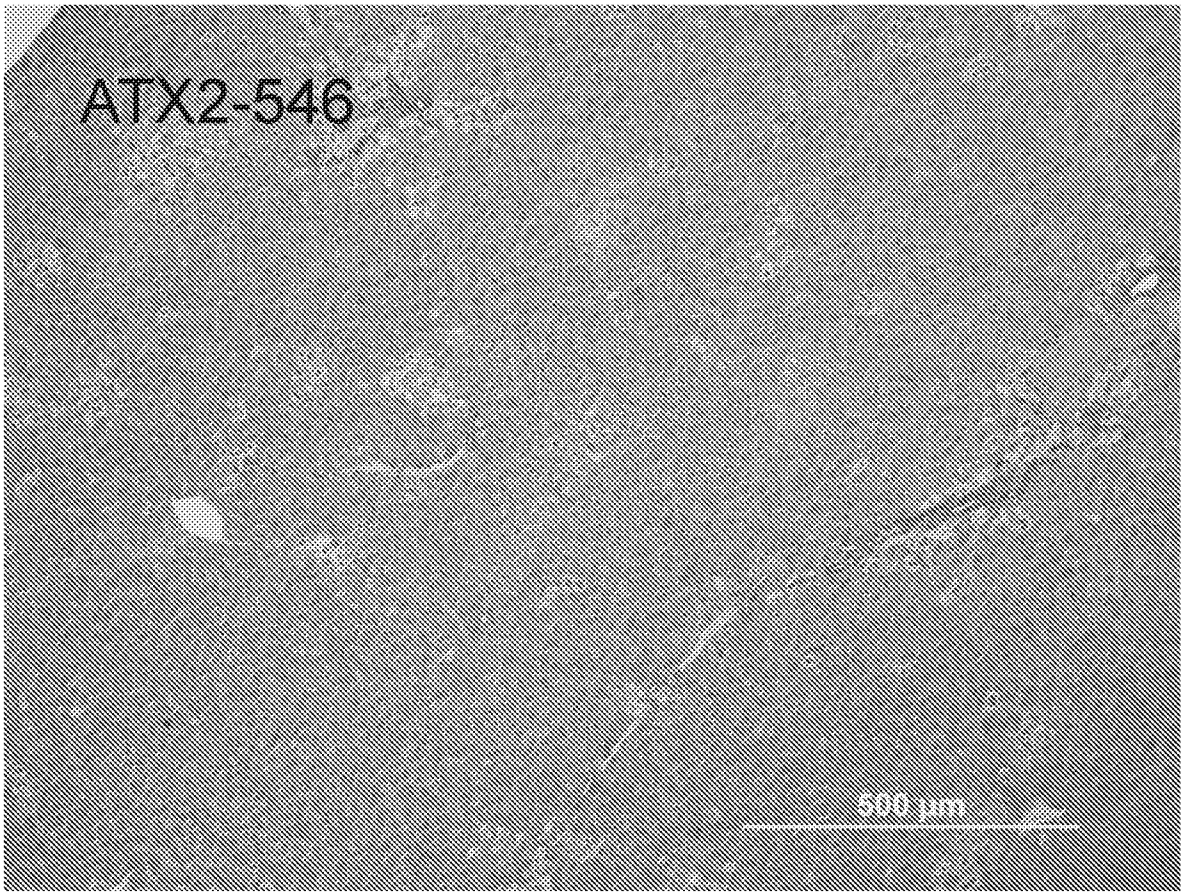


FIG. 9



INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 18/35477

A. CLASSIFICATION OF SUBJECT MATTER
IPC(8) - C12N 9/10, C07K 14/505, C07K 14/81 (2018.01)
CPC - C12N 9/1018, C12N 2840/60, C07K 14/505

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
See Search History Document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
See Search History Document

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
See Search History Document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- A	US 2016/0130567A1 (ARCTURUS THERAPEUTICS, INC.) 12 May 2016 (12.05.2016) para [0021]-[0024]; [0055]; [0056]; [0062]; [0131]-[0162]; [0212]; [0488]-[0491].	1-10, 15-20, 22-27, 29-32 --- 21
A	US 2013/0259924 A1 (MODERNA THERAPEUTICS) 03 October 2013 (03.10.2013) claim 2; para [0288]; Table 6; SEQ ID NO: 1707.	21, 34-37, 58, 59
A	Genbank Accession No. DQ048148 "Homo sapiens AGL gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence." 02-JUN-2005 [online]. [Retrieved on 2 Oct 2018]. Retrieved from the internet <URL: https://www.ncbi.nlm.nih.gov/nucgss/DQ048148> full sequence.	21, 34-37, 58, 59
A	WO 2017/054086 A1 (EXERKINE CORPORATION) 6 April 2017 (06.04.2017) para [0026]; [0086].	1

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search
02 October 2018

Date of mailing of the international search report
22 OCT 2018

Name and mailing address of the ISA/US
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PCT OSP: 571-272-7774

Form PCT/ISA/210 (second sheet) (January 2015)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 18/35477

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 11-14, 28, 33, 38-5/
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. Ill Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group l+, claims 1-10, 15-27, 29-32, 34-37 and 58-65, directed to a polynucleotide comprising a nucleobase sequence encoding a human amylo-alpha-1, 6-glucosidase, 4-alphaglucanotransferase (AGL). The polynucleotide will be searched to the extent that the AGL nucleobase sequence encompasses SEQ ID NO: 7. It is believed that claims 1-10, 15-27, 29-32, 34-37, 58 and 59 encompass this first named invention, and thus these claims will be searched without fee to the extent that the AGL nucleobase sequence encompasses SEQ ID NO: 7. Additional AGL nucleobase sequence(s) will be searched upon the payment of additional fees. Applicants must specify the claims that encompass any additionally elected AGL nucleobase sequence(s). Applicants must further indicate, if applicable, the claims which encompass the first named invention, if different than what was indicated above for this group. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched. An exemplary election would be a AGL nucleobase sequence comprising SEQ ID NO: 8 (claims 1-10, 15-27, 29-32, 34-37, 58 and 59).
-continued on first extra sheet-

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-10, 15-27, 29-32, 34-37, 58, 59 limited to SEQ ID NO: 7

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

No protest accompanied the payment of additional search fees.

International application No.
PCT/US 18/35477

-continued from Box III: Observations where unity of invention is lacking-

The inventions listed as Group I+ do not relate to a single special technical feature under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Special technical features

The inventions of Group I+ each include the special technical feature of a unique amino acid sequence. Each amino acid sequence encodes a unique peptide, and is considered a distinct technical feature.

No technical features are shared between the AGL nucleobase sequences of Group I+ and accordingly, this group lacks unity a priori.

Additionally, even if Group I+ were considered to share the technical features of including: a polynucleotide for expressing a human AGL, or a fragment thereof, wherein the polynucleotide comprises natural and chemically-modified nucleotides and is expressible to provide the human AGL or a fragment thereof having AGL activity, these shared technical features are previously disclosed by WO 2017/054086 A1 to EXERKINE CORPORATION, (hereinafter Exerkine).

Exerkine teaches a polynucleotide for expressing a human AGL, or a fragment thereof, wherein the polynucleotide comprises natural and chemically-modified nucleotides and is expressible to provide the human AGL or a fragment thereof having AGL activity (para [0026] "the protein is encoded by a gene selected from...Amylo-alpha-1, 6-glucosidase, 4-alpha- glucanotransferase (AGL)"; [0086] "a muscle protein or nucleic acid encoding the muscle protein for incorporation into exosomes according to the invention may be a functional native mammalian protein or nucleic acid, including for example, a protein or nucleic acid from human and non-human mammals, or a functionally equivalent protein or nucleic acid. ..includes all isoforms, variants, recombinant produced forms, and naturally -occurring or artificially modified forms. ..Nucleic acid modifications may include one or more base substitutions or alterations, addition of 5' or 3' protecting groups, and the like, preferably maintaining significant sequence similarity").

As the technical features were known in the art at the time of the invention, they cannot be considered special technical features that would otherwise unify the groups.

Therefore, Group I+ inventions lack unity under PCT Rule 13 because they do not share the same or corresponding special technical feature.

NOTE, claims 11-14, 28, 33, 38-57 are held unsearchable because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).