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

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
01 November 2018 (01.11.2018)

WIPO | PCT

(10) International Publication Number
WO 2018/201090 A1

(51) International Patent Classification:
A61K 31/7084 (2006.01) *A61K 9/51* (2006.01)
A61K 47/50 (2017.01) *C12N 15/00* (2006.01)
A61K 9/127 (2006.01)

(21) International Application Number:
PCT/US2018/030021

(22) International Filing Date:
27 April 2018 (27.04.2018)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/492,062 28 April 2017 (28.04.2017) US

(71) Applicant: **EXICURE, INC.** [US/US]; 8045 Lamon Avenue, Suite 410, Skokie, IL 6007-5318 (US).

(72) Inventors: **KANG, Richard**; 212 Thelin Ct., Wilmette, IL 60091 (US). **NALLAGATLA, Subbarao**; 8045 Lamon Avenue, Suite 410, Skokie, IL 60077-5318 (US). **ANDERSON, Bart**; 9408 Ozark Avenue, Morton Grove, IL 60053 (US). **KANDIMALLA, Ekambar**; 8045 Lamon Avenue, Suite 410, Skokie, IL 60077-5318 (US).

(74) Agent: **LOCKHART, Helen, C.**; Wolf, Greenfield & Sacks, P.C., 600 Atlantic Avenue, Boston, MA 02210-2206 (US).

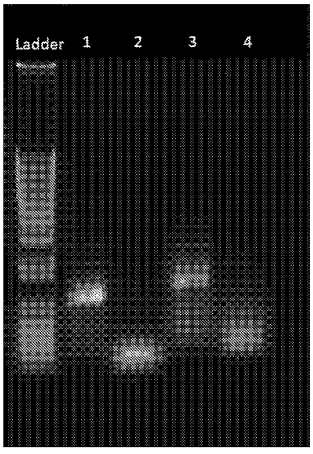
(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS,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

(54) Title: SYNTHESIS OF SPHERICAL NUCLEIC ACIDS USING LIPOPHILIC MOIETIES

(57) Abstract: Spherical nucleic acids (SNA) carrying self-aggregating oligonucleotides are described herein. Compositions of the SNA include discrete nanostructures that are not aggregated. Related methods are also described.

Figure 1



Lane #	Compound # or Oligo No.#
1	D
2	Oligo 1
3	F
4	Oligo 2

WO 2018/201090 A1

[Continued on next page]

Published:
— *with international search report (Art. 21(3))*
— *with sequence listing part of description (Rule 5.2(a))*

SYNTHESIS OF SPHERICAL NUCLEIC ACIDS USING LIPOPHILIC MOIETIES

BACKGROUND OF INVENTION

Spherical Nucleic Acids (SNAs) are a novel class of therapeutic agents that consist of oligonucleotides densely packed and radially oriented around spherical liposomal nanoparticles. SNAs by virtue of their 3-dimentional architecture exhibit the ability to enter cells without the need for auxiliary delivery vehicles or transfection reagents, by engaging scavenger receptors and lipid rafts. Previously, hydrophobic mono-lipophilic moieties, such as cholesterol or tocopherol have been used, and conjugated to oligonucleotides for synthesizing SNAs.

When using single lipophilic moiety, especially cholesterol, oligonucleotides containing G-rich or self-complementary motifs pose a particular challenge. If an oligonucleotide sequence contains self-complementary or G-rich motifs, and is functionalized to the liposome surface using a single lipophilic moiety, such as cholesterol, the resulting SNAs form a cloudy solution, tend to self-aggregate, and eventually precipitate out of solution. These SNA formulations are difficult to filter because the aggregates clog the filter. Bulk synthesis and long term storage are also problematic because the precipitated SNAs may not have the same properties and aggregates may have poor activity or cause unexpected side effects.

SUMMARY OF INVENTION

Some aspects of the present disclosure include a nanostructure comprising a spherical nucleic acid (SNA) comprising a core, a lipid shell having an inner surface surrounding the core and an outer surface with a oligonucleotide functionalized to the outer surface of the nanostructure by a moiety comprised of two or more lipophilic groups. In some embodiments, the core is a hollow or a solid core. In other embodiments, the core is a liposomal core. In some embodiments, the lipid shell is comprised of one type of lipid. In another embodiment, the lipid is a phospholipid. In another embodiment, the phospholipid is 1,2-dioleoyl-sn-glycero-3-phophocholine (DOPC).

In some embodiments, the moiety comprised of two or more lipophilic groups is attached to the oligonucleotide through a linker. In another embodiment, the linker is a hexaethyleneglycol linker. In other embodiments, the oligonucleotide is a single stranded oligonucleotide. In another embodiment, the oligonucleotide is an immunostimulatory

oligonucleotide. In another embodiment, the oligonucleotide contains a self-complementary motif. In another embodiment, the oligonucleotide contains a G-rich motif. In some embodiments, the immunostimulatory oligonucleotide stimulates a toll-like receptor (TLR). In another embodiment, the TLR is TLR9. In some embodiments, the oligonucleotide is an antisense oligonucleotide.

In some embodiments, the moiety comprised of the two or more lipophilic groups is a di-alkyl. In another embodiment, the moiety comprised of the two or more lipophilic groups is distearyl. In other embodiments, the moiety comprised of the two or more lipophilic groups is a tri-alkyl. In other embodiments, the moiety comprised of the two or more lipophilic groups is comprised by an alkyl chain. In another embodiment, the alkyl chain is comprised of at least 10 carbons. In another embodiment, the alkyl chain is comprised of at least 14 carbons.

In some embodiments, the nanostructure contains 26 to 7,000 oligonucleotides. In another embodiment, the nanostructure contains 26 to 500 oligonucleotides. In another embodiment, the nanostructure contains 26 to 80 oligonucleotides. In another embodiment, the nanostructure contains at least 40 oligonucleotides. In yet other embodiments, the nanostructure contains 26 to 5,000, 26 to 2,000, 26 to 1,000, 26 to 800, 25 to 500, 26 to 300, 26 to 200, 26 to 100, 50 to 5,000, 50 to 2,000, 50 to 1,000, 50 to 800, 50 to 500, 50 to 300, 50 to 200, 50 to 100, 100 to 5,000, 100 to 2,000, 100 to 1,000, 100 to 800, 100 to 500, 100 to 300, 100 to 200, or 100 to 150 oligonucleotides.

In some embodiments, the nanostructure moiety comprised of two or more lipophilic groups is more stable in solution than a nanostructure with a moiety comprised of one lipophilic group.

In some embodiments, the nanostructure has a diameter of about 10 nm to about 100 nm. In another embodiment, the nanostructure has a diameter of about 20 nm to about 50 nm. In another embodiment, the nanostructure has a diameter of about 27 nm to about 37 nm. In another embodiment, the nanostructure has a diameter of about 27 nm. In another embodiment, the nanostructure has a diameter of about 37 nm.

Some aspects of the present disclosure include a composition of discrete nanostructures, wherein each nanostructure comprises a spherical nucleic acid (SNA) comprising a core, a lipid shell having an inner surface surrounding the core and an outer surface with 26-7,000 oligonucleotides functionalized to the outer surface of the nanostructure, wherein the

oligonucleotides contain a self-complementary motif. In some embodiments, each discrete nanostructure has a diameter of about 10 nm to about 100 nm. In another embodiment, each discrete nanostructure has a diameter of about 20 nm to about 50 nm. In yet other embodiments, the nanostructure contains 26 to 5,000, 26 to 2,000, 26 to 1,000, 26 to 800, 25 to 500, 26 to 300, 26 to 200, 26 to 100, 50 to 5,000, 50 to 2,000, 50 to 1,000, 50 to 800, 50 to 500, 50 to 300, 50 to 200, 50 to 100, 100 to 5,000, 100 to 2,000, 100 to 1,000, 100 to 800, 100 to 500, 100 to 300, 100 to 200, or 100 to 150 oligonucleotides.

In some embodiments, the oligonucleotides contain a G-rich motif. In another embodiment, the oligonucleotides are immunostimulatory oligonucleotides. In another embodiment, the immunostimulatory oligonucleotides stimulate a toll-like receptor 9 (TLR9). In other embodiments, the oligonucleotides are antisense oligonucleotides.

In some embodiments, the core is a hollow or a solid core. In some embodiments, the composition has a polydispersity (PDI) of 0.1- 0.4. In some embodiments, each discrete nanostructure has a Z average diameter of 30-1,300.

A method for eliciting an immune response is provided according to other aspects of the invention. The method involves contacting a cell with the nanostructure described herein or a composition described herein. In some embodiments, the nanostructure induces cytokine secretion. In another embodiment, the nanostructure activates interferon alpha (IFNα). In some embodiments, the cell is a peripheral blood mononuclear cell.

A method for regulating gene expression is provided according to other aspects of the invention. The method involves contacting a cell with a nanostructure described herein to regulate gene expression.

A method for treating an immune disorder is provided according to other aspects of the invention. The method involves administering to a cell in a subject a nanostructure described herein to deliver an immunostimulatory oligonucleotide that promotes an immune response or to deliver an immunoinhibitory oligonucleotide that decreases or prevents an immune response to treat the immune disorder. In some embodiments, the subject is a mammal. In another embodiment, the subject is a human. In some embodiments, the nanostructure is in contact with the cell at a concentration of 1 nM to 100 μM. In another embodiment, the nanostructure is in contact with the cell at a concentration of 1 μM to 10 μM. In some embodiments, the nanostructure is in contact with the cell for 24 hours.

Kits comprising one or more sealed vials comprising an amount of any of the oligonucleotides and related nanostructure reagents of the present invention are also provided. The kit may optionally include instructions for generating and/or using nanostructures and compositions of the present invention in hard copy or computer readable form.

Each of the limitations of the invention can encompass various embodiments of the invention. It is, therefore, anticipated that each of the limitations of the invention involving any one element or combinations of elements can be included in each aspect of the invention. This invention is not limited in its application to the details of construction and the arrangement of components set forth in the following description or illustrated in the drawings. The invention is capable of other embodiments and of being practiced or of being carried out in various ways. Also, the phraseology and terminology used herein is for the purpose of description and should not be regarded as limiting. The use of "including," "comprising," or "having," "containing", "involving", and variations thereof herein, is meant to encompass the items listed thereafter and equivalents thereof as well as additional items.

BRIEF DESCRIPTION OF DRAWINGS

The accompanying drawings are not intended to be drawn to scale. In the drawings, each identical or nearly identical component that is illustrated in various figures is represented by a like numeral. For purposes of clarity, not every component may be labeled in every drawing. In the drawings:

Figure 1 agarose gel electrophoresis of SNA constructs and oligonucleotide-lipophilic moiety conjugates. Gel electrophoresis of SNA 1_30 (Lane 1), Oligo 1 (Lane 2), SNA 2 (Lane 3), and Oligo 2 (Lane 4), using 0.5 % agarose stained with 0.5 μg/ml ethidium bromide is shown. SNA formation is observed for both SNA 1_30 and SNA 2, which have slower migration than their respective lipophilic moiety-conjugated oligonucleotides.

Figure 2 depicts agarose gel electrophoresis of SNA constructs and oligonucleotide-lipophilic moiety conjugates. Gel electrophoresis of SNA4 (Lane 1), Oligo 5 (Lane 2), SNA 6 (Lane 3), Oligo 9 (Lane 4), SNA 5(Lane 5), Oligo 6 (Lane 6), SNA 10 (Lane 7), Oligo 14 (Lane 8), SNA 13 (Lane 9), Oligo 18 (Lane 10), SNA 8 (Lane 11), Oligo 12 (Lane 12), SNA 15 (Lane 13), Oligo 21 (Lane 14), SNA 16 (Lane 15), Oligo 22 (Lane 16), SNA 14 (Lane 17), Oligo 20 (Lane 18), Oligo 35 (Lane 19), using 0.5 % agarose stained with 0.5 μg/ml ethidium bromide is

shown. SNA formation is observed for SNA 10, SNA 13, SNA 8, SNA 15, SNA 16, and SNA 14, which have distinctive migrations compared to their respective constitutive lipophilic moiety-conjugated oligonucleotides.

Figure 3 shows size exclusion chromatography (SEC) analysis of SNAs functionalized with oligonucleotides with various lipophilic moieties. SNA 1_25, SNA 11, SNA 10, SNA 9, SNA 7, and SNA 3 were analyzed by SEC with PBS running buffer. SNA 3 shows elution of the unbound oligonucleotide only (11-12 minutes) with no SNA peak (6-7 minutes) indicating no self-assembly and formation of SNAs with the corresponding Oligo 3. SNA 1_25, SNA 11, SNA 10, SNA 9, and SNA 7, all elute at 6-7 minutes indicating self-assembly and SNA formation, with no free unbound lipophilic moiety-conjugated oligo.

Figures 4A-4B show SEC analyses of oligonucleotide loading on SNA with various lipophilic moieties. In Figure 4A, SNA 1_10, SNA 1_20, SNA 1_25, SNA 1_30, and SNA 1_50 were analyzed by SEC with PBS running buffer. SNA 1_50 shows elution of the unbound oligonucleotide (11-12 minutes) with SNA peak (6-7 minutes) indicating unbound oligonucleotide when SNAs are loaded with over 25 oligos per nanoparticle with Oligo 1. In Figure 4B, SNA 18_50, SNA 18_60, SNA 18_70, SNA 18_80, SNA 18_90, and SNA 18_100 were analyzed by SEC with PBS running buffer. SNA 18_70 shows elution of the unbound oligonucleotide (9 minutes) with SNA peak (6-7 minutes) indicating unbound oligonucleotide when SNAs are loaded at over 60 oligos per nanoparticle with Oligo 32.

DETAILED DESCRIPTION

Spherical nucleic acids (SNAs) consist of densely packed, radially oriented nucleic acids. This architecture gives them unique properties, enabling cellular uptake of SNAs mediated via scavenger receptors. Cellular uptake of SNAs is fast and efficient and leads to endosomal accumulation.

Spherical nucleic acids (SNAs) are formed by organizing nucleic acids radially around a core. These structures exhibit the ability to enter cells without the need for auxiliary delivery vehicles or transfection reagents by engaging class A scavenger receptors (SR-A) and lipid rafts Once inside the cell, the nucleic acid components of traditional SNAs resist nuclease degradation, leading to longer intracellular lifetimes. Moreover, SNAs, due to their multi-functional chemical structures, have the ability to bind their targets in a multivalent fashion.

It has been discovered herein that SNA structures can be modified to significantly improve loading density with strategically designed lipophilic groups. SNAs have been developed according to the invention which have a densely packed oligonucleotide shell around a lipid structure. It was found that densely packing the oligonucleotides onto the surface can be achieved using a moiety comprised of two or more lipophilic groups, such as di-stearyl.

It has also been discovered herein that SNA formulation technology can be utilized to deliver self-aggregating oligonucleotides that have heretofore produced unacceptable aggregates that prevented their therapeutic use. SNAs composed of self-aggregating oligonucleotides have been developed according to the invention which incorporate oligonucleotides in a densely packed oligonucleotide shell. These unique molecules can be used to efficiently deliver any type of therapeutic or diagnostic self-aggregating oligonucleotide to a cell, and in particular to endosomes. A liposome or lipoplex can be functionalized into an SNA by inserting lipid-conjugated self-aggregating oligonucleotides onto the external surface. It has been discover that one method for densely packing the self-aggregating oligonucleotides onto the surface can be achieved using a moiety comprised of two or more lipophilic groups.

It is shown herein that when oligonucleotides containing self-complementary, e.g., G-rich motifs, are functionalized to liposome surface using two or more lipophilic groups, such as di-stearyl, the resulting SNAs do not aggregate or precipitate. This is particularly advantageous for large scale clinical and non-clinical preparations where SNAs need to be made in bulk, filter sterilized, and stored over extended periods. It is shown that the presence of multiple lipophilic groups enables higher density of oligonucleotides to be added to the liposome surface. The higher oligonucleotide density imparts stability to these SNAs, which are otherwise unstable, presumably by increasing electrostatic repulsion between SNAs, and promoting intra-SNA oligonucleotide interactions instead of inter-SNA oligonucleotide interactions. The resulting SNAs are active in immunostimulatory assays and can be used for other therapeutic indications such as gene regulation when functionalized with the appropriate antisense sequences.

Self-aggregating oligonucleotides in some embodiments have a self-complementary motif or are G-rich or GC rich. A self-complementary motif may be a region of 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 or more nucleotides that base pair with a region of 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 or more nucleotides in the same oligonucleotide or in other

oligonucleotides within the SNAs. In some embodiments nucleotides are consecutive and in other embodiments there are 1 or more intervening nucleotides.

Compositions of SNA of the invention include discrete nanoparticles. The term "discrete" when used in the context of the nanoparticles refers to unaggregated nanoparticles. A composition of discrete nanoparticles includes at least 30% of the nanoparticles in the composition in an aggregated form. In some embodiments a composition of discrete nanoparticles includes at least 40, 45, 50, 55, 60, 65, 70, 75, 80, 85 90, 95, 96, 97, 98, or 99% or in some cases 100% of the nanoparticles in the composition in an unaggregated form.

A moiety comprised of two or more lipophilic groups as used herein is any compound having two lipophilic moieties capable of embedding in a lipid membrane. In some embodiments a moiety comprised of two or more lipophilic groups is a saturated or unsaturated, multi-alkyl chain lipophilic moiety, with carbon chains ranging from, for instance, C10 to C22, or di- and tri-alkyl chain lipophilic moiety. Di- and tri-alkyl chain lipophilic moiety-oligonucleotide conjugates can be synthesized by using symmetrical branching (doubler) and trebler reagents, respectively. As shown in the Examples below, various lipophilic moiety-oligonucleotide conjugates were studied for their ability to form SNAs with 20 nm DOPC liposomes. In contrast to the mono-alkyl lipophilic moiety-oligonucleotide conjugates that did not form SNAs, both di- and tri-alkyl chain lipophilic moiety-oligonucleotide conjugates formed SNAs.

Thus, the nanostructures of the invention are typically composed of lipid nanoparticles having a shell of oligonucleotides, which is formed by arranging oligonucleotides such that they point radially outwards from the core in a densely packed manner. A hydrophobic (e.g. lipophilic moiety) anchor group attached to either the 5'- or 3'-end of the oligonucleotide, depending on whether the oligonucleotides are arranged with the 5'- or 3'-end facing outward from the core preferably is used to embed the oligonucleotides in the lipid nanoparticle. The anchor acts to drive insertion into the lipid nanoparticle and to anchor the oligonucleotides to the lipids.

The density of self-aggregating oligonucleotides on the surface of the SNA of the invention is greater than the density of oligonucleotides positioned on the surface of traditional SNA which have oligonucleotides held on the surface using mono-lipophilic moieties such as cholesterol. Quite surprisingly, the improved density was shown to be associated with less inter-SNA aggregation. Compositions of unaggregated SNA are more stable. The density of the oligonucleotides can be described as a number of oligonucleotides per surface area.

The absolute number of oligonucleotides on the surface of a particle will depend on the size of the particle. For instance, on a 20 nm liposome an ideal number of oligonucleotides on the surface may be about 25-80, 26-80, 25-100, 26-100, 25-60, 26-60, 25-50, 26-50, 30-100, 30-80, 30-70, 30-60, 30-50, 30-40, 40-50, 40-60, or 50-60. Alternatively, on a 100 nm liposome core an ideal number of oligonucleotides on the surface may be about 5,000-6,000, 4,000-6,000, 4,500-6,000, or 5,500-6,000. In other embodiments the surface density of the multi-lipophilic moiety-self-aggregating oligonucleotide- SNAs of the invention is at least 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, or 10% greater than the density of oligonucleotides positioned on the surface of traditional SNA which have oligonucleotides held on the surface using mono-lipophilic moieties such as cholesterol.

A surface density adequate to make the nanoparticles stable and not aggregate and the conditions necessary to obtain it for a desired combination of nanoparticles and oligonucleotides can be determined empirically.

In some aspects the SNAs may be used to deliver a therapeutic oligonucleotide to any tissue in which it is desirable to present the nucleic acid. For instance, it may be desirable to deliver the therapeutic oligonucleotide to the skin, a mucosal membrane, or an internal organ. The stable SNAs described herein are useful for delivering therapeutic oligonucleotides to these tissues for the treatment of disease or for diagnostic purposes.

The invention in some aspects relates to the delivery of an active agent that is a therapeutic nucleic acid. Therapeutic nucleic acids include inhibitory oligonucleotides and oligonucleotides that upregulate expression. In some embodiments the therapeutic nucleic acids specifically downregulate or upregulate the expression of a protein which is useful for being upregulated or downregulated in the eye and in particular in the cornea or retina or other related tissue. In other embodiments the therapeutic nucleic acids specifically downregulate or upregulate the expression of a protein which is useful for being upregulated or downregulated in other tissues. In some embodiments the nucleic acids are selected from the group consisting of a ribozyme, an interfering RNA (RNAi) molecule, a small inhibitory RNA (siRNA) molecule, a triple helix forming molecule, DNA, RNA, plasmids, antisense oligonucleotides, immunostimulatory oligonucleotides, immunoinhibitory oligonucleotides, mRNA, long ncRNA, and miRNA.

The terms "nucleic acid" and "oligonucleotide" are used interchangeably to mean multiple nucleotides (i.e., molecules comprising a sugar (e.g., ribose or deoxyribose) linked to a phosphate group and to an exchangeable organic base, which is either a substituted pyrimidine (e.g., cytosine (C), thymine (T) or uracil (U)) or a substituted purine (e.g., adenine (A) or guanine (G)). As used herein, the terms "nucleic acid" and "oligonucleotide" refer to oligoribonucleotides as well as oligodeoxyribonucleotides. The terms "nucleic acid" and "oligonucleotide" shall also include polynucleosides (i.e., a polynucleotide minus the phosphate) and any other organic base containing polymer. Nucleic acid molecules are preferably synthetic (e.g., produced by nucleic acid synthesis). The oligonucleotides may be any size useful for producing antisense effects. In some embodiments they are 18-23 nucleotides in length. In other embodiments the antisense oligonucleotide is 18 nucleotides in length.

The terms "nucleic acid" and "oligonucleotide" may also encompass nucleic acids or oligonucleotides with substitutions or modifications, such as in the bases and/or sugars. For example, they include nucleic acids having backbone sugars that are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 2' position and other than a phosphate group or hydroxy group at the 5' position. Thus modified nucleic acids may include a 2'-O-alkylated ribose group. In addition, modified nucleic acids may include sugars such as arabinose or 2'-fluoroarabinose instead of ribose. Thus the nucleic acids may be heterogeneous in backbone composition thereby containing any possible combination of polymer units linked together such as peptide-nucleic acids (which have an amino acid backbone with nucleic acid bases). Other examples are described in more detail below.

The oligonucleotides may be DNA, RNA, PNA, LNA, ENA or hybrids including any chemical or natural modification thereof. Chemical and natural modifications are well known in the art. Such modifications include, for example, modifications designed to increase binding to a target strand (i.e., increase their melting temperatures), to assist in identification of the oligonucleotide or an oligonucleotide-target complex, to increase cell penetration, to stabilize against nucleases and other enzymes that degrade or interfere with the structure or activity of the oligonucleotides, to provide a mode of disruption (a terminating event) once sequence-specifically bound to a target, and to improve the pharmacokinetic properties of the oligonucleotide.

Modifications include, but are not limited to, for example, (a) end modifications, e.g., 5' end modifications (phosphorylation dephosphorylation, conjugation, inverted linkages, etc.), 3' end modifications (conjugation, DNA nucleotides, inverted linkages, etc.), (b) base modifications, e.g., replacement with modified bases, stabilizing bases, destabilizing bases, or bases that base pair with an expanded repertoire of partners, or conjugated bases, (c) sugar modifications (e.g., at the 2' position or 4' position) or replacement of the sugar, as well as (d) internucleoside linkage modifications, including modification or replacement of the phosphodiester linkages. To the extent that such modifications interfere with translation (i.e., results in a reduction of 50%, 60%, 70%, 80%, or 90% or more in translation relative to the lack of the modification - e.g., in an *in vitro* translation assay), the modification may not be optimal for the methods and compositions described herein.

Non-limiting examples of modified internucleoside linkages include phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl phosphonates including 3'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein the adjacent pairs of nucleoside units are linked 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, mixed salts and free acid forms are also included.

Modified internucleoside linkages that do not include a phosphorus atom therein have internucleoside linkages that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatoms and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH_2 component parts.

Substituted sugar moieties include, but are not limited to one of the following at the 2' position: H (deoxyribose); OH (ribose); F; 0-, S-, or N-alkyl; 0-, S-, or N-alkenyl; 0-, S- or N-

alkynyl; or O-alkyl- O-alkyl, wherein the alkyl, alkenyl and alkynyl can be substituted or unsubstituted C_1 to C_{10} alkyl or C_2 to C_{1O} alkenyl and alkynyl.

A chemically or naturally modified oligonucleotide may include, for example, at least one nucleotide modified at the 2' position of the sugar, most preferably a 2'-O-alkyl, 2'-O-alkyl-O-alkyl or 2'-fluoro-modified nucleotide or an end cap. In other embodiments, RNA modifications include 2'-fluoro, 2'-amino and 2' O-methyl modifications on the ribose of pyrimidines, abasic residues or an inverted base at the 3' end of the RNA.

The oligonucleotides useful according to the invention may include a single modified nucleoside. In other embodiments the oligonucleotide may include at least two modified nucleosides, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20 or more nucleosides, up to the entire length of the oligonucleotide.

Nucleosides or nucleobases include the natural purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleosides include other synthetic and natural nucleobases such as inosine, xanthine, hypoxanthine, nubularine, isoguanisine, tubercidine, 2-(halo)adenine, 2-(alkyl)adenine, 2- (propyl)adenine, 2 (amino)adenine, 2-(aminoalkyll)adenine, 2 (aminopropyl)adenine, 2 (methylthio) N6 (isopentenyl)adenine, 6 (alkyl)adenine, 6 (methyl)adenine, 7 (deaza)adenine, 8 (alkenyl)adenine, 8- (alkyl)adenine, 8 (alkynyl)adenine, 8 (amino)adenine, 8-(halo)adenine, 8-(hydroxyl)adenine, 8 (thioalkyl) adenine, 8-(thiol)adenine, N6-(isopentyl)adenine, N6 (methyl)adenine, N6, N6 (dimethyl)adenine, 2-(alkyl)guanine,2 (propyl)guanine, 6-(alkyl)guanine, 6 (methyl)guanine, 7 (alkyl)guanine, 7 (methyl)guanine, 7 (deaza)guanine, 8 (alkyl)guanine, 8-(alkenyl)guanine, 8 (alkynyl)guanine, 8-(amino)guanine, 8 (halo)guanine, 8-(hydroxyl)guanine, 8 (thioalkyl)guanine, 8- (thiol)guanine, N (methyl)guanine, 2-(thio)cytosine, 3 (deaza) 5 (aza)cytosine, 3-(alkyl)cytosine, 3 (methyl)cytosine, 5-(alkyl)cytosine, 5-(alkynyl)cytosine, 5 (halo)cytosine, 5 (methyl)cytosine, 5 (propynyl)cytosine, 5 (propynyl)cytosine, 5 (trifluoromethyl)cytosine, 6-(azo)cytosine, N4 (acetyl)cytosine, 3 (3 amino-3 carboxypropyl)uracil, 2-(thio)uracil, 5 (methyl) 2 (thio)uracil, 5 (methylaminomethyl)-2 (thio)uracil, 4-(thio)uracil, 5 (methyl) 4 (thio)uracil, 5 (methylaminomethyl)-4 (thio)uracil, 5 (methyl) 2,4 (dithio)uracil, 5 (methylaminomethyl)-2,4 (dithio)uracil, 5 (2- aminopropyl)uracil, 5-(alkyl)uracil, 5-(alkynyl)uracil, 5-(allylamino)uracil, 5 (aminoallyl)uracil, 5 (aminoalkyl)uracil, 5 (guanidiniumalkyl)uracil, 5 (l,3-diazole-l-alkyl)uracil, 5-(cyanoalkyl)uracil, 5- (dialkylaminoalkyl)uracil, 5 (dimethylaminoalkyl)uracil, 5-(halo)uracil,

5-(methoxy)uracil, uracil-5 oxyacetic acid, 5 (methoxycarbonylmethyl)-2-(thio)uracil, 5 (methoxycarbonyl-methyl)uracil, 5 (propynyl)uracil, 5 (propynyl)uracil, 5 (trifluoromethyl)uracil, 6 (azo)uracil, dihydrouracil, N3 (methyl)uracil, 5-uracil (i.e., pseudouracil), 2 (thio)pseudouracil,4 (thio)pseudouracil,2,4- (dithio)psuedouracil,5-(alkyl)pseudouracil, 5-(methyl)pseudouracil, 5-(alkyl)-2-(thio)pseudouracil, 5- (methyl)-2-(thio)pseudouracil, 5-(alkyl)-4 (thio)pseudouracil, 5-(methyl)-4 (thio)pseudouracil, 5-(alkyl)- 2,4 (dithio)pseudouracil, 5-(methyl)-2,4 (dithio)pseudouracil, 1 substituted pseudouracil, 1 substituted 2(thio)-pseudouracil, 1 substituted 4 (thio)pseudouracil, 1 substituted 2,4-(dithio)pseudouracil, 1 (aminocarbonylethylenyl)-pseudouracil, 1 (aminocarbonylethylenyl)-2(thio)-pseudouracil, 1 (aminocarbonylethylenyl)-4 (thio)pseudouracil, 1 aminocarbonylethylenyl)-2,4-(dithio)pseudouracil, 1 (arninoalkylarninocarbonylethylenyl)-pseudouracil, 1 (arninoalkylarnino-carbonylethylenyl)-2(thio)- pseudouracil, 1(arninoalkylarninocarbonylethylenyl)-4 (thio)pseudouracil, 1 (arninoalkylarninocarbonylethylenyl)-2,4-(dithio)pseudouracil, 1,3-(diaza)-2-(oxo)-phenoxazin-l-yl, 1 - (aza)-2-(thio)-3-(aza)-phenoxazin-l-yl, l,3-(diaza)-2-(oxo)-phenthiazin-l-yl, l-(aza)-2-(thio)-3-(aza)- phenthiazin-l-yl, 7-substituted l,3-(diaza)-2-(oxo)-phenoxazin-l-yl, 7-substituted l-(aza)-2-(thio)-3- (aza)-phenoxazin-l-yl, 7-substituted l,3-(diaza)-2-(oxo)-phenthiazin-l-yl, 7-substituted l-(aza)-2-(thio)- 3-(aza)-phenthiazin-l-yl, 7-(arninoalkylhydroxy)-l,3-(diaza)-2-(oxo)-phenoxazin-l-yl, 7- (arninoalkylhydroxy)-l-(aza)-2-(thio)-3-(aza)-phenoxazin-l-yl, 7-(aminoalkylhydroxy)-l,3-(diaza)-2- (oxo)-phenthiazin-l-yl, 7-(arninoalkylhydroxy)-l-(aza)-2-(thio)-3-(aza)-phenthiazin-l-yl, 7- (guanidiniumalkylhydroxy)-l,3-(diaza)-2-(oxo)-phenoxazin-l-yl, 7-(guanidiniumalkylhydroxy)-l-(aza)- 2-(thio)-3-(aza)-phenoxazin-l-yl, 7-(guanidiniumalkyl-hydroxy)-l,3-(diaza)-2-(oxo)-phenthiazin-l-yl, 7- (guanidiniumalkylhydroxy)-l-(aza)-2-(thio)-3-(aza)-phenthiazin-l-yl, l,3,5-(triaza)-2,6-(dioxa)- naphthalene, inosine, xanthine, hypoxanthine, nubularine, tubercidine, isoguanisine, inosinyl, 2-aza- inosinyl, 7-deaza-inosinyl, nitroimidazolyl, nitropyrazolyl, nitrobenzimidazolyl, nitroindazolyl, aminoindolyl, pyrrolopyrimidinyl, 3-(methyl)isocarbostyrilyl, 5-(methyl)isocarbostyrilyl, 3-(methyl)-7-(propynyl)isocarbostyrilyl, 7-(aza)indolyl, 6-(methyl)-7-(aza)indolyl, imidizopyridinyl, 9-(methyl)- imidizopyridinyl, pyrrolopyrizinyl, isocarbostyrilyl, 7-(propynyl)isocarbostyrilyl, propynyl-7- (aza)indolyl, 2,4,5-(trimethyl)phenyl, 4-(methyl)indolyl, 4,6-(dimethyl)indolyl, phenyl, napthalenyl, anthracenyl, phenanthracenyl, pyrenyl, stilbenyl, tetracenyl, pentacenyl,

diiluorotolyl, 4-(iluoro)-6- (methyl)benzimidazole, 4-(methyl)benzimidazole, 6-(azo)thymine, 2-pyridinone, 5 nitroindole, 3 nitropyrrole, 6-(aza)pyrimidine, 2 (amino)purine, 2,6-(diamino) purine, 5 substituted pyrimidines, N2- substituted purines, N6-substituted purines, 06-substituted purines, substituted 1,2,4-triazoles, pyrrolo- pyrimidin-2-on-3-yl, 6-phenyl-pyrrolo-pyrimidin-2-on-3-yl, para-substituted-6-phenyl-pyrrolo-pyrimidin- 2-on-3-yl, ortho-substituted-6-phenyl-pyrrolo-pyrimidin-2-on-3-yl, bis-ortho-substituted-6-phenyl- pyrrolo-pyrimidin-2-on-3-yl, para-(aminoalkylhydroxy)- 6-phenyl-pyrrolo-pyrimidin-2-on-3-yl, ortho- (aminoalkylhydroxy)- 6-phenyl-pyrrolo-pyrimidin-2-on-3-yl, bis-ortho— (aminoalkylhydroxy)- 6-phenyl- pyrrolo-pyrimidin-2-on-3-yl, pyridopyrimidin-3-yl, 2-oxo-7-amino-pyridopyrimidin-3-yl, 2-oxo-pyridopyrimidine-3-yl, or any O-alkylated or N-alkylated derivatives thereof.

The oligonucleotides of the invention may be chimeric oligonucleotides. Chimeric compounds of the invention may be formed as composite structures of two or more oligonucleotides, modified oligonucleotides, oligonucleotides and/or oligonucleotide mimetics as described above. Such compounds have also been referred to in the art as hybrids or gapmers. In particular a gapmer is an oligonucleotide that has at least three discrete portions, two of which are similar i.e. include one or more backbone modifications, and surround a region that is distinct, i.e., does not include backbone modifications.

In some embodiments, the backbone of the oligonucleotide is modified. In some embodiments, the backbone of the oligonucleotide has a phosphorothioate modification. The backbone of the oligonucleotide may have other modifications apparent to one of ordinary skill in the art.

Aspects of the invention relate to delivery of SNAs to a subject for therapeutic and/or diagnostic use. The SNAs may be administered alone or in any appropriate pharmaceutical carrier, such as a liquid, for example saline, or a powder, for administration in vivo. They can also be co-delivered with larger carrier particles or within administration devices. The SNAs may be formulated. The formulations of the invention can be administered in pharmaceutically acceptable solutions, which may routinely contain pharmaceutically acceptable concentrations of salt, buffering agents, preservatives, compatible carriers, adjuvants, and optionally other therapeutic ingredients. In some embodiments, SNAs associated with the invention are mixed with a substance such as a lotion (for example, aquaphor) and are administered to the skin of a subject, whereby the SNAs are delivered through the skin of the subject. It should be appreciated

that any method of delivery of nanoparticles known in the art may be compatible with aspects of the invention.

For use in therapy, an effective amount of the SNAs can be administered to a subject by any mode that delivers the SNAs to the desired cell. Administering pharmaceutical compositions may be accomplished by any means known to the skilled artisan. Routes of administration include but are not limited to oral, parenteral, intramuscular, intravenous, subcutaneous, mucosal, intranasal, sublingual, intratracheal, inhalation, ocular, vaginal, dermal, rectal, and by direct injection.

In some embodiments the oligonucleotide is a G-rich oligonucleotide. The G-rich nucleic acids may have a sequence that includes at least 50% G's. In some embodiment the G-rich nucleic acids have a sequence that includes at least 60%, 70%, 80% or 90% G's. The G-rich nucleic acids may also have one or multiple G repeats. For instance, a G-rich nucleic acid may have a stretch of at least 4 G's. In other embodiments the G-rich nucleic acid may have one or more stretches of 3 G's. In yet other embodiments the G-rich nucleic acid may have multiple G dimers (e.g., 2, 3, 4, 5, or 6 dimers) separated by one or more other nucleotides.

The oligonuceltide of the SNA in some embodiments is comprised of densely packed, radially oriented nucleic acids which stimulate an immune response, and in particular stimulate the toll-like receptors (TLR) such as TLR9. In some embodiments the SNA is an agonist of a TLR (TLR agonist). A TLR agonist, as used herein is a nucleic acid molecule that interacts with and stimulates the activity of a TLR. The SNA, in some embodiments, is a TLR-9 targeted Immunostimulatory Sperical Nucleic Acid.

Toll-like receptors (TLRs) are a family of highly conserved polypeptides that play a critical role in innate immunity in mammals. At least ten family members, designated TLR1 - TLR10, have been identified. The cytoplasmic domains of the various TLRs are characterized by a Toll-interleukin 1 (IL-1) receptor (TIR) domain. Medzhitov R et al. (1998) Mol Cell 2:253-8. Recognition of microbial invasion by TLRs triggers activation of a signaling cascade that is evolutionarily conserved in Drosophila and mammals. The TIR domain-containing adaptor protein MyD88 has been reported to associate with TLRs and to recruit IL-1 receptor-associated kinase (IRAK) and tumor necrosis factor (TNF) receptor-associated factor 6 (TRAF6) to the TLRs. The MyD88-dependent signaling pathway is believed to lead to activation of NF-κB transcription factors and c-Jun NH2 terminal kinase (Jnk) mitogen-activated protein kinases

(MAPKs), critical steps in immune activation and production of inflammatory cytokines. For a review, see Aderem A et al. (2000) Nature 406:782-87.

TLRs are believed to be differentially expressed in various tissues and on various types of immune cells. For example, human TLR7 has been reported to be expressed in placenta, lung, spleen, lymph nodes, tonsil and on plasmacytoid precursor dendritic cells (pDCs). Chuang T-H et al. (2000) Eur Cytokine Netw 11:372-8); Kadowaki N et al. (2001) J Exp Med 194:863-9. Human TLR8 has been reported to be expressed in lung, peripheral blood leukocytes (PBL), placenta, spleen, lymph nodes, and on monocytes. Kadowaki N et al. (2001) J Exp Med 194:863-9; Chuang T-H et al. (2000) Eur Cytokine Netw 11:372-8. Human TLR9 is reportedly expressed in spleen, lymph nodes, bone marrow, PBL, and on pDCs, and B cells. Kadowaki N et al. (2001) J Exp Med 194:863-9; Bauer S et al. (2001) Proc Natl Acad Sci USA 98:9237-42; Chuang T-H et al. (2000) Eur Cytokine Netw 11:372-8.

Nucleotide and amino acid sequences of human and murine TLR9 are known. See, for example, GenBank Accession Nos. NM_017442, AF259262, AB045180, AF245704, AB045181, AF348140, AF314224, NM_031178; and NP_059138, AAF72189, BAB19259, AAF78037, BAB19260, AAK29625, AAK28488, and NP_112455, the contents of all of which are incorporated herein by reference. Human TLR9 is reported to exist in at least two isoforms, one 1032 amino acids long and the other 1055 amino acids. Murine TLR9 is 1032 amino acids long. TLR9 polypeptides include an extracellular domain having a leucine-rich repeat region, a transmembrane domain, and an intracellular domain that includes a TIR domain.

As used herein, the term "TLR9 signaling" refers to any aspect of intracellular signaling associated with signaling through a TLR9. As used herein, the term "TLR9-mediated immune response" refers to the immune response that is associated with TLR9 signaling. A TLR9-mediated immune response is a response associated with TLR9 signaling. This response is further characterized at least by the production/secretion of IFN-γ and IL-12, albeit at levels lower than are achieved via a TLR8-mediated immune response.

The term "TLR9 agonist" refers to any agent that is capable of increasing TLR9 signaling (i.e., an agonist of TLR9). TLR9 agonists specifically include, without limitation, immunostimulatory oligonucleotides, and in particular CpG immunostimulatory oligonucleotides.

An "immunostimulatory oligonucleotide" as used herein is any nucleic acid (DNA or RNA) containing an immunostimulatory motif or backbone that is capable of inducing an immune response. An induction of an immune response refers to any increase in number or activity of an immune cell, or an increase in expression or absolute levels of an immune factor, such as a cytokine. Immune cells include, but are not limited to, NK cells, CD4+ T lymphocytes, CD8+ T lymphocytes, B cells, dendritic cells, macrophage and other antigen-presenting cells.

As used herein, the term "CpG oligonucleotides," "immunostimulatory CpG nucleic acids" or "immunostimulatory CpG oligonucleotides" refers to any CpG-containing oligonucleotide that is capable of activating an immune cell. At least the C of the CpG dinucleotide is typically unmethylated. Immunostimulatory CpG oligonucleotides are described in a number of issued patents and published patent applications, including U.S. Pat. Nos. 6,194,388; 6,207,646; 6,218,371; 6,239,116; 6,339,068; 6,406,705; and 6,429,199.

In some embodiments, the CpG oligonucleotides are 4-100 nucleotides in length. In other embodiments, the CpG oligonucleotides are 4-90, 4-80, 4-70, 4-60, 4-50, 4-40, 4-30, 4-20, or 4-10 nucleotides in length.

In some embodiments the immunostimulatory oligonucleotides have a modified backbone such as a phosphorothioate (PS) backbone. In other embodiments the immunostimulatory oligonucleotides have a phosphodiester (PO) backbone. In yet other embodiments immunostimulatory oligonucleotides have a mixed PO and PS backbone.

The CpG oligonucleotides may be A-class oligonucleotides, B-class oligonucleotides, or C- class oligonucleotides. "A-class" CpG immunostimulatory oligonucleotides have been described in published PCT application WO 01/22990. These oligonucleotides are characterized by the ability to induce high levels of interferon-alpha while having minimal effects on B cell activation. The A class CpG immunostimulatory nucleic acid may contain a hexamer palindrome GACGTC, AGCGCT, or AACGTT described by Yamamoto and colleagues. Yamamoto S et al. J Immunol 148:4072-6 (1992). Traditional A-class oligonucleotides have poly-G rich 5' and 3' ends and a palindromic center region. Typically the nucleotides at the 5' and 3' ends have stabilized internucleotide linkages and the center palindromic region has phosphodiester linkages (chimeric).

B class CpG immunostimulatory nucleic acids strongly activate human B cells but have minimal effects inducing interferon-α without further modification. Traditionally, the B-class

oligonucleotides include the sequence 5' $TCN_1TX_1X_2CGX_3X_4$ 3' , wherein X_1 is G or A; X_2 is T, G , or A; X_3 is T or C and X_4 is T or C; and N is any nucleotide, and N_1 and N_2 are nucleic acid sequences of about 0-25 N's each. B-class CpG oligonucleotides that are typically fully stabilized and include an unmethylated CpG dinucleotide within certain preferred base contexts are potent at activating B cells but are relatively weak in inducing IFN-α and NK cell activation. See, e.g., U.S. Patent Nos. 6,194,388; 6,207,646; 6,214,806; 6,218,371; 6,239,116; and 6,339,068.

In one embodiment a B class CpG oligonucleotide is represented by at least the formula:

5' $X_1X_2CGX_3X_4$ 3'

wherein X_1, X_2, X_3, and X_4 are nucleotides. In one embodiment X_2 is adenine, guanine, or thymine. In another embodiment X_3 is cytosine, adenine, or thymine.

In another embodiment the invention provides an isolated B class CpG oligonucleotide represented by at least the formula:

5' $N_1X_1X_2CGX_3X_4N_2$ 3'

wherein X_1, X_2, X_3, and X_4 are nucleotides and N is any nucleotide and N_1 and N_2 are nucleic acid sequences composed of from about 0-25 N's each. In one embodiment X_1X_2 is a dinucleotide selected from the group consisting of: GpT, GpG, GpA, ApA, ApT, ApG, CpT, CpA, CpG, TpA, TpT, and TpG; and X_3X_4 is a dinucleotide selected from the group consisting of: TpT, ApT, TpG, ApG, CpG, TpC, ApC, CpC, TpA, ApA, and CpA. Preferably X_1X_2 is GpA or GpT and X_3X_4 is TpT. In other embodiments X_1 or X_2 or both are purines and X_3 or X_4 or both are pyrimidines or X_1X_2 is GpA and X_3 or X_4 or both are pyrimidines. In another preferred embodiment X_1X_2 is a dinucleotide selected from the group consisting of: TpA, ApA, ApC, ApG, and GpG. In yet another embodiment X_3X_4 is a dinucleotide selected from the group consisting of: TpT, TpA, TpG, ApA, ApG, GpA, and CpA. X_1X_2 in another embodiment is a dinucleotide selected from the group consisting of: TpT, TpG, ApT, GpC, CpC, CpT, TpC, GpT and CpG; X_3 is a nucleotide selected from the group consisting of A and T and X_4 is a nucleotide, but wherein when X_1X_2 is TpC, GpT, or CpG, X_3X_4 is not TpC, ApT or ApC.

In another preferred embodiment the CpG oligonucleotide has the sequence 5' $TCN_1TX_1X_2CGX_3X_4$ 3'. The CpG oligonucleotides of the invention in some embodiments include X_1X_2 selected from the group consisting of GpT, GpG, GpA and ApA and X_3X_4 is selected from the group consisting of TpT, CpT and TpC.

The C class immunostimulatory nucleic acids contain at least two distinct motifs have unique and desirable stimulatory effects on cells of the immune system. Some of these ODN have both a traditional "stimulatory" CpG sequence and a "GC-rich" or "B-cell neutralizing" motif. These combination motif nucleic acids have immune stimulating effects that fall somewhere between those effects associated with traditional "class B" CpG ODN, which are strong inducers of B cell activation and dendritic cell (DC) activation, and those effects associated A-class CpG ODN which are strong inducers of IFN-α and natural killer (NK) cell activation but relatively poor inducers of B-cell and DC activation. Krieg AM et al. (1995) *Nature* 374:546-9; Ballas ZK et al. (1996) *J Immunol* 157:1840-5; Yamamoto S et al. (1992) *J Immunol* 148:4072-6. While preferred class B CpG ODN often have phosphorothioate backbones and preferred class A CpG ODN have mixed or chimeric backbones, the C class of combination motif immune stimulatory nucleic acids may have either stabilized, e.g., phosphorothioate, chimeric, or phosphodiester backbones, and in some preferred embodiments, they have semi-soft backbones.

The stimulatory domain or motif is defined by a formula: 5' X_1DCGHX_2 3'. D is a nucleotide other than C. C is cytosine. G is guanine. H is a nucleotide other than G.

X_1 and X_2 are any nucleic acid sequence 0 to 10 nucleotides long. X_1 may include a CG, in which case there is preferably a T immediately preceding this CG. In some embodiments DCG is TCG. X_1 is preferably from 0 to 6 nucleotides in length. In some embodiments X_2 does not contain any poly G or poly A motifs. In other embodiments the immunostimulatory nucleic acid has a poly-T sequence at the 5' end or at the 3' end. As used herein, "poly-A" or "poly-T" shall refer to a stretch of four or more consecutive A's or T's respectively, e.g., 5' AAAA 3' or 5' TTTT 3'.

As used herein, "poly-G end" shall refer to a stretch of four or more consecutive G's, e.g., 5' GGGG 3', occurring at the 5' end or the 3' end of a nucleic acid. As used herein, "poly-G nucleic acid" shall refer to a nucleic acid having the formula 5' X_1X_2GGGX_3X_4 3' wherein X_1, X_2, X_3, and X_4 are nucleotides and preferably at least one of X_3 and X_4 is a G.

Some preferred designs for the B cell stimulatory domain under this formula comprise TTTTTCG, TCG, TTCG, TTTCG, TTTTCG, TCGT, TTCGT, TTTCGT, TCGTCGT.

The second motif of the nucleic acid is referred to as either P or N and is positioned immediately 5' to X_1 or immediately 3' to X_2.

N is a B-cell neutralizing sequence that begins with a CGG trinucleotide and is at least 10 nucleotides long. A B-cell neutralizing motif includes at least one CpG sequence in which the CG is preceded by a C or followed by a G (Krieg AM et al. (1998) *Proc Natl Acad Sci USA* 95:12631-12636) or is a CG containing DNA sequence in which the C of the CG is methylated. As used herein, "CpG" shall refer to a 5' cytosine (C) followed by a 3' guanine (G) and linked by a phosphate bond. At least the C of the 5' CG 3' must be unmethylated. Neutralizing motifs are motifs which has some degree of immunostimulatory capability when present in an otherwise non-stimulatory motif, but, which when present in the context of other immunostimulatory motifs serve to reduce the immunostimulatory potential of the other motifs.

P is a GC-rich palindrome containing sequence at least 10 nucleotides long. As used herein, "palindrome" and, equivalently, "palindromic sequence" shall refer to an inverted repeat, i.e., a sequence such as ABCDEE'D'C'B'A' in which A and A', B and B', etc., are bases capable of forming the usual Watson-Crick base pairs.

As used herein, "GC-rich palindrome" shall refer to a palindrome having a base composition of at least two-thirds G's and C's. In some embodiments the GC-rich domain is preferably 3' to the "B cell stimulatory domain". In the case of a 10-base long GC-rich palindrome, the palindrome thus contains at least 8 G's and C's. In the case of a 12-base long GC-rich palindrome, the palindrome also contains at least 8 G's and C's. In the case of a 14-mer GC-rich palindrome, at least ten bases of the palindrome are G's and C's. In some embodiments the GC-rich palindrome is made up exclusively of G's and C's.

In some embodiments the GC-rich palindrome has a base composition of at least 81 % G's and C's. In the case of such a 10-base long GC-rich palindrome, the palindrome thus is made exclusively of G's and C's. In the case of such a 12-base long GC-rich palindrome, it is preferred that at least ten bases (83 %) of the palindrome are G's and C's. In some preferred embodiments, a 12-base long GC-rich palindrome is made exclusively of G's and C's. In the case of a 14-mer GC-rich palindrome, at least twelve bases (86 %) of the palindrome are G's and C's. In some preferred embodiments, a 14-base long GC-rich palindrome is made exclusively of G's and C's. The C's of a GC-rich palindrome can be unmethylated or they can be methylated.

In general this domain has at least 3 Cs and Gs, more preferably 4 of each, and most preferably 5 or more of each. The number of Cs and Gs in this domain need not be identical. It is preferred that the Cs and Gs are arranged so that they are able to form a self-complementary

duplex, or palindrome, such as CCGCGCGG. This may be interrupted by As or Ts, but it is preferred that the self-complementarity is at least partially preserved as for example in the motifs CGACGTTCGTCG (SEQ ID NO: 4) or CGGCGCCGTGCCG (SEQ ID NO: 5). When complementarity is not preserved, it is preferred that the non-complementary base pairs be TG. In a preferred embodiment there are no more than 3 consecutive bases that are not part of the palindrome, preferably no more than 2, and most preferably only 1. In some embodiments the GC-rich palindrome includes at least one CGG trimer, at least one CCG trimer, or at least one CGCG tetramer.

In other embodiments the oligonucleotide is an inhibitory nucleic acid. The oligonucleotide that is an inhibitory nucleic acid may be, for instance, an siRNA or an antisense molecule that inhibits expression of a protein that will have a therapeutic effect. The inhibitory nucleic acids may be designed using routine methods in the art.

An inhibitory nucleic acid typically causes specific gene knockdown, while avoiding off-target effects. Various strategies for gene knockdown known in the art can be used to inhibit gene expression. For example, gene knockdown strategies may be used that make use of RNA interference (RNAi) and/or microRNA (miRNA) pathways including small interfering RNA (siRNA), short hairpin RNA (shRNA), double-stranded RNA (dsRNA), miRNAs, and other small interfering nucleic acid-based molecules known in the art. In one embodiment, vector-based RNAi modalities (e.g., shRNA expression constructs) are used to reduce expression of a gene in a cell. In some embodiments, therapeutic compositions of the invention comprise an isolated plasmid vector (e.g., any isolated plasmid vector known in the art or disclosed herein) that expresses a small interfering nucleic acid such as an shRNA. The isolated plasmid may comprise a specific promoter operably linked to a gene encoding the small interfering nucleic acid. In some cases, the isolated plasmid vector is packaged in a virus capable of infecting the individual. Exemplary viruses include adenovirus, retrovirus, lentivirus, adeno-associated virus, and others that are known in the art and disclosed herein.

A broad range of RNAi-based modalities could be employed to inhibit expression of a gene in a cell, such as siRNA-based oligonucleotides and/or altered siRNA-based oligonucleotides. Altered siRNA based oligonucleotides are those modified to alter potency, target affinity, safety profile and/or stability, for example, to render them resistant or partially resistant to intracellular degradation. Modifications, such as phosphorothioates, for example, can

be made to oligonucleotides to increase resistance to nuclease degradation, binding affinity and/or uptake. In addition, hydrophobization and bioconjugation enhances siRNA delivery and targeting

Other molecules that can be used to inhibit expression of a gene include antisense nucleic acids (single or double stranded), ribozymes, peptides, DNAzymes, peptide nucleic acids (PNAs), triple helix forming oligonucleotides, antibodies, and aptamers and modified form(s) thereof directed to sequences in gene(s), RNA transcripts, or proteins. Antisense and ribozyme suppression strategies have led to the reversal of a tumor phenotype by reducing expression of a gene product or by cleaving a mutant transcript at the site of the mutation. Ribozymes have also been proposed as a means of both inhibiting gene expression of a mutant gene and of correcting the mutant by targeted trans-splicing.

Triple helix approaches have also been investigated for sequence-specific gene suppression. Triple helix forming oligonucleotides have been found in some cases to bind in a sequence-specific manner. Similarly, peptide nucleic acids have been shown to inhibit gene expression. Minor-groove binding polyamides can bind in a sequence-specific manner to DNA targets and hence may represent useful small molecules for suppression at the DNA level.

Other inhibitor molecules that can be used include antisense nucleic acids (single or double stranded). Antisense nucleic acids include modified or unmodified RNA, DNA, or mixed polymer nucleic acids, and primarily function by specifically binding to matching sequences resulting in modulation of peptide synthesis. Antisense nucleic acid binds to target RNA by Watson Crick base-pairing and blocks gene expression by preventing ribosomal translation of the bound sequences either by steric blocking or by activating RNase H enzyme. Antisense molecules may also alter protein synthesis by interfering with RNA processing or transport from the nucleus into the cytoplasm.

As used herein, the term “antisense nucleic acid” describes a nucleic acid that is an oligoribonucleotide, oligodeoxyribonucleotide, modified oligoribonucleotide, or modified oligodeoxyribonucleotide which hybridizes under physiological conditions to DNA comprising a particular gene or to an mRNA transcript of that gene and, thereby, inhibits the transcription of that gene and/or the translation of that mRNA. The antisense molecules are designed so as to interfere with transcription or translation of a target gene upon hybridization with the target gene or transcript. Those skilled in the art will recognize that the exact length of the antisense

oligonucleotide and its degree of complementarity with its target will depend upon the specific target selected, including the sequence of the target and the particular bases which comprise that sequence.

An inhibitory nucleic acid useful in the invention will generally be designed to have partial or complete complementarity with one or more target genes. The target gene may be a gene derived from the cell, an endogenous gene, a transgene, or a gene of a pathogen which is present in the cell after infection thereof. Depending on the particular target gene, the nature of the inhibitory nucleic acid and the level of expression of inhibitory nucleic acid (e.g. depending on copy number, promoter strength) the procedure may provide partial or complete loss of function for the target gene. Quantitation of gene expression in a cell may show similar amounts of inhibition at the level of accumulation of target mRNA or translation of target protein. "Inhibition of gene expression" refers to the absence or observable decrease in the level of protein and/or mRNA product from a target gene. "Specificity" refers to the ability to inhibit the target gene without manifest effects on other genes of the cell. The consequences of inhibition can be confirmed by examination of the outward properties of the cell or organism or by biochemical techniques such as RNA solution hybridization, nuclease protection, Northern hybridization, reverse transcription, gene expression monitoring with a microarray, antibody binding, enzyme linked immunosorbent assay (ELISA), Western blotting, radioimmunoassay (RIA), other immunoassays, and fluorescence activated cell analysis (FACS). For RNA-mediated inhibition in a cell line or whole organism, gene expression is conveniently assayed by use of a reporter or drug resistance gene whose protein product is easily assayed. Such reporter genes include acetohydroxyacid synthase (AHAS), alkaline phosphatase (AP), beta galactosidase (LacZ), beta glucoronidase (GUS), chloramphenicol acetyltransferase (CAT), green fluorescent protein (GFP), horseradish peroxidase (HRP), luciferase (Luc), nopaline synthase (NOS), octopine synthase (OCS), and derivatives thereof. Multiple selectable markers are available that confer resistance to ampicillin, bleomycin, chloramphenicol, gentamycin, hygromycin, kanamycin, lincomycin, methotrexate, phosphinothricin, puromycin, and tetracyclin. Depending on the assay, quantitation of the amount of gene expression allows one to determine a degree of inhibition which is greater than 10%, 33%, 50%, 90%, 95% or 99% as compared to a cell not treated according to the present invention. As an example, the efficiency of inhibition may be determined by assessing the amount of gene product in the cell: mRNA may be detected

with a hybridization probe having a nucleotide sequence outside the region used for the inhibitory nucleic acid, or translated polypeptide may be detected with an antibody raised against the polypeptide sequence of that region.

An expression enhancing oligonucleotide as used herein is a synthetic oligonucleotide that encodes a protein. The synthetic oligonucleotide may be delivered to a cell such that it is used by a cells machinery to produce a protein based on the sequence of the synthetic oligonucleotide. The synthetic oligonucleotide may be, for instance, synthetic DNA or synthetic RNA. "Synthetic RNA" refers to a RNA produced through an in vitro transcription reaction or through artificial (non-natural) chemical synthesis. In some embodiments, a synthetic RNA is an RNA transcript. In some embodiments, a synthetic RNA encodes a protein. In some embodiments, the synthetic RNA is a functional RNA. In some embodiments, a synthetic RNA comprises one or more modified nucleotides. In some embodiments, a synthetic RNA is up to 0.5 kilobases (kb), 1 kb, 1.5 kb, 2 kb, 2.5 kb, 3 kb, 4 kb, 5 kb, 6 kb, 7 kb, 8 kb, 9 kb, 10 kb, 15 kb, 20 kb, 25 kb, 30 kb or more in length. In some embodiments, a synthetic RNA is in a range of 0.1 kb to 1 kb, 0.5 kb to 2 kb, 0.5 kb to 10 kb, 1 kb to 5 kb, 2 kb to 5 kb, 1 kb to 10 kb, 3 kb to 10 kb, 5 kb to 15 kb, or 1 kb to 30 kb in length.

A diagnostic oligonucleotide is an oligonucleotide that interacts with a cellular marker to identify the presence of the marker in a cell or subject. Diagnostic oligonucleotides are well known in the art and typically include a label or are otherwise detectable.

This invention is not limited in its application to the details of construction and the arrangement of components set forth in the following description or illustrated in the drawings. The invention is capable of other embodiments and of being practiced or of being carried out in various ways. Also, the phraseology and terminology used herein is for the purpose of description and should not be regarded as limiting. The use of "including," "comprising," or "having," "containing," "involving," and variations thereof herein, is meant to encompass the items listed thereafter and equivalents thereof as well as additional items.

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

All references, including patent documents, disclosed herein are incorporated by reference in their entirety.

EXAMPLES

Materials and Methods

Synthesis of oligonucleotide-lipophilic moiety conjugates

Lipophilic moiety conjugated oligonucleotides were synthesized in 5'- to 3'-direction using β-cyanoethyl phosphoramidite chemistry on appropriate solid supports. Syntheses were carried out on Mermade12 DNA/RNA synthesizer. After the synthesis, oligonucleotides were cleaved from the solid support and deprotected by standard protocols using ammonia solution, and purified by RP-HPLC. Oligonucleotide-lipophilic moiety conjugate concentrations were measured using UV absorbance at 260 nm. All the oligonucleotide conjugates synthesized were characterized by MALDI-TOF mass spectrometry for molecular mass.

Liposome synthesis

Liposomes were synthesized by homogenization of 1,2-dioleoyl-sn-glycero-3-phosphocholine (DOPC) hydrated in phosphate buffered saline solution (PBS) (137 mM NaCl, 10 M phosphate, 2.7 mM KCl, pH 7.4, hyclone) using a homogenizer (Avestin). Liposome diameters (~20 nm) were measured using dynamic light scattering using a Malvern Zetasizer Nano (Malvern Instruments). Lipid concentration was determined using a phospholipid assay kit (Sigma).

SNA synthesis and characterization

Oligonucleotide-lipophilic moiety conjugates (see Table 1) were used to synthesize SNAs at various loadings (see Table 2). SNAs were formulated by mixing a molar excess of lipophilic moiety-oligonucleotide conjugate to a liposome in PBS and storing them overnight at 4 °C. SNAs were analyzed using 0.5% agarose gel electrophoresis and staining with 0.5 μg/ml ethidium bromide and size-exclusion chromatography (SEC) on a SEC-4000 column (Phenomenex). Light transmission of SNAs was measured at 700nm using a Cary100Bio UV/VIS Spectrophotometer (Agilent). SNA diameters were measured using dynamic light scattering using a Malvern Zetasizer Nano.

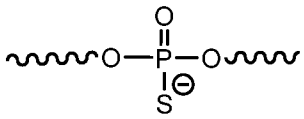
Table 1: Oligonucleotide sequences and modifications

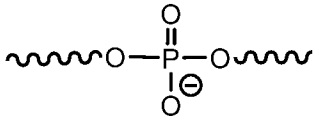
Oligo #	Seq ID No	Sequence and modifications	Molecular weight	
			Calculated	Observed

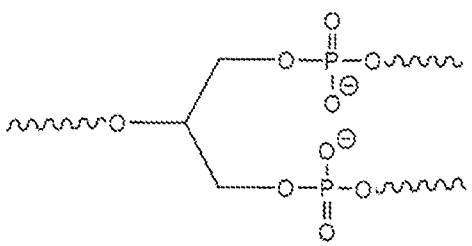
Oligo #	Seq ID No	Sequence and modifications	Molecular weight	
			Calculated	Observed
1	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^R1	9143	9143
2	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^R2	9086	9084
3	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^R4	9035	9058
4	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^R7	8804	8782
5	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^R8	8719	8704
6	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^R9	8746	8740
7	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^R10	8774	8782
8	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^R11	8733	8713
9	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^R12	8756	8742
10	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^X$(R3)_2$	8981	8985
11	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^X$(R5)_2$	9063	9078
12	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^X$(R6)_2$	9119	9123
13	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^X$(R7)_2$	9349	9359
14	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^X(R8)2	9205	9183
15	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^X$(R9)_2$	9261	9250
16	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^X$(R10)_2$	9287	9302
17	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^X$(R11)_2$	9201	9197
18	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^X$(R12)_2$	9297	9272
19	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^Y$(R3)_3$	9419	9419
20	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^Y$(R7)_3$	9966	9992
21	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^Y$(R8)_3$	9755	9742

Oligo #	Seq ID No	Sequence and modifications	Molecular weight	
			Calculated	Observed
22	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T^SP18^SP18^Y(R12)$_3$	9894	9866
23	2	T*C*G*T*T*C*G*T*C*G*A*C*G*A*A^SP18^SP18^R1	6234	6235
24	2	T*C*G*T*T*C*G*T*C*G*A*C*G*A*A^SP18^SP18^R8	5814	5832
25	2	T*C*G*T*T*C*G*T*C*G*A*C*G*A*A^SP18^SP18^R9	5841	5851
26	2	T*C*G*T*T*C*G*T*C*G*A*C*G*A*A^SP18^SP18^R10	5869	5871
27	2	T*C*G*T*T*C*G*T*C*G*A*C*G*A*A^SP18^SP18^X(R3)$_2$	6049	6083
28	2	T*C*G*T*T*C*G*T*C*G*A*C*G*A*A^SP18^SP18^X(R5)$_2$	6157	6176
29	2	T*C*G*T*T*C*G*T*C*G*A*C*G*A*A^SP18^SP18^X(R6)$_2$	6205	6233
30	2	T*C*G*T*T*C*G*T*C*G*A*C*G*A*A^SP18^SP18^X(R7)$_2$	6411	6469
31	2	T*C*G*T*T*C*G*T*C*G*A*C*G*A*A^SP18^SP18^X(R8)$_2$	6269	6290
32	2	T*C*G*T*T*C*G*T*C*G*A*C*G*A*A^SP18^SP18^X(R9)$_2$	6325	9342
33	2	T*C*G*T*T*C*G*T*C*G*A*C*G*A*A^SP18^SP18^X(R10)$_2$	6381	6413
34	2	T*C*G*T*T*C*G*T*C*G*A*C*G*A*A^SP18^SP18^X(R11)$_2$	6295	6287
35	1	T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T	7698	7699
36	3	mUmGmGmGmAmGT*A*G*A*C*A*mAmGmGmUmAmC^SP18^SP18^R1	7485	7487
37	3	mUmGmGmGmAmGT*A*G*A*C*A*mAmGmGmUmAmC^SP18^SP18^X(R9)$_2$	7608	7543

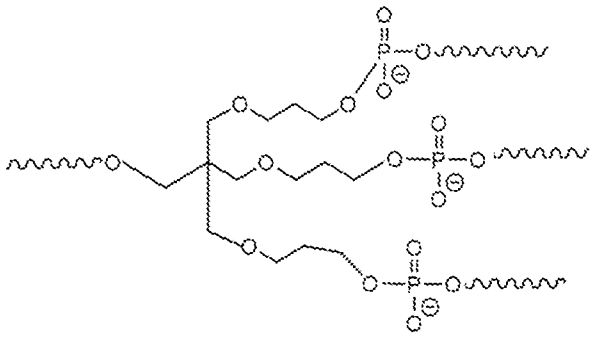
Abreviations:

* = 

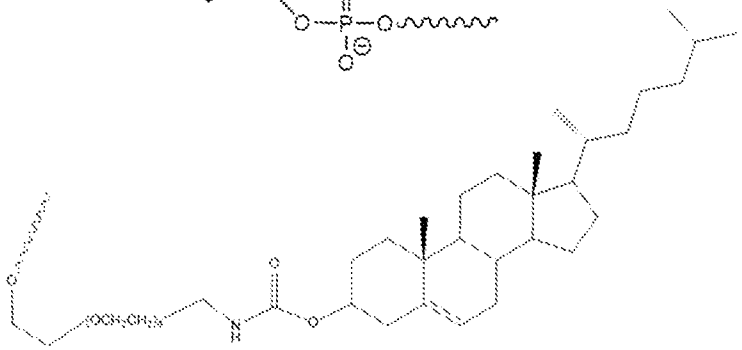
^ = 

X (Doubler) = 

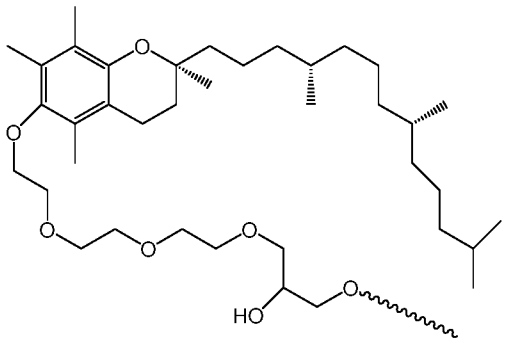
Y (Trebler) =



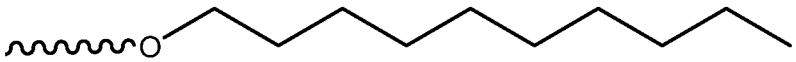
R1 (Cholesterol) =



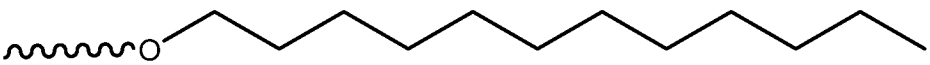
R2 (Tocopherol) =



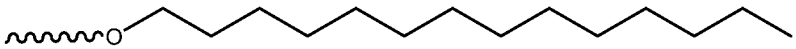
R3 (Decane; C10) =



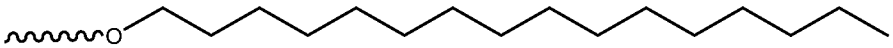
R4 (Dodecane; C12) =

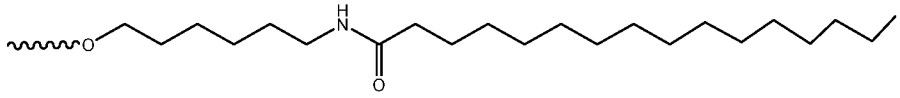


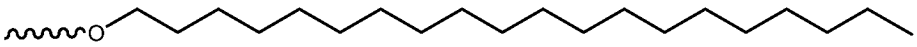
R5 (Myristyl; C14) =

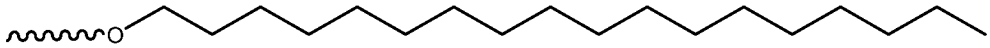


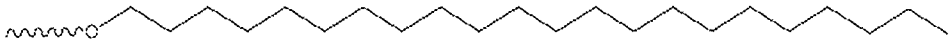
R6 (Palmitoyl; C16) =

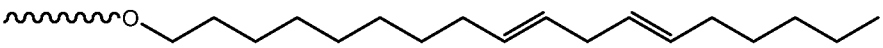


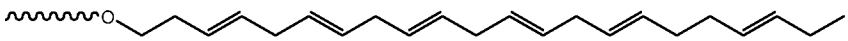
R7 (C6-Palmitoyl; C22) = 

R8 (Arachidyl; C20) = 

R9 (Stearyl; C18) = 

R10 (Behenyl; C22) = 

R11 (Linoleyl; C18) = 

R12 (Docosahexaenoyl; C22) = 

Spherical nucleic acid (SNA) using the oligonucleotides described herein were generated and assigned a SNA number (also referred to by a letter designation in the Figures and Table). The composition of each SNA compound is listed below in Table 3, identifying the oligo number and number of oligo's loaded on the surface.

Table 2: Spherical nucleic acid (SNA) constructs

SNA#	Letter designation	Oligo sequence #	Approximate Oligo Loading per Particle
SNA 1_10	A	Oligo 1	10
SNA 1_20	B	Oligo 1	20
SNA 1_25	C	Oligo 1	25
SNA 1_30	D	Oligo 1	25
SNA 1_50	E	Oligo 1	25
SNA 2	F	Oligo 2	25
SNA 3	G	Oligo 3	0
SNA 4	H	Oligo 5	0
SNA 5	I	Oligo 6	0
SNA 6	J	Oligo 9	0
SNA 7	K	Oligo 11	25
SNA 8	L	Oligo 12	25
SNA 9	M	Oligo 13	25
SNA 10	N	Oligo 14	25
SNA 11	O	Oligo 15	25
SNA 12	P	Oligo 16	25
SNA 13	Q	Oligo 18	25
SNA 14	R	Oligo 20	25
SNA 15	S	Oligo 21	25

SNA 16	T	Oligo 22	25
SNA 17	U	Oligo 23	30
SNA 18_30	V	Oligo 32	30
SNA 18_50	W	Oligo 32	50
SNA 18_60	X	Oligo 32	60
SNA 18_70	Y	Oligo 32	60
SNA 18_80	Z	Oligo 32	60
SNA 18_90	AA	Oligo 32	60
SNA 18_100	AB	Oligo 32	60
SNA 19_30	AC	Oligo 36	25
SNA 20_30	AD	Oligo 37	30
SNA 20_60	AE	Oligo 37	60

Human PBMC cultures

Fresh human peripheral blood mononuclear cells (PBMCs) from five different donors (Zenbio) were cultured in RPMI supplemented with 10 % fetal bovine serum, 2 mM L-glutamine, 50 U/mL penicillin, and 50 mg/mL streptomycin. Cells were maintained at 37 °C in a 5 % CO_2 humidified incubator. SNAs were applied to PBMCs in 96-well tissue culture plates for 24 hours at concentrations listed in Table 4 and Table 5. After 24 hours of treatment, PBMC culture supernatants were collected for cytokine analysis.

Table 3: Characterization of SNAs with various oligonucleotide loading densities

SNA#	Oligo Loading per Particle	Number Mean Diameter	Polydispersity (PDI)	Z-Average Diameter	@700nm % Transmission
SNA17	25	831.5	0.404	1345.0	0.76
SNA18_30	30	544.8	0.221	1260.3	2.58
SNA18_60	60	27.6	0.223	54.2	97.3
SNA19_30	25	2462.7	0.21	2358.3	1.5
SNA20_30	30	26.6	0.42	121.1	41.5
SNA20_60	60	36.6	0.36	104.6	72.8

Table 4: In vitro cytokine secretion in human PBMC cultures

Donor 1

Compound[a]	IL-6 (pg/ml)	IL-12p70 (pg/mL)	TNFα (pg/mL)

PBS	28.6	7.4	30.2
SNA 1_30	1128.9	12.2	129.1
SNA 2	558.0	12.1	59.7
SNA 9	875.8	13.1	95.4
SNA 10	1039.7	8.0	182.7
SNA 13	782.7	12.9	55.7
SNA 14	684.4	7.7	175.9
SNA 16	474.2	11.1	71.8

[a] At 2.5 μM oligonucleotide concentration

Donor 2

Compound[a]	IL-6 (pg/ml)	IL-12p70 (pg/mL)	TNFα (pg/mL)	IFNγ (pg/mL)
PBS	21.2	25.5	36.6	138.4
SNA 1_30	997.3	75.9	221.6	245.3
SNA 2	709.5	49.3	123.8	276.6
SNA 9	955.0	69.2	267.4	236.5
SNA 10	1336.8	27.2	411.4	271.3
SNA 13	1395.4	25.6	122.2	268.6
SNA 14	1057.9	25.5	283.5	356.7
SNA 16	1236.5	53.6	318.8	264.1

[a] At 2.5 μM oligonucleotide concentration

Donor 3

Compound[a]	IL-6 (pg/ml)	IL-12p70 (pg/mL)	TNFα (pg/mL)	IFNγ (pg/mL)
PBS	5	5	5	7
SNA 1_30	367	249	65	23
SNA 8	538	186	57	45
SNA 9	382	232	57	24
SNA 10	431	237	62	55
SNA 11	503	167	71	69

SNA 12	791	81	167	32

[a] At 2.5 μM oligonucleotide concentration

Table 5: In vitro cytokine secretion in human PBMC cultures with SNA 18_60

Donor 1

Compound	IL-6 (pg/ml) [a]	IL-12p40 (pg/mL) [a]	TNFα (pg/mL) [a]	IFNα (pg/mL) [b]
PBS	28.3	6.82	16.69	6.38
SNA 18_60	709.79	33.80	173.14	4642.07

[a] At 3.33 μM oligonucleotide concentration

[b] At 0.123 μM oligonucleotide concentration

Donor 2

Compound	IL-6 (pg/ml) [a]	IL-12p40 (pg/mL) [a]	TNFα (pg/mL) [a]	IFNα (pg/mL) [b]
PBS	12.94	12.78	30.2	0.3
SNA 18_60	529.58	176.67	376.0	3885.0

[a] At 5.00 μM oligonucleotide concentration

[b] At 0.312 μM oligonucleotide concentration

Cytokine induction in mouse serum

Female, 6-week old C57BL6 mice were administered 7.5 mg/kg SNA subcutaneously. At 10 hours following SNA administration, serum was collected for cytokine analysis.

Cytokine analysis using Q-Plex array

The cytokine levels in human PBMC culture supernatants and mouse seum were measured using a Q-Plex chemiluminescent arrays (Quansys) following the manufacturer's instructions. The plates were imaged using a Bio-Rad ChemiDoc XRS+ imager and the data were analyzed using the Q-view software (Quansys).

Results

Nature and number of lipophilic moieties conjugated to oligonucleotide determine SNA assembly

To determine the effect of the lipophilic moiety on SNA formation, SNAs were synthesized using oligonucleotide-lipophilic moiety conjugates listed in Table 1. Agarose gel electrophoresis was used to identify the formation of SNAs. Oligonucleotides conjugated to lipophilic moieties alone were run alongside the SNAs that were self-assembled with the same oligonucleotide. SNA formation results in a characteristic band which migrates between 1000-1500 bases which can be differentiated from the lipophilic moiety-conjugated oligonucleotide. It was observed that oligonucleotide conjugates of mono-alkyl lipophilic moieties did not form SNAs, but di- and tri-alkyl lipophilic moieties (≥C14) formed SNAs on DOPC liposomes (see Figure 1 and Figure 2). Further, size-exclusion chromatography (SEC) was used to characterize SNA formation from non-functionalized oligonucleotide-lipophilic moiety conjugates and observed that a mono-alkyl lipid moiety did not form SNA (SNA 3 through SNA 6) as demonstrated by late retention of the oligonucleotide-mono alkyl lipophilic moiety conjugate (11-12 mins). Mono-cholesterol- and di-alkyl lipophilic moiety-oligonucleotide conjugates formed SNAs as demonstrated by elution of the SNAs in the void volume (6-8 mins) (see Figure 3).

Oligonucleotide-stearyl lipophilic moiety conjugate results in higher SNA loading

Based on evidence of SNA formation determined using gel electrophoresis (Figures 1 and 2) it was sought to determine the loading capacities of oligonucleotide-lipophilic moieties per particle using SEC method. Oligonucleotide conjugates 1, 2, 11-16 and 18-22 with mono-cholesterol, mono-tocopherol, or different alkyl chain lipophilic moieties resulted in up to 25 oligonucleotides per particle (see Figure 4A; Table 2). In contrast to other alkyl lipophilic moieties, cholesterol, and tocopherol, oligonucleotide-di-stearyl conjugates had the capability of loading up to 60-oligonucleotides per nanoparticle (see Figure 4B).

Increased loading density allows SNAs without aggregation for secondary structure-forming oligonucleotides

The oligonucleotide sequences 23-34 and 36-37 (see Table 1) have a self-complementary or a G-rich nucleotide sequence, respectively. Synthesis of SNAs with these oligonucleotide-cholesterol conjugates (25-oligonucleotides per particle) leads to aggregation of SNA to a suspension as determined by enlarged particle diameters and low light transmission (SNA 17 and

SNA 19_30, see Table 3). This aggregation is inherent to SNAs that are synthesized with oligonucleotides that contain a self-complementary or a G-rich sequence that can potentially form secondary structures such as duplexes or G-quadruplexes, respectively, due to inter-particle interactions of oligonucleotides. When the self-complementary oligonucleotide was conjugated with a di-stearyl lipophilic moiety and synthesized SNA at 60-oligonucleotides per nanoparticle, the resulting SNAs did not aggregate as demonstrated by the small 27 nm particle diameter and high light transmission (SNA 18_60, see Table 3). However, loading of only 30-self-complementary oligonucleotide-di-stearyl moiety conjugates on liposomes resulted in SNA aggregation as in the case of cholesterol-oligonucleotide SNAs with enlarged particle diameters and low light transmission (SNA 18_30, see Table 3). Similarly, SNAs synthesized with G-rich oligonucleotide-di-stearyl moiety conjugates also at 60-oligonucleotides per nanoparticle abrogated aggregation significantly as demonstrated by the small 36.6 nm particle diameter and high light transmission (SNA 20_60, see Table 3). SNAs synthesized with a loading of only 30-oligonucleotides per nanoparticle of G-rich oligonucleotide-di-stearyl conjugates showed more aggregation than SNA 20_60, but less than that of cholesterol-oligonucleotide SNA 19_30 as demonstrated by decreased light transmission (SNA 20_30, see Table 3).

Immunostimulatory activity of SNAs with various oligonucleotide-lipophilic moiety conjugates

Immunostimulatory activity of SNAs synthesized with a TLR9 stimulating oligonucleotide with various lipophilic moieties that formed SNAs was also evaluated. Human PBMCs from three different donors were treated with SNAs synthesized to characterize their cytokine release profiles. In general, SNAs exhibited similar cytokine induction profiles characteristic of TLR9 activation regardless of the type of lipophilic moiety conjugated to the oligonucleotide to synthesize the SNA (see Table 4). Self-complementary oligonucleotide sequence in SNA 18_60 is designed to elicit a strong IFNα response. As expected, SNA 18_60 stimulated IFNα induction in PBMCs from two different healthy human donors (see Table 5).

Cytokine induction in mouse serum following SNA administration was used to assess the *in vivo* immunostimulatory activity of SNAs with a TLR9 stimulating oligonucleotide and two different lipophilic moieties. SNAs with both lipophilic moieties induced similar cytokine profiles in mouse serum (see Table 6).

Table 6: *In vivo* cytokine induction in mouse serum

Compound	IL-6	IL-12p40	MCP-1	RANTES
PBS	128 ± 0	73 ± 0	63 ± 1	68 ± 1
SNA 1_25	1343 ± 292	159 ± 44	4389 ± 294	748 ± 118
SNA 2	530 ± 53	270 ± 36	4300 ± 137	579 ± 77

Mean serum cytokine level (pg/mL) ± SEM of n=4 mice per group

Together, these results demonstrate that multiple lipophilic moieties, including di- or tri-alkyl lipophilic moieties, conjugated to oligonucleotides permit synthesis of SNAs with desired characteristics without significant effect on their biological activity.

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

All references, including patent documents, disclosed herein are incorporated by reference in their entirety.

What is claimed is:

CLAIMS

1. A nanostructure comprising:

a spherical nucleic acid (SNA) comprising a core, a lipid shell having an inner surface surrounding the core and an outer surface, and an oligonucleotide linked to a lipophilic moiety wherein the oligonucleotide is functionalized to the lipid shell through interaction between the lipid shell and at least a portion of the lipophilic moiety and wherein the lipophilic moiety is comprised of two or more lipophilic groups and has the following structure:

$$–L1-(Spacer)_n-L2-(Spacer)_{n1}-L3-X-(alkyl\ group)_m,$$

wherein L1, L2, and L3 are each linkers independent of one another and may be a phosphodiester or phosphorothioate bond or short chain linkage, wherein the spacer is an oligoethylene spacer, wherein n and n1 are independently 0-3, wherein X is a doubler or trebler, the alkyl group is a C_6-C_{30} saturated or unsaturated alkyl group and m is 2-3.

2. The nanostructure of claim 1, wherein the oligoethylene spacer is a HEG spacer (hexaethylene glycol).

3. The nanostructure of claim 1 or 2, wherein L1, L2, and L3 are phosphodiester linkages.

4. The nanostructure of any one of claims 1-3, wherein n is 1 and n1 is 0.

5. The nanostructure of any one of claims 1-3, wherein n is 1 and n1 is 1.

6. The nanostructure of any one of claims 1-5, wherein X is a doubler.

7. The nanostructure of any one of claims 1-6, wherein the alkyl group is a C_{12}-C_{22} alkyl group.

8. A nanostructure comprising:

a spherical nucleic acid (SNA) comprising a core, a lipid shell having an inner surface surrounding the core and an outer surface with a oligonucleotide functionalized to the outer surface of the nanostructure by a moiety comprised of two or more lipophilic groups.

9. The nanostructure of claim 8, wherein the core is a hollow or a solid core.

10. The nanostructure of claim 8, wherein the core is a liposomal core.

11. The nanostructure of claim 8, wherein the lipid shell is 1,2-dioleoyl-sn-glycero-3-phophocholine (DOPC).

12. The nanostructure of any one of claims 8-10, wherein the moiety comprised of two or more lipophilic groups is attached to the oligonucleotide through a linker.

13. The nanostructure of claim 12, wherein the linker is a hexaethyleneglycol linker.

14. The nanostructure of any one of claims 8-13, wherein the oligonucleotide is a single stranded oligonucleotide and/or an immunostimulatory oligonucleotide.

15. The nanostructure of claim 8, wherein the oligonucleotide is a self-aggregating oligonucleotide containing a self-complementary motif, which optionlly includes a G-rich motif.

16. The nanostructure of any one of claims 8-15, wherein the moiety comprised of the two or more lipophilic groups is a di-alkyl.

17. The nanostructure of any one of claims 8-15, wherein the moiety comprised of the two or more lipophilic groups is distearyl.

18. The nanostructure of any one of claims 8-15, wherein the moiety comprised of the two or more lipophilic groups is a tri-alkyl.

19. The nanostructure of any one of claims 8-18, wherein the moiety comprised of the two or more lipophilic groups is comprised by an alkyl chain.

20. The nanostructure of claim 19, wherein the alkyl chain is comprised of at least 10 carbons.

21. The nanostructure of claims 19 or 20, wherein the alkyl chain is comprised of at least 14 carbons.

22. The nanostructure of any one of claims 8-21, wherein the nanostructure contains 26 to 7,000 oligonucleotides.

23. The nanostructure of any one of claims 8-21, wherein the nanostructure contains 26 to 500 oligonucleotides.

24. The nanostructure of any one of claims 8-21, wherein the nanostructure contains 26 to 80 oligonucleotides.

25. The nanostructure of any one of claims 9-21, wherein the nanostructure contains at least 40 oligonucleotides.

26. The nanostructure of any one of claims 8-25, wherein the nanostructure moiety comprised of two or more lipophilic groups is more stable in solution than a nanostructure with a moiety comprised of one lipophilic group.

27. The nanostructure of any one of claims 8-26, wherein the nanostructure has a diameter of about 10 nm to about 100 nm.

28. The nanostructure of any one of claims 8-26, wherein the nanostructure has a diameter of about 20 nm to about 50 nm.

29. The nanostructure of any one of claims 8-26, wherein the nanostructure has a diameter of about 27 nm to about 37 nm.

30. The nanostructure of any one of claims 8-26, wherein the nanostructure has a diameter of about 27 nm.

31. The nanostructure of any one of claims 8-26, wherein the nanostructure has a diameter of about 37 nm.

32. A composition of discrete nanostructures, wherein each nanostructure comprises:

a spherical nucleic acid (SNA) comprising a core, a lipid shell having an inner surface surrounding the core and an outer surface with 26-200 oligonucleotides functionalized to the outer surface of the nanostructure, wherein the oligonucleotides contain a self-complementary motif.

33. The composition of claim 32, wherein each discrete nanostructure has a diameter of about 10 nm to about 100 nm.

34. The composition of claim 32, wherein each discrete nanostructure has a diameter of about 20 nm to about 50 nm.

35. The composition of claim 32, wherein the oligonucleotides contain a G-rich motif.

36. The composition of claim 32, wherein the oligonucleotides are immunostimulatory oligonucleotides.

37. The composition of claim 36, wherein the immunostimulatory oligonucleotides stimulate a toll-like receptor 9 (TLR9).

38. The composition of claim 32, wherein the oligonucleotides are antisense oligonucleotides.

39. The composition of any one of claims 32-38, wherein the core is a hollow or a solid core.

40. The composition of any one of claims 32-39, wherein the composition has a polydispersity (PDI) of 0.1- 0.4.

41. The composition of any one of claims 32-39, wherein each discrete nanostructure has a Z average diameter of 30-1,300.

42. A method for eliciting an immune response, comprising

contacting a cell with the nanostructure of any one of claims 1-31 or a composition of any one of claims 32-41.

43. The method of claim 42, wherein the nanostructure induces cytokine secretion.

44. The method of claim 42, wherein the nanostructure activates interferon alpha (IFNα).

45. The method of any one of claims 42-44, wherein the cell is a peripheral blood mononuclear cell.

46. A method for regulating gene expression, comprising contacting a cell with a nanostructure of any one of claims 1-12 and 15-31 to regulate gene expression.

47. A method for treating an immune disorder, comprising administering to a cell in a subject a nanostructure of any one of claims 1-31 to deliver an immunostimulatory oligonucleotide that promotes an immune response or to deliver an immunoinhibitory oligonucleotide that decreases or prevents an immune response to treat the immune disorder.

48. The method of claim 47, wherein the subject is a mammal.

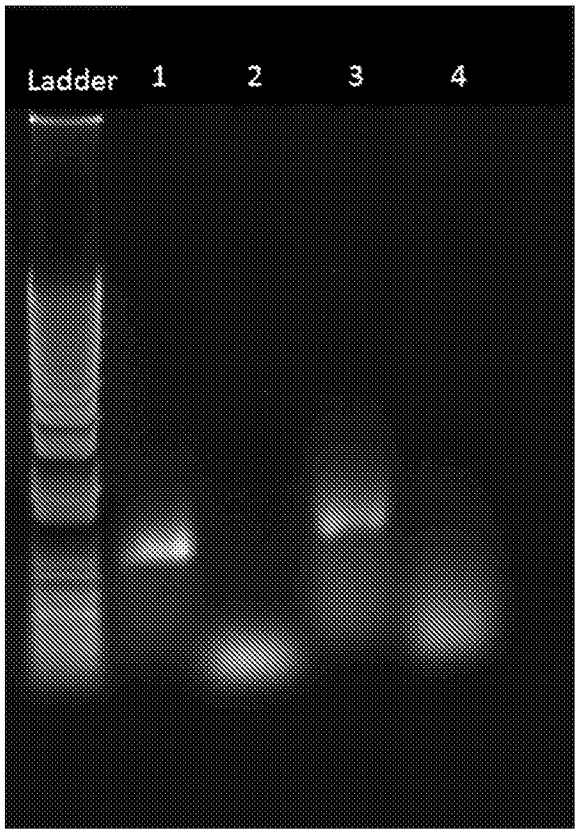
49. The method of claim 47, wherein the subject is a human.

50. The method of any one of claims 47-49, wherein the nanostructure is in contact with the cell at a concentration of 1 nM to 100 μM.

51. The method of any one of claims 47-49, wherein the nanostructure is in contact with the cell at a concentration of 1 μM to 10 μM.

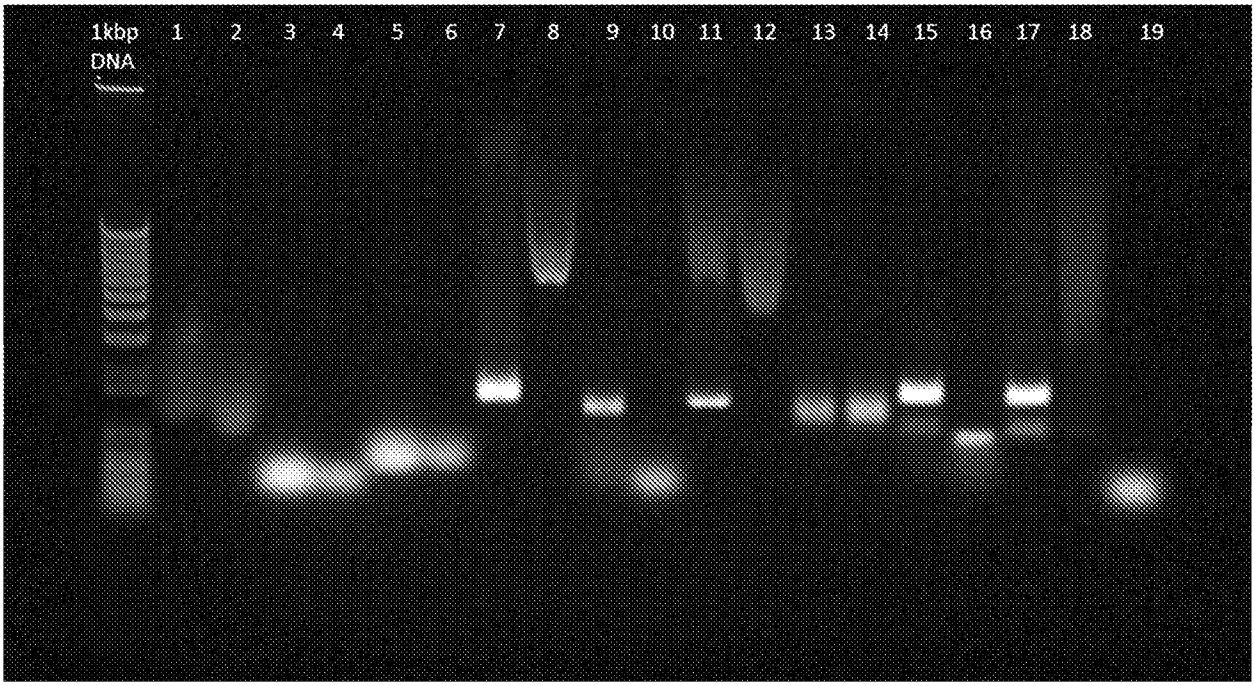
52. The method of any one of claims 47-51, wherein the nanostructure is in contact with the cell for 24 hours.

Figure 1



Lane #	Compound # or Oligo No.#
1	D
2	Oligo 1
3	F
4	Oligo 2

Figure 2



Lane #	Compound or Oligo sequence #	Lane #	Compound or Oligo sequence #
1	H	11	L
2	Oligo 5	12	Oligo 12
3	J	13	S
4	Oligo 9	14	Oligo 21
5	I	15	T
6	Oligo 6	16	Oligo 22
7	N	17	R
8	Oligo 14	18	Oligo 20
9	Q	19	Oligo 35
10	Oligo 18		

Figure 3

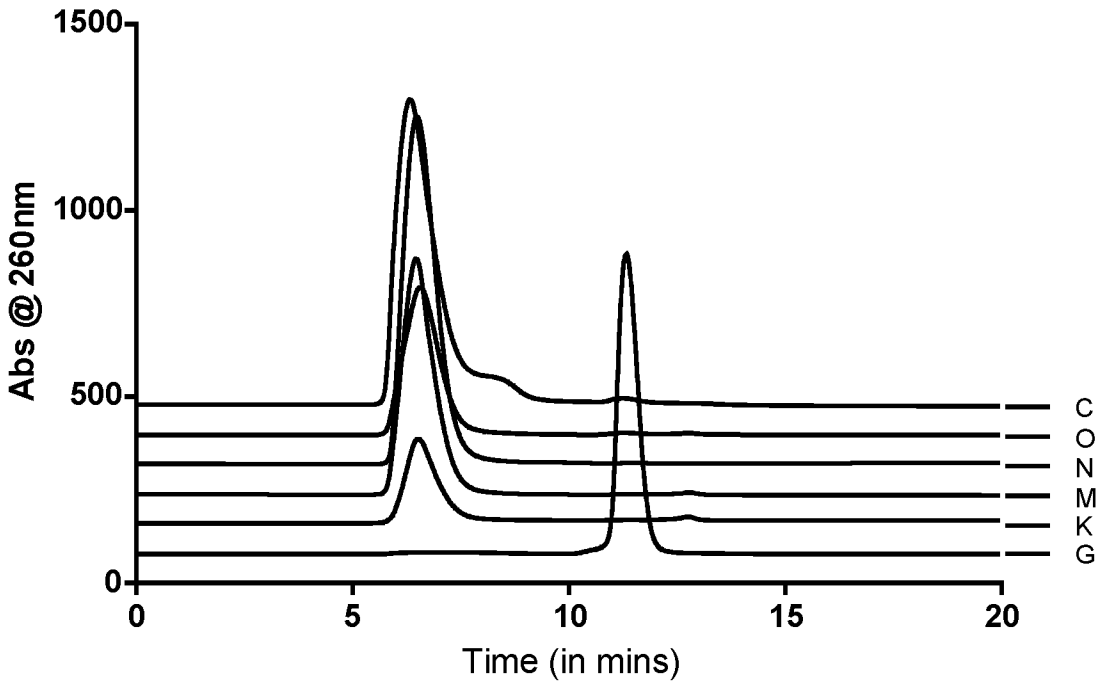


Figure 4A

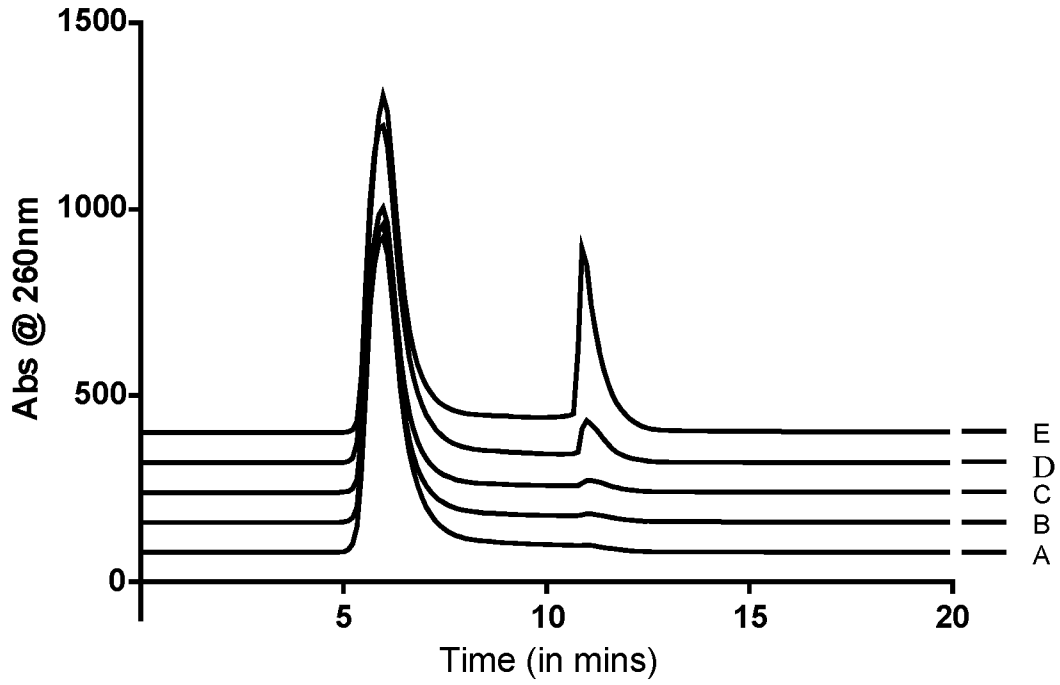
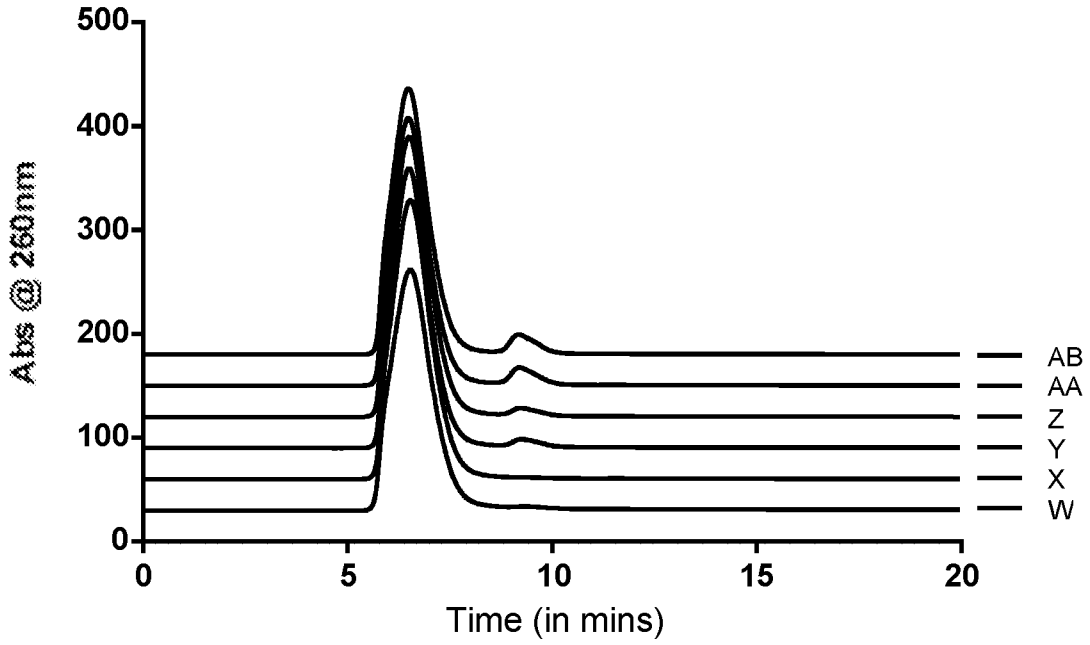


Figure 4B



INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2018/030021

A. CLASSIFICATION OF SUBJECT MATTER

A61K 31/7084 (2006.01) A61K 47/50 (2017.01) A61K 9/127 (2006.01) A61K 9/51 (2006.01) C12N 15/00 (2006.01)

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)

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

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

EPODOC, WPIAP, MEDLINE, CAPLUS, EMBASE. Keywords: nanostructure, spherical nucleic acid, SNA, oligonucleotide.

Applicant/Inventor search.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	Documents are listed in the continuation of Box C	

[X] Further documents are listed in the continuation of Box C

[X] 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	Date of mailing of the international search report
1 August 2018	01 August 2018
Name and mailing address of the ISA/AU	**Authorised officer**
AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA Email address: pct@ipaustralia.gov.au	Geoffrey Peters AUSTRALIAN PATENT OFFICE (ISO 9001 Quality Certified Service) Telephone No. +61262832184

INTERNATIONAL SEARCH REPORT C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		International application No. **PCT/US2018/030021**
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	WO 2017/011662 A1 (EXICURE, INC.) 19 January 2017	
X	Pages 1-3, 6, claims.	32-35, 38, 39
A	Pages 1-3, 6, claims.	1-31, 36, 37, 40-52
	WO 2016/115320 A1 (EXICURE, INC.) 21 July 2016	
X	Pages 1-3, 23, claims.	32-45
A	Pages 1-3, 23, claims.	1-31, 46-52

INTERNATIONAL SEARCH REPORT Information on patent family members	International application No. **PCT/US2018/030021**

This Annex lists known patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document/s Cited in Search Report		Patent Family Member/s	
Publication Number	**Publication Date**	**Publication Number**	**Publication Date**
WO 2017/011662 A1	19 January 2017	WO 2017011662 A1	19 Jan 2017
		AU 2016294594 A1	08 Feb 2018
		EP 3322407 A1	23 May 2018
WO 2016/115320 A1	21 July 2016	WO 2016115320 A1	21 Jul 2016
		AU 2016206658 A1	03 Aug 2017
		CA 2973702 A1	21 Jul 2016
		CN 108064295 A	22 May 2018
		EP 3247796 A1	29 Nov 2017
		JP 2018503377 A	08 Feb 2018
		KR 20170104550 A	15 Sep 2017

End of Annex

Due to data integration issues this family listing may not include 10 digit Australian applications filed since May 2001.