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## (54) COMPOSITIONS AND METHODS FOR TUMOR IMMUNOTHERAPY

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- (60) Provisional application No. 62/630,022, filed on Feb. 13, 2018.

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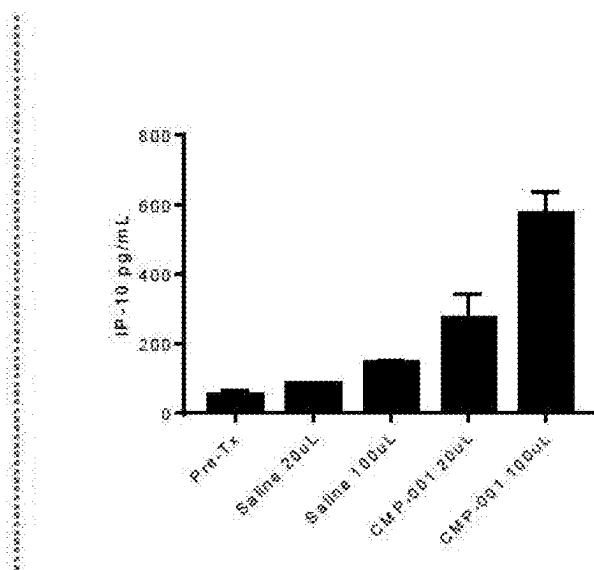
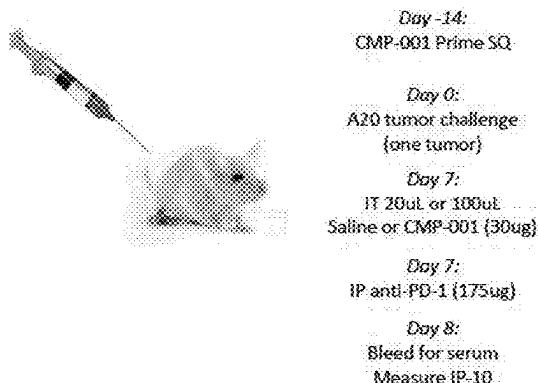
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## (57)

## ABSTRACT

Provided are compositions and methods for treating cancer using administration of certain volumes of CpG oligonucleotides (CpG ODN) and, optionally, administration of a checkpoint inhibitor such as an anti-PD-1 antibody, an anti-PD-L1 antibody, and/or an anti-CTLA-4 antibody. In preferred embodiments, the CpG ODN are selected based on their propensity to induce high amounts of interferon alpha (IFN- $\alpha$ ) and T-cell activation relative to interleukin-10 (IL-10) and B-cell activation. In certain embodiments, the methods further include pretreatment with radiotherapy, to potentiate the combination immunotherapy.

Specification includes a Sequence Listing.



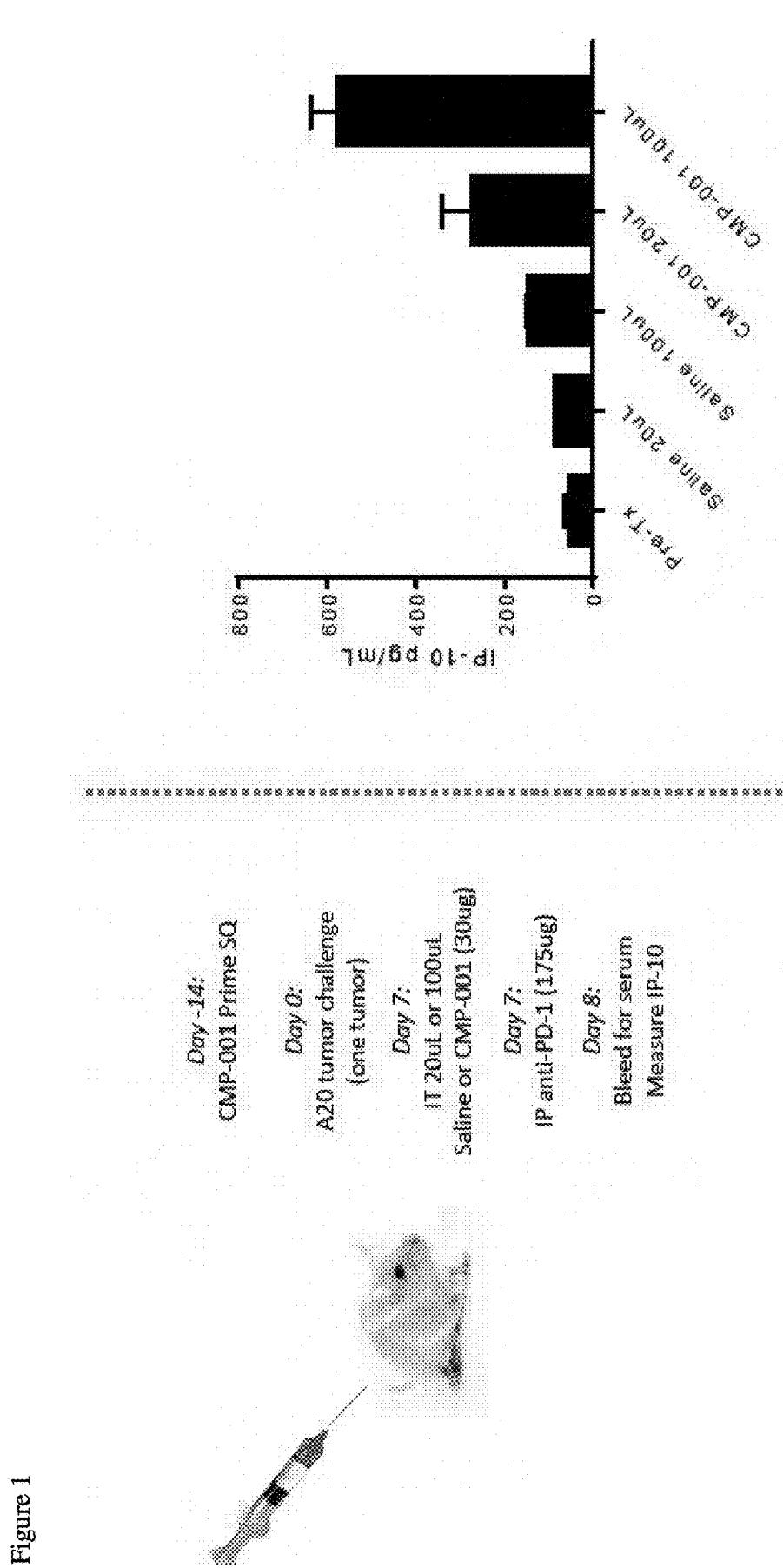


Figure 1

Figure 2

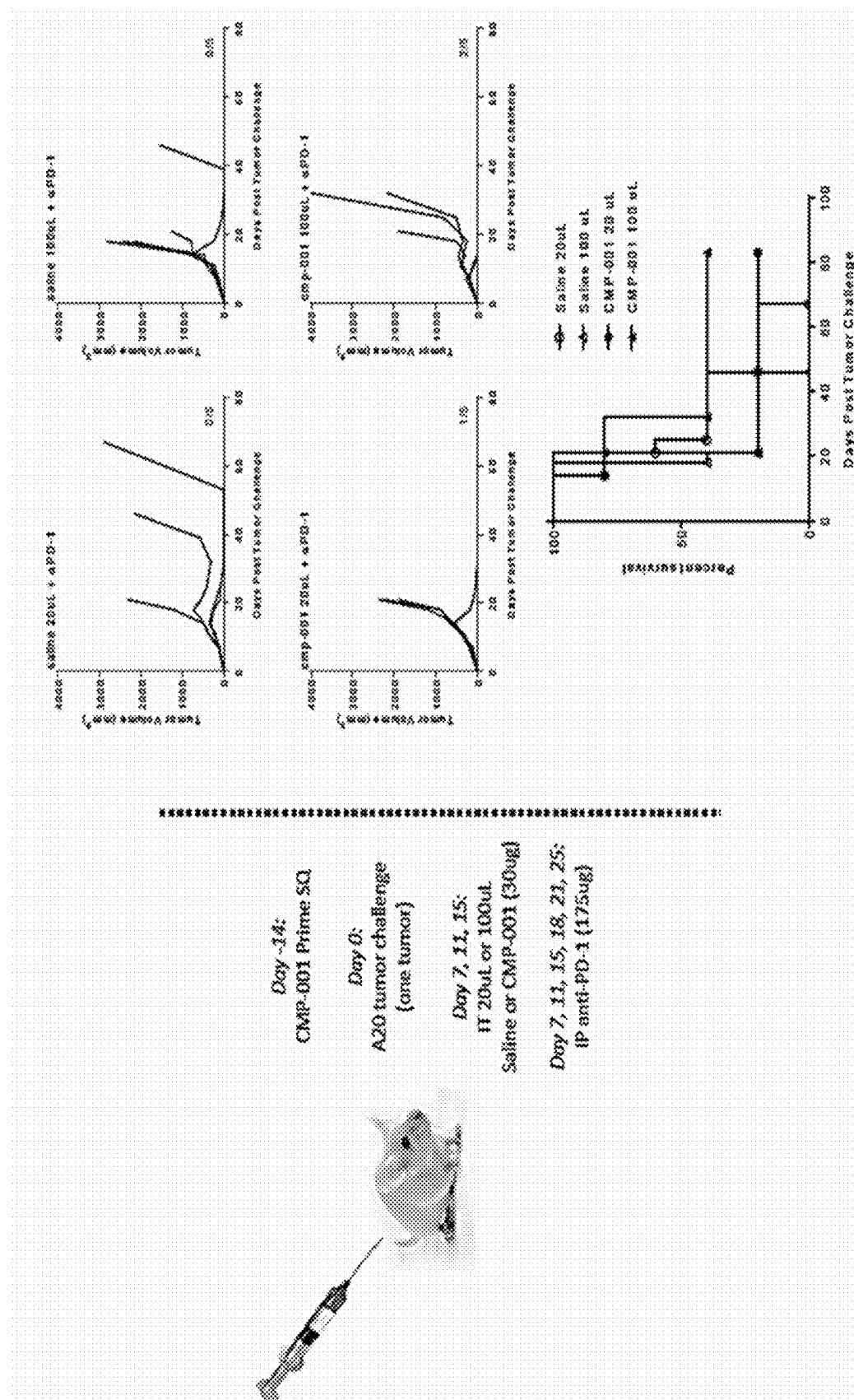


Figure 3

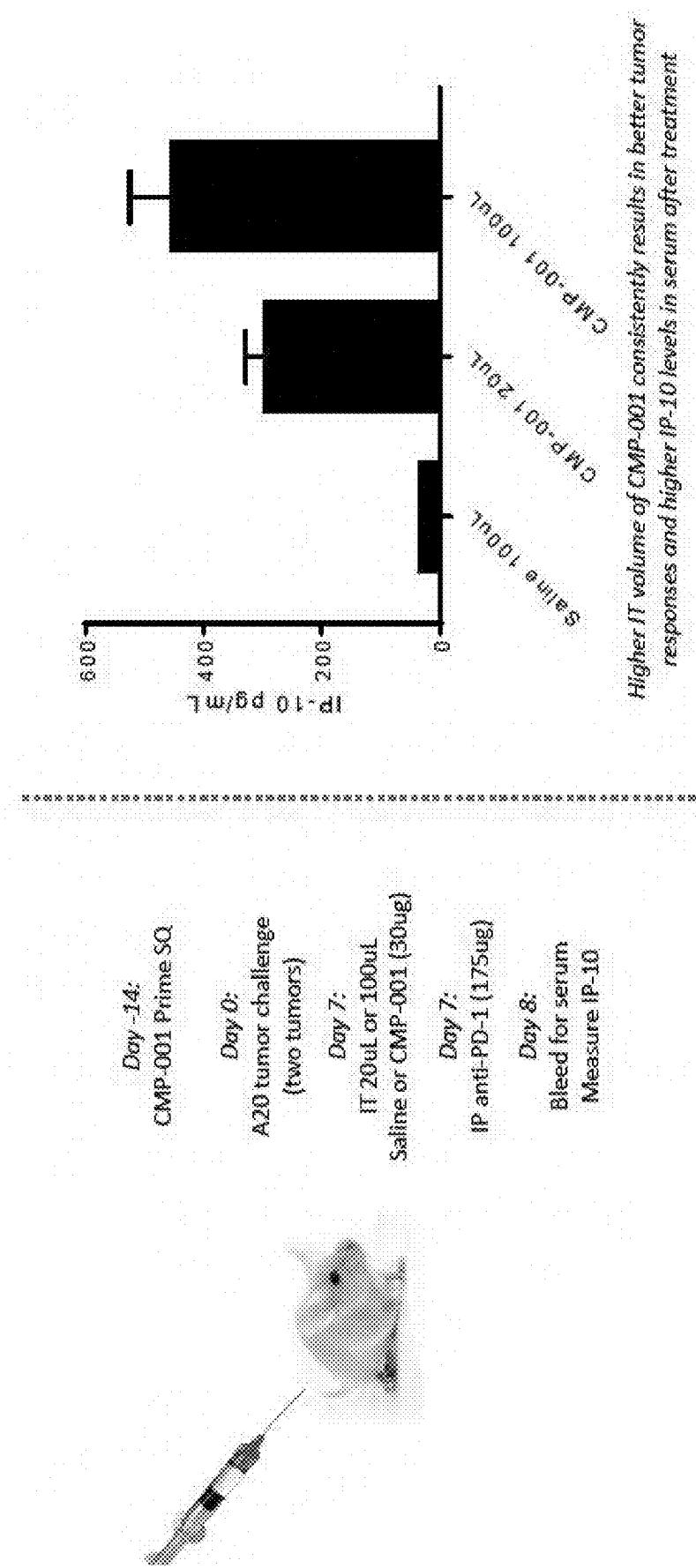


Figure 4

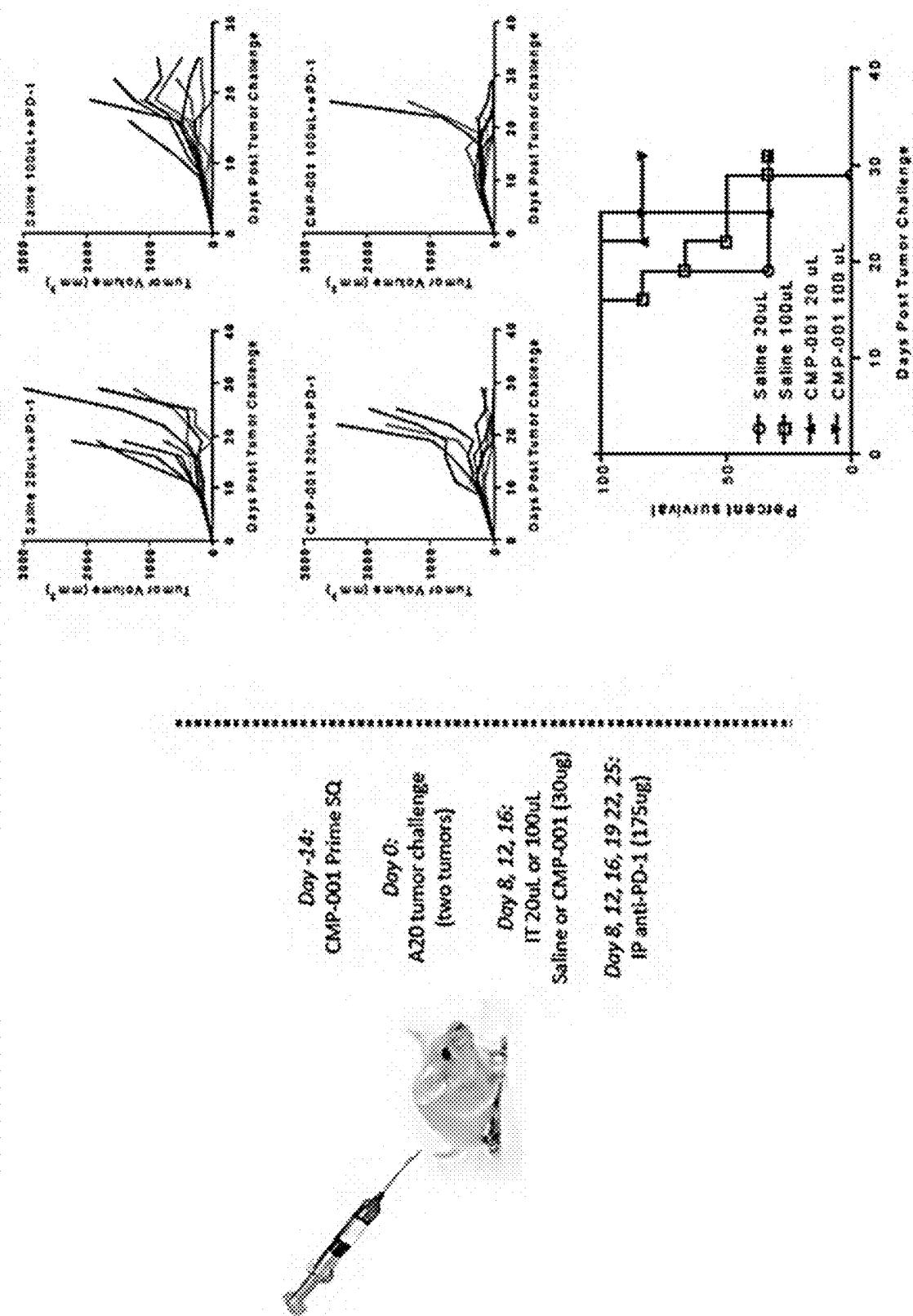


Figure 5

Group (n=15)	CMV-001	CMV-004
Priming Regimen	Treatment	
1	100 µg/ 100 µL	Vehicle: 100 µL
2	Vehicle: 100 µL	
3	1 µg/ 10 µL	
4	10 µg/ 10 µL	
5	10 µg/ 10 µL (-OT1)	100 µg/ 100 µL
6	100 µg/ 10 µL	D5, D10 & D15
7	1 µg/ 100 µL	
8	10 µg/ 100 µL	
9	10 µg/ 100 µL (-OT1)	
10	100 µg/ 100 µL	

- \* Female C57Bl/6 mice (6-8 wks old); 5x10<sup>6</sup> B16-OVA cells injected SC (lower dorsal region) on D0
- \* CMV-001: SC delivery
  - Prime: scruff of neck (D-14)
  - Treatment: Peritumoral (D5, D10, D15)
- \* 10<sup>6</sup> splenocytes from OT1 mice (OVA-specific CD8 T cells) injected IV (RO) on D3 (Except groups 5 & 9)
- \* Immune readouts
  - Serum cytokines: 3 hours post prime & initial Tx (D-14 & D5; n=5)
  - Anti-Qbeta IgG/IgM: D-1, D14 (n=15)
  - ELISpot (n=5): OVA & Qbeta antigens (D14) from splenocytes & TILs
- \* Mice followed for long-term survival (n=10)
  - Humans endpoint: >20% loss in BW relative to D0 and/or tumor size >300 mm<sup>2</sup>

Figure 6

No.	No. SC CHP-001 Priming dose: 100 μl of G10 Img Chp-001*	IT CHP-001 Treatment dose: 100 μl of G10 Img Chp-001*	C87073 IT Treatment schedule	3hr post-treatment serum analysis	24hr post-treatment serum analysis	24hr post-treatment serum analysis
1	priming only control	10 16.7[0.067] 100μl of 0.67mg/ml	Untreated (100μl vehicle)	-	Lumines 25-plex	T Cell response
2		10 16.7[0.067] 100μl of 0.67mg/ml	1.67[0.067] 100μl of 0.67mg/ml	1x or 2x	Lumines 25-plex	T Cell response
3		10 16.7[0.067] 100μl of 0.67mg/ml	16.7[0.067] 100μl of 0.7mg/ml	1x or 2x	Lumines 25-plex	T Cell response
4	Low conc. Std dose high vol prime	10 16.7[0.067] 100μl of 0.67mg/ml	1.67[0.067] 100μl of 0.67mg/ml	1x or 2x	Lumines 25-plex	T Cell response
5	low/high vol Tx dose	10 16.7[0.067] 100μl of 0.67mg/ml	1.67[0.067] 100μl of 0.067mg/ml	1x or 2x	Lumines 25-plex	T Cell response
6		10 16.7[0.067] 100μl of 0.67mg/ml	16.7[0.067] 100μl of 0.67mg/ml	1x or 2x	Lumines 25-plex	T Cell response
7	range	10 16.7[0.067] 100μl of 0.67mg/ml	16.7[0.067] 100μl of 0.7mg/ml	1x or 2x	Lumines 25-plex	T Cell response
8		10 16.7[0.067] 100μl of 0.67mg/ml	5.00[2.0] 100μl of 20mg/ml	1x or 2x	Lumines 25-plex	T Cell response
	And/or					
9	priming only control	10 16.7[0.067] 100μl of 0.7mg/ml	Untreated (100μl vehicle)	-	Lumines 25-plex	T Cell response
10		10 16.7[0.067] 100μl of 0.7mg/ml	1.67[0.067] 100μl of 0.67mg/ml	1x or 2x	Lumines 25-plex	T Cell response
11	High conc. Std dose	10 16.7[0.067] 100μl of 0.7mg/ml	16.7[0.067] 100μl of 0.7mg/ml	1x or 2x	Lumines 25-plex	T Cell response
12	low vol prime:	10 16.7[0.067] 100μl of 0.7mg/ml	1.67[0.067] 100μl of 0.67mg/ml	1x or 2x	Lumines 25-plex	T Cell response
13	low/high vol Tx dose	10 16.7[0.067] 100μl of 0.7mg/ml	1.67[0.067] 100μl of 0.067mg/ml	1x or 2x	Lumines 25-plex	T Cell response
14		10 16.7[0.067] 100μl of 0.7mg/ml	16.7[0.067] 100μl of 0.67mg/ml	1x or 2x	Lumines 25-plex	T Cell response
15	range	10 16.7[0.067] 100μl of 0.7mg/ml	16.7[0.067] 100μl of 0.7mg/ml	1x or 2x	Lumines 25-plex	T Cell response
16		10 16.7[0.067] 100μl of 0.7mg/ml	5.00[2.0] 100μl of 20mg/ml	1x or 2x	Lumines 25-plex	T Cell response
	And/or					
17	priming only control	10 16.7[0.067] 100μl of 0.7mg/ml	Untreated (100μl vehicle)	-	Lumines 25-plex	T Cell response
18		10 16.7[0.067] 100μl of 0.7mg/ml	1.67[0.067] 100μl of 0.67mg/ml	1x or 2x	Lumines 25-plex	T Cell response
19	High conc. High dose high vol prime	10 16.7[0.067] 100μl of 0.7mg/ml	16.7[0.067] 100μl of 0.7mg/ml	1x or 2x	Lumines 25-plex	T Cell response
20	low/high vol Tx dose	10 16.7[0.067] 100μl of 0.7mg/ml	1.67[0.067] 100μl of 0.67mg/ml	1x or 2x	Lumines 25-plex	T Cell response
21		10 16.7[0.067] 100μl of 0.7mg/ml	1.67[0.067] 100μl of 0.067mg/ml	1x or 2x	Lumines 25-plex	T Cell response
22	range	10 16.7[0.067] 100μl of 0.7mg/ml	16.7[0.067] 100μl of 0.67mg/ml	1x or 2x	Lumines 25-plex	T Cell response
23		10 16.7[0.067] 100μl of 0.7mg/ml	16.7[0.067] 100μl of 0.7mg/ml	1x or 2x	Lumines 25-plex	T Cell response
24		10 16.7[0.067] 100μl of 0.7mg/ml	5.00[2.0] 100μl of 20mg/ml	1x or 2x	Lumines 25-plex	T Cell response

Figure 7

Cy5.5 Cell ( $\mu$ g)	Cy5.5 Volume ( $\mu$ L)	Route of Administration
1	20	Subcutaneous (scruff of neck)
2	100	
5	500	
10		Intratumoral
25		
50		
7	100	Peritumoral
10		
100		
100	0	N/A

- Female BALB/c mice (4-6 weeks old)
  - 1x10<sup>6</sup> CT-26 cells implanted SC in the right flank on D0
- Animals primed w/ 12.5 $\mu$ g/100 $\mu$ L CMP-001 SC (scruff of neck) at D-14
- Cy5.5-labeled CMP-001 injected on ~D12 (2 days later than previous IVIS study – allows IT injection of slightly higher volumes)
- Imaging Timepoints:
  - Fast Kinetics: 2, 5, 10, 20, 40, 60 min
  - Short-term: 2, 6 & 24 hours
- At 24hrs, animals perfused, lymph nodes (axial, inguinal and mesenteric) collected, imaged ex vivo and quantitative analysis conducted on tissue homogenates *in vitro*

## COMPOSITIONS AND METHODS FOR TUMOR IMMUNOTHERAPY

### RELATED APPLICATIONS

[0001] This application is a divisional of U.S. patent application Ser. No. 16/969,076, filed Aug. 11, 2020, now U.S. Pat. No. 12,246,031, which is a 35 U.S.C. § 371 filing of International Patent Application No. PCT/US2019/017680, filed Feb. 12, 2019, which claims priority to U.S. Provisional Patent Application Ser. No. 62/630,022, filed Feb. 13, 2018, the entire disclosures of which are hereby incorporated herein by reference.

### SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in XML format and is hereby incorporated by reference in its entirety. Said XML file, created on May 6, 2025, is named 761214\_RGN9-007USDIV\_ST26.xml and is 1,682,697 bytes in size.

### BACKGROUND OF THE INVENTION

[0003] Many scientists have sought to treat cancer by activating the immune system against the tumor. However, despite occasional successes, durable responses to immune therapy have been rare and limited to just a few tumor types. Current understanding of cancer immunotherapy among those skilled in the art has been summarized in recent review articles, including for example Chen and Mellman, *Immunity* 2013 39 (1): 1-10. The cycle for induction of therapeutic immune responses against tumors may be broken down into seven distinct steps: Release of cancer cell antigens; Presentation of cancer cell antigens by antigen-presenting cells (APC, usually in draining lymph nodes); T-cell priming and activation; Trafficking of CD8<sup>+</sup> T cells to tumors; Infiltration of CD8<sup>+</sup> T cells into tumors; Recognition of cancer cells by the infiltrating CD8<sup>+</sup> T cells; and Killing of cancer cells.

[0004] The art teaches that there are multiple negative and positive mediators of each step of the anti-tumor response. Recent research interest has focused on understanding and addressing the role that negative mediators play in inhibiting the anti-tumor immune response. For example, interleukin-10 (IL-10) is a factor that can have complicated effects, locally immune suppressive in the tumor, but systemically can actually have anti-tumor activity (reviewed in Vicari and Trinchieri, *Immunol. Rev.*, 2004). Although Toll-like receptor (TLR) agonists such as TLR9-activating CpG oligonucleotides (CpG ODN) have immune stimulatory effects that can promote anti-tumor responses, they are also known in the art to induce immune suppressive factors such as IL-10 (reviewed in Lu, *Frontiers Immunol.*, 2014). The art does not teach designs of TLR9 agonists that have improved anti-tumor effects as a result of inducing lower amounts of IL-10 production. Nevertheless, this increasing recent understanding of the cycle of tumor immunity has heightened awareness that it may be possible to increase the clinical efficacy of cancer immunotherapy by using combinations of agents that act at different points in this cycle for induction of therapeutic immune responses against tumors, but the art does not provide a deep enough understanding of the immunobiology of cancer to predict which of the many different possible combinations will be preferred.

[0005] Another possible way to consider the development of the anti-cancer T-cell response is the 3-signal model for

the induction of a T-cell response, summarized by Kim and Cantor, *Cancer Immunol Res* 2014 2:929-936). In this model a signal to the T cell comes from the presentation of antigen by an APC on the appropriate MHC to the T cell receptor. A second signal is the requirement for a costimulatory signal through the interaction of CD28 on the T cell by B7-1 or B7-2 on the APC (this signal is antagonized by CTLA-4 present on Treg; the efficacy of anti-CTLA-4 antibodies in cancer immunotherapy results from their inhibition of this “off” signal). Finally, a third signal is the modulation of T cell function resulting from signals via inflammatory cytokine receptors and PD-1. In particular for the induction of optimal CD8<sup>+</sup> T cell responses, which are known to be critical for successful cancer immunotherapy, type I IFN signaling is a very positive signal, but when chronic or prolonged also can paradoxically lead to T cell exhaustion and unresponsiveness, which is mediated through upregulation of PD-1 expression. Blocking of PD-1 (e.g., by anti-PD-1 antibodies, or by antibodies to its major ligand regulating anti-tumor immunity, PD-L1) restores the ability of the T cell to proliferate and produce cytokines in the tumor microenvironment.

[0006] Recently there have been several early clinical successes with the use of “checkpoint inhibitor” (CPI) compounds, such as antibodies, which block the negative immune effects of the checkpoint molecules such as CTLA-4, PD-1, and its ligand, PD-L1. Systemic administration of anti-CTLA-4 antibodies has led to durable responses in ~10% of patients with melanoma, and some encouraging early results in other tumor types, but at the cost of a high rate of adverse effects, including death in some patients. Anti-PD-1/PD-L1 human clinical trials also have been reporting encouraging results, apparently with a lower rate of severe toxicity. However, analyses of the responding patients have revealed that across multiple different types of cancer, responses to anti-PD-L1 therapy are relatively restricted to patients with tumor-infiltrating lymphocytes (TIL) and a Th1 pattern of gene expression in the tumor (Powles et al., *Nature* 2014 515:558; Herbst et al., *Nature* 2014 515:563; Tumeh et al., *Nature* 2014 515:568). That is, responses can be seen in some patients with preexisting immunity to the tumor, but are quite unlikely to occur in patients without this. Aside from melanoma, in which pre-existing anti-tumor immunity is relatively common, TIL are relatively uncommon in most other tumor types, indicating that CPI may be of limited benefit in most types of cancer.

[0007] Thus, there is a need to improve the efficacy of for cancer therapy and for therapies that include the use of CPI.

### SUMMARY OF THE INVENTION

[0008] The present disclosure provides compositions and methods for treating cancer. As described herein, the volume of the one or more compositions that are administered to a subject in need of cancer therapy is an important consideration to maximize efficacy. In various embodiments, the volume that is administered is higher than what has previously been described. (See, for example, PCT/US2015/067269 which is incorporated by reference herein in its entirety)

[0009] The present disclosure also provides compositions and methods for promoting immune activation and reducing immune inhibition, thus metaphorically both “stepping on the gas” and “releasing the brakes” of the immune system, to treat cancer. The disclosure can be used, for example, to

convert "cold" (treatment-resistant or -refractory) cancers or tumors to "hot" ones amenable to treatment, including treatment with checkpoint inhibition.

[0010] The present disclosure provides in some embodiments specific subtypes of CpG ODN with reduced amounts of phosphorothioate modifications compared to the CpG ODN most widely used in past cancer immunotherapy, and methods for their intratumoral and peritumoral administration in combination with CPI and/or radiotherapy (XRT), for the improved immunotherapy of cancer, including cancers that would be unlikely to respond to any of these therapies alone, or in other combinations.

[0011] CpG ODN bind and stimulate TLR9, an innate immune receptor which is constitutively expressed in only two types of human immune cell: B cells, which respond to TLR9 stimulation by proliferating and secreting immunoglobulin; and plasmacytoid dendritic cells (pDC), which respond to TLR9 stimulation by secreting large amounts of type I IFN (IFN- $\alpha$  and IFN- $\beta$ ). The present disclosure is based, at least in part, on the finding that the IFN- $\alpha$  response to CpG ODN is important for tumor immunotherapy. The present disclosure is based, at least in part, on the finding that a strong IFN- $\alpha$  response to CpG ODN is important for tumor immunotherapy, including tumor immunotherapy using intratumoral administration of CpG ODN.

[0012] Preferred CpG ODN of the disclosure are characterized, at least in part, by their propensity to induce high amounts of type I IFN.

[0013] Type I IFN is believed to play a key role in tumor rejection. For example, Type I IFN augments CD8+ T-cell survival, expansion, and effector differentiation; promotes dendritic cell (DC) maturation, cross-presentation of tumor-associated antigens to CD8+ T cells; is required for immune surveillance against carcinogen-induced tumors; and is required for rejection of implanted tumors. Additionally, levels of type I IFN-related mRNA correlate with tumor-infiltrating lymphocytes (TILs) in human metastases.

[0014] In addition to inducing higher levels of type I IFN than anything else, TLR9 ligands such as CpG ODN also activate pDC and induce secretion of hundreds of other Th1-promoting genes and factors; and convert pDC from immature/tolerance-promoting phenotype to mature, activated, cytotoxic T lymphocyte (CTL)-inducing phenotype.

[0015] The present disclosure also is based, at least in part, on the finding that delivery of the CpG ODN into tumors (directly or indirectly) induces the expression of adhesion molecules in the local vasculature in and around the tumor, and promotes the egress of activated T cells (CD4+ and CD8+) from capillaries into the tumor and surrounding region. Some of these T cells will be specific to the unmuted and mutated tumor-associated antigens (TAA). In the absence of checkpoint inhibitors and/or XRT, these T cells may be inhibited by the tumor, but in combination, this creates a much more powerful anti-tumor effect than can be achieved with CpG or the checkpoint inhibitors or XRT on their own.

[0016] The present disclosure in certain aspects is based on the use of CpG ODN classes other than those that have historically been used for cancer immunotherapy. In particular, the present disclosure in certain aspects is based on the use of high IFN- $\alpha$  secreting classes, the A-class and E-class, with reduced amounts of phosphorothioate (PS) modifications compared to B-class CpG ODN that have been widely used in the past. B-class CpG ODN are typi-

cally completely phosphorothioate-modified to increase their resistance to nucleases and the magnitude of the B-cell activation. In contrast, since a focus of the present disclosure is on achieving a high type I IFN response, rather than B-cell activation, the preferred CpG ODN of the present disclosure have either no phosphorothioate modifications, or only 1 or 2 phosphorothioate modifications at the 5' end and 1 to 4 phosphorothioate modifications at the 3' end. Preferred E-class ODN of the disclosure also contain phosphodiester (PO) linkages at the CpG dinucleotides, and optionally at other positions within the ODN, in order to reduce the B cell activation (and concomitant IL-10 and indoleamine 2,3-dioxygenase (IDO) induction), and they also preferably contain one or more palindromes to form duplexes or concatamers.

[0017] Those skilled in the art understand that intra- or peritumoral CpG in human cancer patients will activate APC in the tumor draining lymph nodes, enhancing one step of the cancer immunity cycle. However, what is not well understood by those skilled in the art is that this route of administration of high IFN-inducing CpG ODN will also induce TIL and convert the tumor microenvironment to a more Th1-like state that is more conducive to induction of clinically beneficial anti-tumor immunity. The intratumoral administration of high IFN-inducing CpG ODN induces T cell infiltration into the tumors, notably including CD8+ T cell infiltration. The importance of this is that this CD8+ T cell infiltration into tumors is believed to be the best predictor of response to treatment with anti-PD-1 or anti-PD-L1. Because the human clinical trials performed in the past with intratumoral administration of CpG oligonucleotides used B-class ODN, there would have been significant local production of IL-10 in the tumor that would have inhibited the anti-tumor immune response. The present disclosure features improved preferred CpG ODN as well as designs and screens for identifying the same, which induce lower amounts of IL-10 production and higher amounts of type I IFN secretion compared to the B-class ODN used in the past. Such preferred CpG ODN will provide improved synergy in cancer therapy when combined with checkpoint inhibitors using the methods of the disclosure.

[0018] In various embodiments of the present disclosure, virus-like particles (VLP) are used to formulate one or more CpG ODN.

[0019] In one embodiment of the present disclosure, a method of treating cancer in a subject is provided, said method comprising administering at least one dose of a composition comprising a TLR9 agonist, wherein said composition comprising the TLR9 agonist is administered in a volume of greater than 4 mL. As will be appreciated and as described herein, the composition comprising the TLR9 agonist may include, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, etc. TLR9 agonists, and that "at least one dose" includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc. doses over a period of time. In one embodiment, the composition comprising the TLR9 agonist is administered in a volume of between 5 and 20 mL. In another embodiment, the composition comprising the TLR9 agonist is administered in a volume of between 5 and 10 mL. In another embodiment, the composition comprising the TLR9 agonist is administered in a volume of 5 mL. In still another embodiment, the composition comprising the TLR9 agonist is administered in a volume of 7 mL.

[0020] In another embodiment of the disclosure, the TLR9 agonist induces IFN- $\gamma$ ,  $\alpha$ , or  $\beta$ . In a related embodiment, the TLR9 agonist induces IFN- $\alpha$ .

[0021] In yet another embodiment, the TLR9 agonist is CpG DNA. In a related embodiment, the CpG DNA is selected from the group consisting of A-class CpG DNA, C-class CpG DNA, E-class CpG DNA, A/E-class CpG DNA, P-class CpG DNA, and any combination thereof. In one embodiment, the TLR9 agonist is an A-class CpG DNA. In a related embodiment, the sequence of the A-class CpG DNA is GGGGGGGGGGGAC-GATCGTCGGGGGGGG (SEQ ID NO:82). In still another embodiment, the TLR9 agonist is a C-class CpG DNA.

[0022] In yet another embodiment of the disclosure, the composition comprising the TLR9 agonist is formulated as a virus-like particle (VLP). In a related embodiment, the aforementioned TLR9 agonist is an A-class CpG DNA. In still another embodiment, the A-class CpG DNA formulated as a virus-like particle (VLP) is CMP-001.

[0023] In various embodiments, the composition comprising the TLR9 agonist is administered via intratumoral, peritumoral, systemic, intravenous, intraperitoneal, enteric, oral, intramuscular, subcutaneous, transmucosal, topical and/or transdermal routes. In one embodiment, the composition comprising the TLR9 agonist is administered intratumorally.

[0024] In one embodiment, the cancer is associated with a cancerous tumor. In various embodiments, the cancerous tumor is a lymphoma or a cancerous tumor of a tissue or organ selected from the group consisting of skin, head and neck, esophagus, stomach, liver, colon, rectum, pancreas, lung, breast, cervix, ovary, kidney, bladder, prostate, thyroid, brain, muscle, and bone. In one embodiment, the cancerous tumor is a melanoma. In another embodiment, the cancerous tumor is a lymphoma. In still another embodiment, the cancerous tumor is resistant to a treatment regimen comprising administration of a checkpoint inhibitor (CPI).

[0025] In various embodiments, the subject is a human.

[0026] In yet another embodiment of the present disclosure, a method of treating cancer in a subject is provided, said method comprising (a) administering to the subject at least dose of a composition comprising a TLR9 agonist and (b) administering to the subject at least one dose of a composition comprising a CPI, wherein the composition comprising the TLR9 agonist is administered in a volume of greater than 4 mL. As will be appreciated and as described herein, the composition comprising the TLR9 agonist and/or the composition comprising a CPI may include, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, etc. TLR9 agonists and/or CPI, and that “at least one dose” includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc. doses over a period of time. In one embodiment, the composition comprising the TLR9 agonist is administered in a volume of between 5 and 20 mL. In another embodiment, the composition comprising the TLR9 agonist is administered in a volume of between 5 and 10 mL. In still another embodiment, the composition comprising the TLR9 agonist is administered in a volume of 5 mL. In yet another embodiment, the composition comprising the TLR9 agonist is administered in a volume of 7 mL.

[0027] In another embodiment of the disclosure, the TLR9 agonist induces IFN- $\gamma$ ,  $\alpha$ , or  $\beta$ . In a related embodiment, the TLR9 agonist induces IFN- $\alpha$ .

[0028] In yet another embodiment, the TLR9 agonist is CpG DNA. In a related embodiment, the CpG DNA is selected from the group consisting of A-class CpG DNA, C-class CpG DNA, E-class CpG DNA, A/E-class CpG DNA, P-class CpG DNA, and any combination thereof. In one embodiment, the TLR9 agonist is an A-class CpG DNA. In a related embodiment, the sequence of the A-class CpG DNA is GGGGGGGGGGGAC-GATCGTCGGGGGGGG (SEQ ID NO:82). In still another embodiment, the TLR9 agonist is a C-class CpG DNA.

[0029] In yet another embodiment of the disclosure, the composition comprising the TLR9 agonist is formulated as a virus-like particle (VLP). In a related embodiment, the aforementioned TLR9 agonist is an A-class CpG DNA. In still another embodiment, the A-class CpG DNA formulated as a virus-like particle (VLP) is CMP-001.

[0030] In various embodiments, the composition comprising the TLR9 agonist is administered via intratumoral, peritumoral, systemic, intravenous, intraperitoneal, enteric, oral, intramuscular, subcutaneous, transmucosal, topical and/or transdermal routes. In one embodiment, the composition comprising the TLR9 agonist is administered intratumorally.

[0031] In one embodiment, the cancer is associated with a cancerous tumor. In various embodiments, the cancerous tumor is a lymphoma or a cancerous tumor of a tissue or organ selected from the group consisting of skin, head and neck, esophagus, stomach, liver, colon, rectum, pancreas, lung, breast, cervix, ovary, kidney, bladder, prostate, thyroid, brain, muscle, and bone. In one embodiment, the cancerous tumor is a melanoma. In another embodiment, the cancerous tumor is a lymphoma. In still another embodiment, the cancerous tumor is resistant to a treatment regimen comprising administration of a checkpoint inhibitor (CPI).

[0032] In various embodiments, the subject is a human.

[0033] In still other embodiments of the present disclosure, the composition comprising the CPI is administered via intratumoral, peritumoral, systemic, intravenous, intraperitoneal, enteric, oral, intramuscular, subcutaneous, transmucosal, topical and/or transdermal routes.

[0034] In other embodiments, the CPI is an antibody or antigen-binding fragment thereof which binds specifically to an antigen selected from the group consisting of PD-1, PD-L1, and CTLA-4. In one embodiment, the CPI is an antibody or antigen-binding fragment thereof which binds specifically to PD-1. In another embodiment, the CPI is an antibody or antigen-binding fragment thereof which binds specifically to PD-L1. In yet another embodiment, the CPI is an antibody or antigen-binding fragment thereof which binds specifically to CTLA-4. In some embodiments, the composition comprising the CPI comprises a combination of CPIs selected from the group consisting of: (a) a first antibody or antigen-binding fragment thereof which binds specifically to CTLA-4, and a second antibody or antigen-binding fragment thereof which binds specifically to PD-1; (b) a first antibody or antigen-binding fragment thereof which binds specifically to CTLA-4, and a second antibody or antigen-binding fragment thereof which binds specifically to PD-L1; (c) a first antibody or antigen-binding fragment thereof which binds specifically to PD-1, and a second antibody or antigen-binding fragment thereof which binds specifically to PD-L1.

[0035] In related embodiments, the composition comprising the TLR9 agonist is administered prior to administration of the composition comprising the CPI. In another embodiment, the composition comprising the TLR9 agonist and the composition comprising the CPI are administered substantially at the same time. In another embodiment, the composition comprising the TLR9 agonist and the composition comprising the CPI are administered via different routes. In another embodiment, the composition comprising the TLR9 agonist and the composition comprising the CPI are administered via the same route.

[0036] In still another embodiment, at least two doses of the composition comprising the TLR9 agonist are administered or wherein at least two doses of the composition comprising the CPI are administered. In another embodiment, (a) two doses; (b) three doses; (c) four doses; or (d) five doses of the composition comprising the TLR9 agonist are administered.

[0037] In another embodiment, the two doses of the composition comprising the TLR9 agonist are administered prior to administration of the composition comprising the CPI.

[0038] In another embodiment, the composition comprising the CPI is administered prior to administration of the composition comprising the TLR9 agonist. In another embodiment, the composition comprising the TLR9 agonist and the composition comprising the CPI are administered concurrently and at least two doses of each composition are administered. In still another embodiment, the composition comprising the TLR9 agonist and the composition comprising the CPI are administered sequentially and at least two doses of each composition are administered. In yet another embodiment, the composition comprising the TLR9 agonist and the composition comprising the CPI are administered sequentially and by the same route. In another embodiment, the composition comprising the TLR9 agonist and the composition comprising the CPI are administered sequentially and by different routes. In another embodiment, the composition comprising the TLR9 agonist is administered 1 to 3 weeks before the composition comprising the CPI.

[0039] In another embodiment, the aforementioned methods are provided further comprising administering one or more additional therapeutic agents or treatments. In a related embodiment, the one or more additional therapeutic agents or treatments is selected from the group consisting of an immune checkpoint inhibitor, an antibody that activates a co-stimulatory pathway, a cancer chemotherapy, and radiation therapy.

#### BRIEF DESCRIPTION OF THE DRAWINGS

[0040] FIG. 1 shows the effect of treatment volume on serum IP-10 response to CMP-001 in a single tumor model.

[0041] FIG. 2 shows the effect of treatment volume on tumor growth, survival in a single tumor model.

[0042] FIG. 3 shows the effect of treatment volume on serum IP-10 response to CMP-001 in a bilateral tumor model.

[0043] FIG. 4 shows the effect of treatment volume on tumor growth, survival in a bilateral tumor model.

[0044] FIG. 5 shows a varied priming dose study in a mouse B16-OVA model.

[0045] FIG. 6 shows a mouse study of dose and concentration effects of SC priming and IT Tx doses in a B16-OVA model with bilateral tumors.

[0046] FIG. 7 shows a mouse study of dosing volume impact on biodistribution of CMP-001 using IVIS imaging of CT-26 tumor-bearing BALB/c mice.

#### DETAILED DESCRIPTION OF THE INVENTION

[0047] Toll-like receptor (TLR) ligands in general are known to be potential inducers of the presentation of cancer cell antigens by APC. However, it is not previously known what particular TLR ligands are preferred, and even in the case of TLR9 ligands, it is not previously known which, if any, class of CpG ODN is preferred, nor are their preferred doses and routes of administration previously known. Nearly all human clinical trials of CpG ODN in oncology have used B-class ODN administered via a systemic route, while a few trials have explored intratumoral administration (discussed further below).

[0048] The invention of immune stimulatory CpG oligodeoxynucleotides (ODN) and subsequent inventions of various classes and designs of CpG ODN provided new opportunities for cancer immunotherapy. Based on encouraging preclinical data in rodent models, human clinical trials of CpG ODN have been performed in oncology patients using systemic and intratumoral administration of several different CpG ODN alone or in combination with various chemotherapy regimens, vaccines, antibodies, and radiotherapy, but again, clinical responses have been uncommon, and despite some encouraging early clinical trial results, phase 3 trials have so far failed (reviewed in Krieg, Nucleic Acid Ther. 2012 22 (2): 77-89). Therefore, there exists a need to provide improved oligonucleotide therapeutic approaches to increase the success rate of cancer immunotherapy.

[0049] Tumor vaccines in which a cancer patient is vaccinated with a conserved unmutated self antigen together with an adjuvant have been a goal of immuno-oncologists for many years, yet despite successfully inducing immunity against the selected antigen, have almost uniformly failed to deliver clear clinical benefits. B-class CpG ODN have enhanced the induction of anti-tumor CD8<sup>+</sup> T cell responses in multiple cancer vaccine clinical trials (for example, Kruit et al., J Clin Oncol 2013; Tarhini et al., J Immunother 2013; Lovgren et al., Cancer Immunol Immunother 2012; Karbach et al., Clin Cancer Res 2011; Karbach et al., Int J Cancer 2010; Speiser et al., JCI 2005, and in a single trial an unmodified A-class CpG ODN was used as a vaccine adjuvant (Speiser et al., J. Immunother 2010), yet these have seldom been associated with clinical responses, and a phase 3 clinical trial of this approach conducted by GSK (GlaxoSmithKline) using the MAGE-3 tumor antigen so far appears to have been a failure. In particular it is noteworthy that the vaccine clinical trial using an A-class CpG ODN showed relatively weak induction of a CTL response that increased approximately two-fold from baseline in only about half of the patients, compared to an approximate average 10-fold increased CTL response in those melanoma patients previously vaccinated using B-class CpG ODN, indicating the state of the art. It is possible that the immune system will not easily overcome self-tolerance to unmutated self-antigens to a degree sufficient to reject a tumor, leading many of those skilled in the art to search for ways to induce tumor immunity against alternative, mutated tumor antigens. Recent studies using deep sequencing of tumor transcriptomes have revealed that all cancers contain variable num-

bers of unique mutated antigens, referred to as tumor-specific neoantigens (Rajasagi et al., *Blood* 2014 124 (3): 453-462), and those skilled in the art have sought ways to direct the anti-tumor immune response against such antigens. One approach being pursued is to synthesize some or all of these neoantigens as peptides, and to vaccinate a cancer patient with the appropriate antigenic peptides to be presented on Class II MHC in a formulation such as viral-like particle and using a very strong adjuvant, such as a CpG B-class ODN. Such an approach would be extremely complex and expensive to develop. Therefore, there is a need for improved methods to induce anti-tumor immune responses against tumor-specific neoantigens.

[0050] The present disclosure provides a superior approach by turning the tumor itself into a vaccine, due to altering the tumor microenvironment in such a way as to disengage the "brakes" with checkpoint inhibitors, while inducing strong cell-mediated immunity, using TLR9 agonists.

[0051] Radiotherapy has long been used in the treatment of cancer, and it is currently employed in the treatment of approximately 60% of patients with solid tumors (reviewed in Prasanna et al., *J Thoracic Dis.* 2014 6 (4): 287-302). Although radiotherapy often can shrink tumors, this effect is most commonly palliative, and durable responses are extremely uncommon. Moreover, radiotherapy is generally only suitable for treating one or a small number of tumor lesions, and thus is not generally used in the treatment of metastatic cancer.

[0052] In some unusual cases, XRT can lead to regression of distant tumor masses as a result of the induction of a specific immune response against tumor antigens present not only in the irradiated lesion, but also in distant metastases. This has been termed an "abscopal effect", and particularly since a recent case report by Postow et al. (*N. Engl. J. Med.* 2012 366 (10): 925-31), this term has come to be used to include other forms of localized tumor therapy besides just radiotherapy.

[0053] Abscopal effects can be seen when XRT is given either before or after anti-CTLA-4 therapy: for example, more than half of 21 melanoma patients treated with XRT following anti-CTLA-4 therapy showed evidence for distal tumor regressions (Grimaldi et al., *Oncoimmunol.* 2014 3: e28780).

### I. Definitions

[0054] Unless otherwise defined herein, scientific and technical terms used in connection with the present disclosure shall have the meanings that are commonly understood by those of ordinary skill in the art. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. Generally, nomenclatures used in connection with, and techniques of, cell and tissue culture, molecular biology, immunology, microbiology, genetics and protein and nucleic acid chemistry and hybridization described herein are those well-known and commonly used in the art.

[0055] The methods and techniques of the present disclosure are generally performed according to methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification unless otherwise indicated. Such references include, e.g., Sambrook and Russell, *Molecular Cloning, A Laboratory Approach*, Cold Spring

Harbor Press, Cold Spring Harbor, N.Y. (2001), Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley & Sons, NY (2002), and Harlow and Lane *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1990), which are incorporated herein by reference. Enzymatic reactions and purification techniques are performed according to manufacturer's specifications, as commonly accomplished in the art or as described herein. The nomenclatures used in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well-known and commonly used in the art. Standard techniques are used for chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, and delivery, and treatment of patients.

[0056] As used herein, each of the following terms has the meaning associated with it in this section.

[0057] The articles "a" and "an" are used herein to refer to one or to more than one (i.e., to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

[0058] As used herein, the twenty conventional amino acids and their abbreviations follow conventional usage. See *Immunology—A Synthesis* (2nd Edition, E. S. Golub and D. R. Gren, Eds., Sinauer Associates, Sunderland, Mass. (1991)), which is incorporated herein by reference.

[0059] Conventional notation is used herein to portray polypeptide sequences: the left-hand end of a polypeptide sequence is the amino-terminus; the right-hand end of a polypeptide sequence is the carboxyl-terminus.

[0060] A "conservative amino acid substitution" is one in which an amino acid residue is substituted by another amino acid residue having a side chain R group with similar chemical properties (e.g., charge or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of a protein. In cases where two or more amino acid sequences differ from each other by conservative substitutions, the percent sequence identity or degree of similarity may be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well-known to those of skill in the art. See, e.g., Pearson, *Methods Mol. Biol.* 243:307-31 (1994).

[0061] Examples of groups of amino acids that have side chains with similar chemical properties include 1) aliphatic side chains: glycine, alanine, valine, leucine, and isoleucine; 2) aliphatic-hydroxyl side chains: serine and threonine; 3) amide-containing side chains: asparagine and glutamine; 4) aromatic side chains: phenylalanine, tyrosine, and tryptophan; 5) basic side chains: lysine, arginine, and histidine; 6) acidic side chains: aspartic acid and glutamic acid; and 7) sulfur-containing side chains: cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, glutamate-aspartate, and asparagine-glutamine.

[0062] Alternatively, a conservative replacement is any change having a positive value in the PAM250 log-likelihood matrix disclosed in Gonnet et al., *Science* 256:1443-45 (1992), incorporated herein by reference. A "moderately conservative" replacement is any change having a nonnegative value in the PAM250 log-likelihood matrix.

[0063] Preferred amino acid substitutions are those which: (1) reduce susceptibility to proteolysis, (2) reduce susceptibility to oxidation, (3) alter binding affinity for forming protein complexes, and (4) confer or modify other physicochemical or functional properties of such analogs. Analogs comprising substitutions, deletions, and/or insertions can include various muteins of a sequence other than the naturally-occurring peptide sequence. For example, single or multiple amino acid substitutions (preferably conservative amino acid substitutions) may be made in the naturally-occurring sequence (preferably in the portion of the polypeptide outside the domain(s) forming intermolecular contacts). A conservative amino acid substitution should not substantially change the structural characteristics of the parent sequence (e.g., a replacement amino acid should not tend to break a helix that occurs in the parent sequence, or disrupt other types of secondary structure that characterizes the parent sequence). Examples of art-recognized polypeptide secondary and tertiary structures are described in Proteins, Structures and Molecular Principles (Creighton, Ed., W. H. Freeman and Company, New York (1984)); Introduction to Protein Structure (C. Branden and J. Tooze, eds., Garland Publishing, New York, N.Y. (1991)); and Thornton et al., Nature 354:105 (1991), which are each incorporated herein by reference.

[0064] Sequence similarity for polypeptides, and similarly sequence identity for polypeptides, is typically measured using sequence analysis software. Protein analysis software matches similar sequences using measures of similarity assigned to various substitutions, deletions and other modifications, including conservative amino acid substitutions. For instance, GCG contains programs such as "Gap" and "Bestfit" which can be used with default parameters to determine sequence homology or sequence identity between closely related polypeptides, such as homologous polypeptides from different species of organisms or between a wild type protein and a mutein thereof. See, e.g., GCG Version 6.1. Polypeptide sequences also can be compared using FASTA using default or recommended parameters, a program in GCG Version 6.1. FASTA (e.g., FASTA2 and FASTA3) provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences (Pearson, Methods Enzymol. 183:63-98 (1990); Pearson, Methods Mol. Biol. 132:185-219 (2000)). Another preferred algorithm when comparing a sequence of the invention to a database containing a large number of sequences from different organisms is the computer program BLAST, especially blastp or tblastn, using default parameters. See, e.g., Altschul et al., J. Mol. Biol. 215:403-410 (1990); Altschul et al., Nucleic Acids Res. 25:3389-402 (1997); incorporated herein by reference.

[0065] An intact "antibody" comprises at least two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds. See generally, Fundamental Immunology, Ch. 7 (Paul, W., ed., 2nd ed. Raven Press, N.Y. (1989)) (incorporated herein by reference in its entirety for all purposes). Each heavy chain is comprised of a heavy chain variable region (HCVR or  $V_H$ ) and a heavy chain constant region (CH). The heavy chain constant region is comprised of three domains, CH1, CH2 and CH3. Each light chain is comprised of a light chain variable region (LCVR or  $V_L$ ) and a light chain constant region. The light chain constant region is comprised of one domain,  $C_L$ . The  $V_H$  and  $V_L$  regions can be further subdivided into regions of hypervariability,

termed complementarity determining regions (CDR), interspersed with regions that are more conserved, termed framework regions (FR). Each  $V_H$  and  $V_L$  is composed of three CDRs and four FRs, arranged from amino-terminus to carboxyl-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. The assignment of amino acids to each domain is in accordance with the definitions of Kabat, Sequences of Proteins of Immunological Interest (National Institutes of Health, Bethesda, Md. (1987 and 1991)), or Chothia & Lesk, J. Mol. Biol. 196:901-917 (1987); Chothia et al., Nature 342:878-883 (1989).

[0066] The variable regions of the heavy and light chains contain a binding domain that interacts with an antigen. The constant regions of the antibodies may mediate the binding of the immunoglobulin to host tissues or factors, including various cells of the immune system (e.g., effector cells) and the first component (C1q) of the classical complement system.

[0067] The term "antibody" can include antigen-binding portions of an intact antibody that retain capacity to specifically bind the antigen of the intact antibody, e.g., PD-1. Antigen-binding portions may be produced by recombinant DNA techniques or by enzymatic or chemical cleavage of intact antibodies.

[0068] Examples of antigen-binding portions include (i) a Fab fragment, a monovalent fragment consisting of the  $V_L$ ,  $V_H$ ,  $C_L$  and CH1 domains; (ii) a  $F(ab')_2$  fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the  $V_H$  and CH1 domains; (iv) a Fv fragment consisting of the  $V_L$  and  $V_H$  domains of a single arm of an antibody, (v) a single domain antibody ("dAb"), which consists of a  $V_H$  domain as described in Ward et al., Nature 341:544-546 (1989); and (vi) an isolated complementarity determining region (CDR). Furthermore, although the two domains of the Fv fragment,  $V_H$  and  $V_L$ , are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the  $V_H$  and  $V_L$  regions pair to form monovalent molecules (known as single chain Fv (scFv); See, e.g., Bird et al. Science 242:423-426 (1988); and Huston et al. Proc. Natl. Acad. Sci. USA 85:5879-5883 (1988)). Such single chain antibodies are included by reference to the term "antibody".

[0069] A "bispecific antibody" has two different binding specificities, see, e.g., U.S. Pat. Nos. 5,922,845 and 5,837,243; Zeilder J. Immunol. 163:1246-1252 (1999); Somasundaram Hum. Antibodies 9:47-54 (1999); Keler Cancer Res. 57:4008-4014 (1997). For example, the invention provides bispecific antibodies having one binding site for a cell surface antigen, such as human PD-1, and a second binding site for an Fc receptor on the surface of an effector cell. The invention also provides multispecific antibodies, which have at least three binding sites.

[0070] Contemplated by the present disclosure are bispecific antibodies which bind any two different checkpoint molecules. For example, the different checkpoints may be selected from the group consisting of PD-1, PD-L1, CTLA-4, TIM3, and LAG3. Thus, for example, bispecific antibodies may bind PD-1 and PD-L1, PD-1 and CTLA-4, PD-1 and TIM3, PD-1 and LAG3, PD-L1 and CTLA-4, PD-L1 and TIM3, PD-L1 and LAG3, CTLA-4 and TIM3, and CTLA-4 and LAG3, or TIM3 and LAG3. In certain embodiments, the bispecific antibodies may bind PD-1 and PD-L1, PD-1 and

CTLA-4, PD-1 and TIM3, or PD-1 and LAG3. In certain embodiments, the bispecific antibodies may bind PD-L1 and CTLA-4, PD-L1 and TIM3, PD-L1 and LAG3. In certain embodiments, the bispecific antibodies may bind PD-1 and PD-L1, or PD-1 and CTLA-4. In certain embodiments, the bispecific antibodies may bind PD-1 and PD-L1. In certain embodiments, the bispecific antibodies may bind PD-L1 and CTLA-4. In certain embodiments, the bispecific antibodies may bind PD-L1 and CTLA-4.

[0071] Also contemplated by the present disclosure are methods of the invention using bispecific antibodies which bind any two different checkpoint molecules. For example, the different checkpoints may be selected from the group consisting of PD-1, PD-L1, CTLA-4, TIM3, and LAG3. Thus, for example, bispecific antibodies may bind PD-1 and PD-L1, PD-1 and CTLA-4, PD-1 and TIM3, PD-1 and LAG3, PD-L1 and CTLA-4, PD-L1 and TIM3, PD-L1 and LAG3, CTLA-4 and TIM3, and CTLA-4 and LAG3, or TIM3 and LAG3. In certain embodiments, the bispecific antibodies may bind PD-1 and PD-L1, PD-1 and CTLA-4, PD-1 and TIM3, or PD-1 and LAG3. In certain embodiments, the bispecific antibodies may bind PD-L1 and CTLA-4, PD-L1 and TIM3, PD-L1 and LAG3. In certain embodiments, the bispecific antibodies may bind PD-1 and PD-L1, or PD-1 and CTLA-4. In certain embodiments, the bispecific antibodies may bind PD-1 and PD-L1. In certain embodiments, the bispecific antibodies may bind PD-L1 and CTLA-4. In certain embodiments, the bispecific antibodies may bind PD-L1 and CTLA-4.

[0072] The term “bispecific antibodies” further includes “diabodies.” Diabodies are bivalent, bispecific antibodies in which the  $V_H$  and  $V_L$  domains are expressed on a single polypeptide chain, but using a linker that is too short to allow for pairing between the two domains on the same chain, thereby forcing the domains to pair with complementary domains of another chain and creating two antigen binding sites (See, e.g., Holliger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993); Pollak et al., Structure 2:1121-1123 (1994)).

[0073] The terms “human antibody” or “human sequence antibody”, as used interchangeably herein, include antibodies having variable and constant regions (if present) derived from human germline immunoglobulin sequences. The human sequence antibodies of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis in vitro or by somatic mutation in vivo). However, the term “human antibody”, as used herein, is not intended to include “chimeric” antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences (i.e., “humanized” or PRIMATIZED™ antibodies).

[0074] The term “chimeric antibody” as used herein means an antibody that comprises regions from two or more different antibodies. For example, in one embodiment, one or more of the CDRs are derived from a human anti-CTLA-4 antibody. In another embodiment, all of the CDRs are derived from a human anti-CTLA-4 antibody. In another embodiment, the CDRs from more than one human anti-CTLA-4 antibody are combined in a chimeric human antibody. For instance, a chimeric antibody may comprise a CDR1 from the light chain of a first human anti-CTLA-4 antibody, a CDR2 from the light chain of a second human

anti-CTLA-4 antibody, and a CDR3 from the light chain of a third human anti-CTLA-4 antibody; and similarly the CDRs from the heavy chain may be derived from one or more other anti-CTLA-4 antibodies. Further, the framework regions may be derived from one of the same anti-CTLA-4 antibodies or from one or more different human(s).

[0075] As another example, in one embodiment, one or more of the CDRs are derived from a human anti-PD-1 antibody. In another embodiment, all of the CDRs are derived from a human anti-PD-1 antibody. In another embodiment, the CDRs from more than one human anti-PD-1 antibody are combined in a chimeric human antibody. For instance, a chimeric antibody may comprise a CDR1 from the light chain of a first human anti-PD-1 antibody, a CDR2 from the light chain of a second human anti-PD-1 antibody, and a CDR3 from the light chain of a third human anti-PD-1 antibody; and similarly the CDRs from the heavy chain may be derived from one or more other anti-PD-1 antibodies. Further, the framework regions may be derived from one of the same anti-PD-1 antibodies or from one or more different human(s).

[0076] As yet another example, in one embodiment, one or more of the CDRs are derived from a human anti-PD-L1 antibody. In another embodiment, all of the CDRs are derived from a human anti-PD-L1 antibody. In another embodiment, the CDRs from more than one human anti-PD-L1 antibody are combined in a chimeric human antibody. For instance, a chimeric antibody may comprise a CDR1 from the light chain of a first human anti-PD-L1 antibody, a CDR2 from the light chain of a second human anti-PD-L1 antibody, and a CDR3 from the light chain of a third human anti-PD-L1 antibody; and similarly the CDRs from the heavy chain may be derived from one or more other anti-PD-L1 antibodies. Further, the framework regions may be derived from one of the same anti-PD-L1 antibodies or from one or more different human(s).

[0077] Moreover, as discussed previously herein, chimeric antibody includes an antibody comprising a portion derived from the germline sequences of more than one species.

[0078] By the term “compete”, as used herein with regard to an antibody, is meant that a first antibody, or an antigen-binding portion thereof, competes for binding with a second antibody, or an antigen-binding portion thereof, where binding of the first antibody with its cognate epitope is detectably decreased in the presence of the second antibody compared to the binding of the first antibody in the absence of the second antibody. The alternative, where the binding of the second antibody to its epitope is also detectably decreased in the presence of the first antibody, can, but need not be the case. That is, a first antibody can inhibit the binding of a second antibody to its epitope without that second antibody inhibiting the binding of the first antibody to its respective epitope. However, where each antibody detectably inhibits the binding of the other antibody with its cognate epitope or ligand, whether to the same, greater, or lesser extent, the antibodies are said to “cross-compete” with each other for binding of their respective epitope(s). For instance, cross-competing antibodies can bind to the epitope, or portion of the epitope, to which antibodies of the invention bind. Both competing and cross-competing antibodies are encompassed by the present disclosure. Regardless of the mechanism by which such competition or cross-competition occurs (e.g., steric hindrance, conformational change, or binding to a common epitope, or portion thereof, and the like), the skilled

artisan would appreciate, based upon the teachings provided herein, that such competing and/or cross-competing antibodies are encompassed and can be useful for the methods disclosed herein.

[0079] The term “epitope” includes any protein determinant capable of specific binding to an immunoglobulin or T-cell receptor. Epitopic determinants usually consist of chemically active surface groupings of molecules such as amino acids or sugar side chains and usually have specific three-dimensional structural characteristics, as well as specific charge characteristics. Conformational and non-conformational epitopes are distinguished in that the binding to the former but not the latter is lost in the presence of denaturing solvents.

[0080] By the phrase “specifically binds,” as used herein, is meant a compound, e.g., a protein, a nucleic acid, an antibody, and the like, which recognizes and binds a specific molecule, but does not substantially recognize or bind other molecules in a sample. For instance, the phrase “specifically binds” may characterize an antibody or a peptide inhibitor which recognizes and binds a cognate ligand (e.g., an anti-PD-1 antibody that binds with its cognate antigen, PD-1) in a sample, but does not substantially recognize or bind other molecules in the sample. Thus, under designated assay conditions, the specified binding moiety (e.g., an antibody or an antigen-binding portion thereof) binds preferentially to a particular target molecule and does not bind in a significant amount to other components present in a test sample. A variety of assay formats may be used to select an antibody that specifically binds a molecule of interest. For example, solid-phase ELISA immunoassay, immunoprecipitation, BIAcore and Western blot analysis are used to identify an antibody that specifically reacts with PD-1. Typically a specific or selective reaction will be at least twice background signal or noise and more typically more than 10 times background, even more specifically, an antibody is said to “specifically bind” an antigen when the equilibrium dissociation constant ( $K_D$ ) is  $\leq 1 \mu\text{M}$ , preferably  $\leq 100 \text{ nM}$ , and most preferably  $\leq 10 \text{ nM}$ .

[0081] Preferably, an “antibody which binds specifically to a checkpoint molecule” is an antibody or antigen-binding fragment thereof, which, in addition to binding its target CPI, interferes with reciprocal interaction between the bound target CPI and its cognate ligand. For example, an antibody which binds specifically to PD-1 preferably is an antibody or antigen-binding fragment thereof, which, in addition to binding PD-1, interferes with reciprocal interaction between PD-1 and its cognate ligand, PD-L1.

[0082] The term “ $K_D$ ” refers to the equilibrium dissociation constant of a particular antibody-antigen interaction.

[0083] As used herein, “substantially pure” means an object species is the predominant species present (i.e., on a molar basis it is more abundant than any other individual species in the composition), and preferably a substantially purified fraction is a composition wherein the object species (e.g., an anti-PD-1 antibody) comprises at least about 50 percent (on a molar basis) of all macromolecular species present. Generally, a substantially pure composition will comprise more than about 80 percent of all macromolecular species present in the composition, more preferably more than about 85%, 90%, 95%, and 99%. Most preferably, the object species is purified to essential homogeneity (contaminant species cannot be detected in the composition by

conventional detection methods) wherein the composition consists essentially of a single macromolecular species.

[0084] By the term “therapeutically effective amount,” as used herein, is meant an amount that when administered to a mammal, preferably a human, mediates a detectable therapeutic response compared to the response detected in the absence of the compound. A therapeutic response, such as, but not limited to, inhibition of and/or decreased tumor growth (including tumor size stasis), tumor size, metastasis, and the like, can be readily assessed by a plethora of art-recognized methods, including, e.g., such methods as disclosed herein.

[0085] The skilled artisan would understand that the effective amount of the compound or composition administered herein varies and can be readily determined based on a number of factors such as the disease or condition being treated, the stage of the disease, the age and health and physical condition of the mammal being treated, the severity of the disease, the particular compound being administered, and the like.

[0086] A “therapeutically effective amount” is intended to qualify the amount of an agent required to detectably reduce to some extent one or more of the symptoms of a neoplastic disorder, including, but not limited to: 1) reduction in the number of cancer cells; 2) reduction in tumor size; 3) inhibition (i.e., slowing to some extent, preferably stopping) of cancer cell infiltration into peripheral organs; 4) inhibition (i.e., slowing to some extent, preferably stopping) of tumor metastasis; 5) inhibition, to some extent, of tumor growth; 6) relieving or reducing to some extent one or more of the symptoms associated with the disorder; and/or 7) relieving or reducing the side effects associated with the administration of anticancer agents.

[0087] A “therapeutically effective amount” of a TLR9 agonist can also be defined based on a biomarker response using any of the well-defined blood or tissue markers for TLR9 activation that are well known to those skilled in the art. The CpG ODN of the present disclosure are broadly similar to other CpG ODN (e.g., B-class) in their induction of a Th1-like cytokine and chemokine response in the serum, plasma, PBMC, and/or tissues or biopsies, which can be measured as described by Krieg et al., *J. Immunother.*, 2004 27:460-471 using for example cytokine assays for IP-10, I-TAC, MIG, MIP-1B, MIP-3B, IL-6, IL-12p40, or IFN- $\alpha$  from serum or plasma collected approximately 24 hr after the treatment, or can also be assessed by RT-PCR assays of PBMC. A therapeutically effective amount of the CpG ODN that is injected intratumorally into a cancer patient will increase serum IP-10 levels by 24 hours to at least 100  $\mu\text{g/ml}$ , and preferably to between 100-100,000  $\mu\text{g/ml}$ , and most preferably to between 1,000 to 10,000  $\mu\text{g/mL}$ .

[0088] In contrast to chemotherapy drugs, for which the dose is generally escalated to the maximal tolerated dose (MTD), immune stimulatory drugs such as the CpG ODN of the present disclosure function best at an optimal biologic dose (OBD), which is generally below the MTD. The serum cytokines and chemokines provide one simple measure to estimate the optimal biologic dose. The intended biologic effect of the CpG ODN of the present disclosure is to convert the tumor microenvironment (and that of the draining lymph nodes) from immunosuppressive—with a low level of IFN production and lacking in activated TIL—to an immune activated microenvironment that shows increased production of IFN, especially type I IFN, and which now has

increased TIL that display activation markers such as PD-L1, as reflected for example in the tumor biopsy characteristics of patients responding to treatment with anti-PD-1 or anti-PD-L1 reported by Tumeh et al., *Nature* 2014 515:568-571; and by Herbst et al., *Nature* 2014 515:563-567, respectively, or additionally by Taube et al., *Clin Cancer Res.* 2014. Expressed another way, recent studies have demonstrated that anti-PD-1 or anti-PD-L1 therapy is generally only effective in patients who already have TIL, and already have a tumor microenvironment that reflects IFN effects (such as expression of PD-L1, which is induced by IFN). Patients who lack these characteristics on a pre-treatment tumor biopsy are unlikely to respond to therapy with anti-PD-1 or anti-PD-L1 unless they also receive treatment with an agent that induces TIL and high production of type I IFN: the CpG ODN of the present disclosure are the perfect agent for this purpose.

[0089] The major endogenous source of type I IFN in humans and other animals is the plasmacytoid dendritic cell (pDC). pDC produce more than 99% of the type I IFN that is made in response to pathogen infection (Siegal et al., *Science* 1999). Yet very few molecularly-defined stimuli have been shown to activate the pDC to secrete high levels of type I IFN. In fact, to date A-class CpG ODN are by far the strongest stimulus for pDC production of type I IFN that have been reported in the scientific literature, and, surprisingly, the CpG ODN of the present disclosure are even more effective than those previously known in the art.

[0090] Certain preferred CpG ODN induce high or large amounts of type I IFN. Assays for measuring type I IFN are well known in the art and include in vitro enzyme-linked immunosorbent assay (ELISA) and cell-based assays, such as are described herein. Without meaning to be limiting, large or high amounts of type I IFN can refer to greater than or equal to about 1000 µg/mL IFN- $\alpha$  as measured according to such in vitro assays. In certain embodiments, large or high amounts of type I IFN can refer to greater than or equal to about 2000 µg/mL IFN- $\alpha$  as measured according to such in vitro assays. In certain embodiments, large or high amounts of type I IFN can refer to greater than or equal to about 3000 µg/mL IFN- $\alpha$  as measured according to such in vitro assays. In certain embodiments, large or high amounts of type I IFN can refer to greater than or equal to about 4000 µg/mL IFN- $\alpha$  as measured according to such in vitro assays. In certain embodiments, large or high amounts of type I IFN can refer to greater than or equal to about 5,000 µg/mL IFN- $\alpha$  as measured according to such in vitro assays.

[0091] Combined with the teachings provided herein, by choosing among the various active compounds and weighing factors such as potency, relative bioavailability, patient body weight, severity of adverse side-effects and preferred mode of administration, an effective prophylactic or therapeutic treatment regimen can be planned which does not cause substantial toxicity and yet is effective to treat the particular subject. The effective amount for any particular application can vary depending on such factors as the disease or condition being treated, the severity of the disease or condition, and the health and size of the subject. One of ordinary skill in the art can empirically determine the effective amount of TLR9 agonist (e.g., CpG ODN), CPI (e.g., anti-PD-1 antibodies, anti-PD-L1 antibodies, anti-CTLA-4 antibodies), and/or other therapeutic agent(s) without necessitating undue experimentation.

[0092] For example, a human clinical trial of a B-class CpG ODN together with an anti-CTLA-4 antibody was reported by Millward et al., 2013. The clinical trial demonstrated a way to combine a TLR9 agonist given by subcutaneous injection with an anti-CTLA-4 antibody given systemically that could be used in future clinical trials of other CpG ODN and other checkpoint inhibitors, but the trial failed to demonstrate significant clear clinical benefit from the combination. This failure demonstrates the non-obviousness of the present disclosure. Even though there have been publications of A-class CpG ODN with high IFN- $\alpha$  secretion, it was not obvious to the investigators running the clinical trial to use such a CpG ODN instead of the B-class CpG ODN. It was not obvious to give the CpG ODN or anti-CTLA-4 antibody locally into the tumor instead of by the systemic route. As a result, the approach was abandoned following the completion of the trial. Likewise, Mangsbo et al. (*J. Immunother.* 2010 33:225) reported the combination of an intratumoral B-class CpG ODN with anti-CTLA-4 or anti-PD-1 in mouse tumor models. Positive results were seen with the combinations, but again, there was no guidance to perform such therapy using a high IFN-inducing type of CpG ODN, such as the A-class or other ODN of the present disclosure.

[0093] To date, there appears to be no realization among those skilled in the field of the desirability and advantage to combine a high-IFN-inducing class of CpG ODN together with checkpoint inhibitor therapy. For a combination of agents to have optimal synergy in cancer immunotherapy, the immune suppressive effects of one agent should be reversed by another. For example, IFN induce the expression of PD-L1 on tumors, which suppresses the immune response. High IFN-inducing CpG ODN of the invention induce the expression of PD-L1, but when they are used in combination with an anti-PD-L1 antibody or an anti-PD-L1 antibody, the potential immune suppressive effects of the PD-L1 are overcome by the antibody. On the other hand, the present disclosure is based, at least in part, on the discovery that the combination of an intratumoral B-class CpG ODN with a systemic checkpoint inhibitor will be less than optimally synergistic (or not synergistic at all) because the induction of IL-10 results in pleiotropic immune suppressive effects that are not reversed by checkpoint inhibitor therapy. Thus, the present disclosure provides combinations of agents that together provide unexpected, e.g., synergistic, benefits in cancer immunotherapy.

[0094] The therapeutically effective amount of CpG ODN and/or antibodies alone or together can be initially determined from in vitro and/or animal models. A therapeutically effective dose can also be determined from human data for the specific CpG ODN and/or specific antibodies or for other compounds which are known to exhibit similar pharmacological activities. The applied dose can be adjusted based on the relative bioavailability and potency of the administered compound. Adjusting the dose to achieve maximal efficacy based on the methods described above and other methods as are well-known in the art is well within the capabilities of the ordinarily skilled artisan.

[0095] "Instructional material", as that term is used herein, includes a publication, a recording, a diagram, or any other medium of expression which can be used to communicate the usefulness of the compound, combination, and/or composition of the invention in the kit for affecting, alleviating or treating the various diseases or disorders recited herein.

Optionally, or alternately, the instructional material can describe one or more methods of alleviating the diseases or disorders in a cell, a tissue, or a mammal, including as disclosed elsewhere herein.

[0096] The instructional material of the kit may, for example, be affixed to a container that contains the compound and/or composition of the invention or be shipped together with a container which contains the compound and/or composition. Alternatively, the instructional material may be shipped separately from the container with the intention that the recipient uses the instructional material and the compound cooperatively.

[0097] The CpG ODN and/or antibody of the invention may be provided in a medicinal dispenser. A medical dispenser is a package defining a plurality of medicinal storage compartments, each compartment for housing an individual unit of medicament. In an embodiment, an entire medicinal course of treatment is housed in a plurality of medicinal storage compartments.

[0098] A package defining a plurality of medicinal storage compartments may be any type of disposable pharmaceutical package or card which holds medicaments in individual compartments. For example, the package is a blister package constructed from a card, which may be made from stiff paper material, a blister sheet and backing sheet. Such cards are well known to those of ordinary skill in the art.

[0099] As an example, a medicinal dispenser may house an entire medicinal course of treatment. The dispenser may include the day indicia to indicate which day the individual units of medicament are to be taken. These may be marked along a first side of the medicinal package. The dose indicia may also be marked, for example along a second side of the medicinal package perpendicular to the first side of the medicinal package, thereby indicating the time which the individual unit of medicament should be taken. The unit doses may be contained in the dispenser which is a blister pack.

[0100] Except when noted, the terms "patient" or "subject" are used interchangeably and refer to mammals such as human patients and non-human primates, as well as veterinary subjects such as rabbits, rats, and mice, and other animals. Preferably, "patient" or "subject" refers to a human.

[0101] In certain embodiments, a subject is an adult human.

[0102] In certain embodiments, a subject is a child. In certain embodiments, a subject is less than about 18 years of age. In certain embodiments, a subject is less than about 12 years of age.

[0103] As used herein, to "treat" means reducing the frequency with which symptoms of a disease (i.e., tumor growth and/or metastasis, or other effect mediated by the numbers and/or activity of immune cells, and the like) are experienced by a patient. Treatment may be prophylactic (to prevent or delay the onset of the disease, or to prevent the manifestation of clinical or subclinical symptoms thereof) or therapeutic suppression or alleviation of symptoms after the manifestation of the disease. The term "treat" includes the administration of the compounds or agents of the present disclosure to (i) prevent or delay the onset of the symptoms, complications, or biochemical indicia of, (ii) alleviate the symptoms of, and/or (iii) inhibit or arrest the further development of, the disease, condition, or disorder.

[0104] "Combination therapy" embraces the administration of a TLR9 agonist, e.g., certain CpG ODN, and a

checkpoint inhibitor as part of a specific treatment regimen intended to provide a beneficial effect from the co-action of these therapeutic agents. In some embodiments, the checkpoint inhibitor is a CPI-specific antibody or antigen-binding fragment thereof. In some embodiments, the checkpoint inhibitor is a bispecific CPI-specific antibody or bispecific antigen-binding fragment thereof. The beneficial effect of the combination includes, but is not limited to, pharmacokinetic or pharmacodynamic co-action resulting from the combination of therapeutic agents. Administration of these therapeutic agents in combination typically is carried out over a defined time period (usually minutes, hours, days, or weeks depending upon the combination selected). "Combination therapy" generally is not intended to encompass the administration of two or more of these therapeutic agents as part of separate monotherapy regimens that incidentally and arbitrarily result in the combinations of the present disclosure.

[0105] "Combination therapy" embraces administration of these therapeutic agents in a sequential manner, that is, wherein each therapeutic agent is administered at a different time, as well as administration of these therapeutic agents, or at least two of the therapeutic agents, in a substantially simultaneous manner. Sequential or substantially simultaneous administration of each therapeutic agent can be effected by any appropriate route as described herein, including, but not limited to, intratumoral and peritumoral routes; systemic routes, e.g., intravenous, intraperitoneal, enteric (including oral), intramuscular, subcutaneous, and transmucosal routes; and topical and transdermal routes. As described herein, generally a first therapeutic agent (e.g., CpG ODN) can be administered by intratumoral or peritumoral injection, and a second agent (e.g., anti-PD-1 antibody) can be administered systemically (e.g., intravenously).

[0106] "Combination therapy" also can embrace the administration of the TLR9 agonist, e.g., certain CpG ODN, and checkpoint inhibitor therapeutic agents as described above in further combination with non-drug therapies (such as, but not limited to, radiotherapy (XRT) or surgery). In some embodiments, the checkpoint inhibitor is a checkpoint-specific antibody or antigen-binding fragment thereof. In some embodiments, the checkpoint inhibitor is a bispecific CPI-specific antibody or bispecific antigen-binding fragment thereof. Where the combination therapy further comprises radiation treatment, the radiation treatment may be conducted at any suitable time so long as a beneficial effect from the co-action of the combination of the therapeutic agents and radiation treatment is achieved. For example, in appropriate cases, the beneficial effect is still achieved when the radiation treatment is temporally removed from the administration of the therapeutic agents, by days or even weeks.

[0107] "Combination therapy" also can embrace the administration of the TLR9 agonist, e.g., certain CpG ODN, and checkpoint inhibitor therapeutic agents as described above in further combination with other biologically active ingredients (such as, but not limited to, a further and different antineoplastic agent, a dendritic vaccine or other tumor vaccine). In some embodiments, the checkpoint inhibitor is an antibody or antigen-binding fragment thereof. In some embodiments, the checkpoint inhibitor is a bispecific antibody or bispecific antigen-binding fragment

thereof. However, in certain embodiments, "combination therapy" specifically excludes the administration of a dendritic cell or tumor vaccine.

## II. CpG DNA

[0108] CpG oligonucleotides (CpG DNA; CpG ODN) contain specific sequences found to elicit an immune response. These specific sequences are referred to as "immunostimulatory motifs", and the oligonucleotides that contain immunostimulatory motifs are referred to as "immunostimulatory oligonucleotide molecules" and equivalently, "immunostimulatory oligonucleotides". Immunostimulatory oligonucleotides include at least one immunostimulatory motif, and preferably that motif is an internal motif. The term "internal immunostimulatory motif" refers to the position of the motif sequence within an oligonucleotide sequence which is at least one nucleotide longer (at both the 5' and 3' ends) than the motif sequence.

[0109] CpG oligonucleotides include at least one unmethylated CpG dinucleotide. An oligonucleotide containing at least one unmethylated CpG dinucleotide is an oligonucleotide molecule which contains a cytosine-guanine dinucleotide sequence (i.e., "CpG DNA" or DNA containing a 5' cytosine linked by a phosphate bond to a 3' guanine) and activates the immune system. The entire CpG oligonucleotide can be unmethylated or portions may be unmethylated, but at least the C of the 5' CG 3' must be unmethylated.

[0110] CpG ODN are generally about 8-100 nucleotides long. In certain embodiments, CpG ODN are about 8-50 nucleotides long, about 8-40 nucleotides long, about 8-30 nucleotides long, about 8-24 nucleotides long, about 8-20 nucleotides long, or about 8-16 nucleotides long.

[0111] By 2004, structure-activity relationship studies of CpG ODN had defined three families with distinct structural and biological characteristics (Hartmann et al., Eur. J. Immunol. 2003, 33:1633-1641; Marshall et al., J. Leukocyte Biol. 2003 73:781-792; Vollmer et al., Eur. J. Immunol. 2004 34:251-262). Typical B-class ODN have a completely phosphorothioate backbone, do not form higher-ordered structures, and are strong B cell stimulators, inducing relatively high levels of IL-10 secretion, but induce relatively little NK activity or IFN- $\alpha$  secretion (Krieg, 2002, and Krieg, unpublished observations). B-class CpG ODN induce immunosuppressive counter-regulatory effects including not only the secretion of IL-10, but also the expression of IDO, which can promote the development of Treg cells in vitro (Moseman et al., J. Immunol. 2004 173 (7): 4433-4442; Chen et al., J. Immunol. 2008 181 (8): 5396-5404). The relevance of these in vitro data to in vivo tumor immunotherapy has been uncertain, and has not delayed the clinical development of B-class ODN, but the present disclosure is based in part on a new discovery that these effects of B-class ODN will suppress anti-tumor immune responses, which can be avoided using other classes of CpG ODN that are structurally designed not to activate the NF- $\kappa$ B pathway leading to IL-10 secretion.

[0112] The phosphorothioate backbone used in B-class CpG ODN has multiple complex effects on the resulting immune response compared to that seen with a CpG ODN with the same sequence but without a phosphorothioate backbone. One very important effect of the phosphorothioate (PS) backbone is protection against nuclease degradation. Completely PS-modified ODN are nearly completely stable in serum and tissues for at least 24 hr, whereas

unmodified and unprotected ODN are degraded within a few minutes. In serum the major nuclease activity is a 3' exonuclease against which CpG ODN can be protected with just 1 or a few PS linkages at the 3' end of the ODN. But in tissues there also are 5' exonucleases as well as endonucleases, and these can degrade native DNA that is not otherwise protected. Native DNA can be protected against exonucleases by circularization using techniques well described in the literature. See, for example, U.S. Pat. Nos. 8,017,591; 7,635,468; 7,074,772; 6,849,725; 6,451,593; and 6,451,563; and U.S. Published Patent Application No. 2003/0125279; the entire contents of all of which are hereby incorporated by reference. Alternatively or in addition, the native (i.e., otherwise unmodified and unprotected) ODN can be formulated in nanoparticles or other formulations well known in the art to block nuclease access to the ODN.

[0113] In general, native CpG DNA (phosphodiester) activates TLR9 in both B cells and pDC. B cells produce cytokine and start to proliferate (this is predominantly driven through NF- $\kappa$ B activation), but unless the TLR9 stimulation is sustained, the proliferation is usually modest, and relatively little stimulation of Ig secretion and class switching occurs. pDC are activated by native CpG DNA to secrete type I IFN and to express costimulatory receptors, but the magnitude of the stimulation depends critically on the form of the DNA. In contrast to these effects of native CpG DNA, B-class phosphorothioate CpG DNA provides a far more powerful and sustained TLR9 signal for B cells, inducing them to proliferate strongly and leading to Ig secretion and class switching as reported in the literature. But the phosphorothioate backbone has a very different effect on the TLR9-mediated pDC response, reducing substantially the IFN secretion (apparently through suppressing IRF7-mediated signaling), but usually still providing strong induction of costimulatory molecule expression. Thus, for the present disclosure, the use of native DNA usually will provide higher type I IFN responses and will be therapeutically effective as long as the native DNA is protected from degradation. From 1 to 3 phosphorothioate modifications can be added onto the 5' and 3' termini of native DNA to protect it from nuclease degradation without diminishing the type I IFN response.

[0114] Early on in the development of CpG ODN for cancer immunotherapy, those skilled in the art generally believed that B-cell activation was desirable, and therefore focused development efforts on the B-class ODN. Indeed, perhaps B-cell activation is desirable for a tumor vaccine, in order to drive the production of anti-tumor Ab, which are well known in the field to be able to contribute to the anti-tumor response. Some early human clinical trials employing intratumoral administration of B-class CpG gave encouraging evidence of dendritic cell activation in the tumor draining lymph nodes (e.g., Molenkamp B G et al., Clin Cancer Res. 2007 13 (10): 2961-2969). However, clinical responses to this local intratumoral therapy were quite limited, and studies of the total lymphocyte population in the draining lymph nodes showed an approximate two-fold increase in the release of IL-10 in CpG-treated patients (Table 2 in Molenkamp et al.). Considering the negative effects of IL-10 for tumor immunotherapy, and the need for improved CpG ODN that do not induce its production, or which induce a lower level of this production, the present disclosure further provides improved CpG ODN with reduced induction of IL-10.

**[0115]** Nevertheless, it has now been discovered, in accordance with the present disclosure, that for intratumoral administration in particular, B cell activation with the concomitant IL-10 and IDO induction, is undesirable, and perhaps deleterious. This is difficult or impossible to demonstrate using mouse models because of the species-specific differences in the TLR9 expression and differences in the cytokine responses. The present disclosure is based on a new analysis of previously published and unpublished data on the human immune cell responses to various CpG ODN, together with a new analysis of the immune effects and deficiencies of other cancer immunotherapies and XRT.

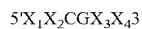
**[0116]** For cancer immunotherapy IL-10 can sometimes have positive effects (especially with systemic therapy, see for example Mumm and Oft, Bioessays 2013 35 (7): 623-631), but IL-10 is generally considered to have negative immune effects in the local tumor microenvironment, inhibiting immune rejection (reviewed in Sato et al., Immunol Res. 2011 51 (2-3): 170-182). Thus, the present disclosure is based in part on the discovery that B-class CpG ODN, which induce high levels of IL-10, are not preferred for intratumoral therapy.

**[0117]** The B-class of CpG oligonucleotides is represented by the formula:



wherein  $X_1$  and  $X_2$  are nucleotides. In some embodiments,  $X_1$  may be adenine, guanine, or thymine and/or  $X_2$  may be cytosine, adenine, or thymine.

**[0118]** The B-class of CpG oligonucleotides is also represented by the formula:



wherein  $X_1$ ,  $X_2$ ,  $X_3$ , and  $X_4$  are nucleotides.  $X_2$  may be adenine, guanine, or thymine.  $X_3$  may be cytosine, adenine, or thymine.

**[0119]** The B-class of CpG oligonucleotides also includes oligonucleotides represented by at least the formula:



wherein  $X_1$ ,  $X_2$ ,  $X_3$ , and  $X_4$  are nucleotides and  $N$  is any nucleotide and  $N_1$  and  $N_2$  are oligonucleotide sequences composed of from about 0-25 N's each.  $X_1X_2$  may be a dinucleotide selected from the group consisting of: GpT, GpG, GpA, ApA, ApT, ApG, CpT, CpA, CpG,TpA, TpT, and TpG; and  $X_3X_4$  may be a dinucleotide selected from the group consisting of: TpT, ApT, TpG, ApG, CpG, TpC, ApC, CpC, TpA, ApA, and CpA.

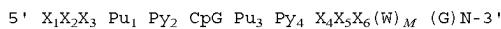
**[0120]** The B-class of CpG oligonucleotides is disclosed in PCT Published Patent Applications PCT/US95/01570 and PCT/US97/19791, and U.S. Pat. No. 6,194,388 B1 and U.S. Pat. No. 6,239,116 B1, issued Feb. 27, 2001 and May 29, 2001 respectively.

**[0121]** In contrast to the B-class CpG ODN, A-class CpG ODN are potent activators of natural killer cells and IFN- $\alpha$  secretion from plasmacytoid dendritic cells (pDC), but only weakly stimulate B cells, and induce very little IL-10 secretion. Canonical A-class ODN contain polyG motifs at the 5' and/or 3' ends which are capable of forming complex higher-ordered structures known as G-tetrads and a central phosphodiester region containing one or more CpG motifs within a self-complementary palindrome (reviewed in (Krieg, 2006).

**[0122]** The A-class of CpG oligodeoxynucleotides is represented by the formula:

**[0123]** wherein  $N_1$  comprises 0-20 guanosines,  $N_2$  is from 4-40 bases in length and which contains at least 1 unmethylated CpG dinucleotide, and  $N_3$  comprises 3-20 guanosines. In preferred embodiments  $N_1$  comprises between 4-15 G and in some preferred embodiments it comprises 10 G. In some preferred embodiments,  $N_2$  comprises a palindrome (a self-complementary DNA sequence, such as ACGT) that is from 4-20 bases in length. In some embodiments there are additional bases on the 5' and/or 3' side of the palindrome within  $N_2$ , and in preferred embodiments these bases comprise a plurality of T. In some embodiments, some or all of the nucleotides comprising  $N_1$  and/or  $N_3$  are linked by phosphorothioate internucleotide linkages. In preferred embodiments the nucleotides comprising  $N_2$  are linked by phosphodiesters. In some embodiments all of the bases in the CpG-A ODN are linked by phosphodiesters.

**[0124]** In one embodiment, a CpG-A ODN is at least about 16 nucleotides in length and includes a sequence represented by the formula:



**[0125]** wherein the central CpG motif is unmethylated, Pu is a purine nucleotide, Py is a pyrimidine nucleotide, X and W are any nucleotide, M is any integer from 0 to 20, and N is any integer from 4 to 20.

**[0126]** For example, U.S. Pat. Nos. 6,949,520 and 7,776,344 show that in certain preferred embodiments the A-class CpG ODN has a sequence corresponding to any of the following:

(SEQ ID NO: 43)  
ggGGTCAACGTTGAggggggG;  
  
(SEQ ID NO: 44)  
tcgtcgtttgcgttttgcgtt;  
  
(SEQ ID NO: 45)  
ggggtcgtcgtttgggggg;  
  
(SEQ ID NO: 46)  
tcgtcgtttgcgtttgggggg;  
  
(SEQ ID NO: 47)  
ggggtcgtcgacgtcgagggggg;  
  
(SEQ ID NO: 48)  
ggggtcatcgatgagggggg;  
  
(SEQ ID NO: 49)  
ggGGGACGATCGTCggggggG;  
  
(SEQ ID NO: 50)  
gggggtcgtacgacgggggg;  
  
(SEQ ID NO: 51)  
ggGGGACGATATCGTCggggggG;  
  
(SEQ ID NO: 52)  
ggGGGACGACGTGTCggggggG;  
  
(SEQ ID NO: 53)  
ggGGGACGAGCTGCTCggggggG;

-continued

(SEQ ID NO: 54)  
ggGGGACGTACGTCgggggg;  
(SEQ ID NO: 55)  
ggGGGACGATCGTTGgggggg;  
(SEQ ID NO: 56)  
ggGGAACGATCGTCggggG;  
(SEQ ID NO: 57)  
ggGGGGACGATCGTCgggggg;  
(SEQ ID NO: 58)  
ggGGGACGATCGTCGgggggg;  
(SEQ ID NO: 59)  
ggGGGTACATCGATGAgggggg;  
(SEQ ID NO: 60)  
ggGGTCGTCGACGAgggggg;  
(SEQ ID NO: 61)  
ggGGTCGTTCGAACGAgggggG;  
(SEQ ID NO: 62)  
ggGGACGTTCGAACGTgggggg;  
(SEQ ID NO: 63)  
ggGGAACGACGTCGTTgggggg;  
(SEQ ID NO: 64)  
ggGGAACGTACGTCgggggg;  
(SEQ ID NO: 65)  
ggGGAACGTACGTACGTTgggggg;  
(SEQ ID NO: 66)  
ggGGTCACCGGTGAgggggg;  
(SEQ ID NO: 67)  
ggGGTCGACGTACGTCGAgggggG;  
(SEQ ID NO: 68)  
ggGGACCGGTACCGGTgggggg;  
(SEQ ID NO: 69)  
ggGTCGACGTCGAgggggG;  
(SEQ ID NO: 70)  
ggGGTCGACGTCGAggggg;  
(SEQ ID NO: 71)  
ggGGAACGTTAACGTTgggggg;  
(SEQ ID NO: 72)  
ggGGACGTCGACGTgggggg;  
(SEQ ID NO: 73)  
ggGGGTGTTCGTTgggggg;  
(SEQ ID NO: 74)  
ggGACGATCGTCGgggggg;  
(SEQ ID NO: 75)  
ggGTCGTCGACGAggggggG;  
(SEQ ID NO: 76)  
ggTCGTCGACGAggggggG;  
(SEQ ID NO: 77)  
ggGGACGATCGTCGgggggg;

-continued

(SEQ ID NO: 78)  
ggGGTCGACGTCGACGTCGAGgggggg;  
and  
(SEQ ID NO: 79)  
ggGGACGACGTCGTTGgggggg;

wherein each lower case letter represents a nucleotide linked to its 3'-adjacent nucleotide by a phosphorothioate (PS) linkage; and each upper case letter represents a nucleotide linked to its 3'-adjacent nucleotide (if present) by a phosphodiester (PO) linkage, except that the 3'-terminal nucleotide is represented by an upper case letter since it has no 3'-adjacent nucleotide.

**[0127]** In certain more preferred embodiments the immunostimulatory nucleic acid has a sequence corresponding to

(SEQ ID NO: 80)  
ggGGGACGAGCTCGTCgggggg;  
(SEQ ID NO: 58)  
ggGGGACGATCGTCGgggggg;  
(SEQ ID NO: 81)  
ggGGACGATCGAACGTTgggggg;  
(SEQ ID NO: 78)  
ggGGTCGACGTCGACGTCGAGgggggg;  
or  
(SEQ ID NO: 79)  
ggGGACGACGTCGTTGgggggg;

wherein each lower case letter represents a nucleotide linked to its 3'-adjacent nucleotide by a phosphorothioate (PS) linkage; and each upper case letter represents a nucleotide linked to its 3'-adjacent nucleotide (if present) by a phosphodiester (PO) linkage, except that the 3'-terminal nucleotide is represented by an upper case letter since it has no 3'-adjacent nucleotide.

**[0128]** In certain embodiments, an A-class CpG ODN for use in accordance with the methods of the instant invention has a sequence provided as:

**[0129]** 5'-GGGGGGGGGGGG-3' (SEQ ID NO:82; also referred to herein as "G10"). Such oligonucleotide and formulations thereof useful in accordance with the present disclosure are described in PCT/2015/067269, WO 2003/024481; US 2003/0099668; US 2012/0301499; WO 2004/084940; U.S. Pat. No. 7,517,520; US 2010/0098722; WO 2007/068747; US 2007/0184068; U.S. Pat. No. 8,574,564; WO 2007/144150; U.S. Pat. No. 8,541,559; WO 2008/073960; and U.S. Pat. No. 8,586,728, the entire contents of each of which is incorporated herein by reference.

**[0130]** CpG-A oligonucleotides are also known in the art as D-type CpG as defined by Klinman and colleagues, and as disclosed in U.S. Pat. Nos. 7,521,063, 7,892,569, and US Appln. No. 2013/0012922, each of which are incorporated by reference in their entirety. Table 2 and SEQ ID NOS 43-62 from US Appln. No. 2013/0012922 is particularly noted and incorporated by reference herein.

**[0131]** The structure of C-class ODN is typically based on a phosphorothioate backbone, but is distinct in that the CpG motifs are followed by a 3' palindrome, which may form a duplex. C-class ODN are described in U.S. Pat. No. 7,566,

703 to Krieg et al.; U.S. Pat. No. 8,198,251 to Vollmer et al.; and U.S. Pat. No. 8,834,900 to Krieg et al. The C-class CpG ODN have immune properties intermediate between the A and B classes (Hartmann et al., 2003; Marshall et al., 2003; Marshall et al., 2005; Vollmer et al., 2004).

[0132] Examples of C-class ODN include:

(SEQ ID NO: 83)  
TCGTCGTTTCGGCGCGCGCCG;  
(SEQ ID NO: 84)  
TCGTCGTTTCGGCGCGCCGCG;  
(SEQ ID NO: 85)  
TCGTCGTTTCGGCGCGCCGCG;  
(SEQ ID NO: 86)  
TCGTCGTTTCGGCGCGCCGCG;  
(SEQ ID NO: 87)  
TCGTCGTTTCGGCGCGCCGCG;  
(SEQ ID NO: 88)  
TCGTCGTTTCGGCGCGCGCGTTT;  
(SEQ ID NO: 89)  
TCCTGACGTTCGGC CGCCGCCG;  
(SEQ ID NO: 90)  
TZGTZGTTTZGGZGZGZGZZG;  
(SEQ ID NO: 91)  
TCCTGACGTTCGGC CGCCGCC;  
(SEQ ID NO: 92)  
TCGGCGCGCGCCGTCGTCGTTT;  
(SEQ ID NO: 93)  
TCGTCGTTTCGGCGGCCGACG;  
(SEQ ID NO: 94)  
TCGTCGTTTCGTCGGCCGCCG;  
(SEQ ID NO: 95)  
TCGTCGTTTCGACGGCCGCCG;  
(SEQ ID NO: 96)  
TCGTCGTTTCGGCGGCCGTCG;  
(SEQ ID NO: 97)  
TCGTCGTTTCGACGGCCGTCG;  
(SEQ ID NO: 98)  
TCGTCGTTTCGACGATCGTCG;  
(SEQ ID NO: 99)  
TCGTCGTTTCGACGTA CGTCG;  
(SEQ ID NO: 100)  
TCGTCGCGACGCCGTCG;  
(SEQ ID NO: 101)  
TCGTCGCGACGATCGTCG;  
(SEQ ID NO: 102)  
TCGTCGCGACGTA CGTCG;  
(SEQ ID NO: 103)  
TCGTTTTTCGACGGCCGTCG;

-continued

(SEQ ID NO: 104)

TCGTTTTTCGACGATCGTCG;  
and

(SEQ ID NO: 105)  
TCGTTTTTTCGACGTACGTTCG,

wherein each Z is 5-methylcytosine.

[0153] According to certain embodiments the immunostimulatory nucleic acid includes the sequence TCGGCGCGGCCGTCGTCTT (SEQ ID NO:92).

[0134] The oligonucleotide may comprise 5' T\*T\*T\*C\_G\*T\*C\_G\*T\*T\*C\_G\*T\*C\_G\*T\*T 3' (SEQ ID NO:106), wherein \* represents a stabilized internucleotide linkage. Optionally, when specifically stated, 5' may refer to the free 5' end of the oligonucleotide and 3' may refer to the free 3' end of the oligonucleotide.

[0135] In some embodiments of the invention the oligonucleotide has one of the following formulas:  
TCGTCGTTCGCGCGCCG (SEQ ID NO:107),  
TCGTCGTCGTTCGCGCGCGCCG (SEQ ID NO:108),  
TCGTCGACGATCGCGCGCGCCG (SEQ ID NO:552),  
TTCGTCGTTTGTCGTT (SEQ ID NO:110), or  
TTTCGTCGTTTCGTCGTT (SEQ ID NO:551).

[0136] In other embodiments of the invention the oligonucleotide has one of the following formulas: TCGTCGTC, CGTCGTG, GTCGTCG, TCGTCGTT, CGTCGTT, GTCGTTG, TCGTTCGG, CGTTCGGC, GTTCGGCG, TTCGGCGC, TCGCGCG, CGGCGCGC, GGCGCGCG, GCGCGCGC, CGCGCGCC, or GCGCGCCG.

[0137] In other embodiments of the invention the oligonucleotide has one of the following formulas:  $T^*C\_G^*T^*C\_G^*T^*C$ ,  $C\_G^*T^*C\_G^*T^*C\_G$ ,  $G^*T^*C\_G^*T^*C\_G^*T$ ,  $T^*C\_G^*T^*C\_G^*T^*T$ ,  $C\_G^*T^*C\_G^*T^*T^*C$ ,  $G^*T^*C\_G^*T^*T^*C\_G$ ,  $T^*C\_G^*T^*T^*C\_G^*G$ ,  $C\_G^*T^*T^*C\_G^*G^*C$ ,  $G^*T^*T^*C\_G^*G^*C^*G$ ,  $T^*T^*C\_G^*G^*C^*G^*C$ ,  $T^*C\_G^*G^*C^*G^*C\_G$ ,  $C\_G^*G^*C^*G^*C\_G^*C$ ,  $G^*G^*C^*G^*C\_G^*C^*G$ ,  $G^*C^*G^*C\_G^*C^*G^*C$ ,  $C^*G^*C\_G^*C^*G^*C^*C$ , or  $G^*C\_G^*C^*G^*C^*C^*G$ , wherein \* represents a stabilized internucleotide linkage.

**[0138]** In other embodiments of the invention an oligonucleotide comprising: T\*C\_G\*T\*C\_G\*T\*C, wherein \* represents a stabilized internucleotide linkage and represents phosphodiester or phosphodiester-like internucleotide linkage is provided. Optionally the oligonucleotide may be 5' T\*C\_G\*T\*C\_G\*T\*C\_G\*T\*C\_G\*G\*C\*G\*C\_G\*C\*G\*C\*G\*C 3' (SEQ ID NO:111), 5' T\*C\_G\*T\*C\_G\*T\*C\_G\*T\*C\_G\*T\*T\*C\_G\*G\*C\*G\*C 3' (SEQ ID NO:112), or 5' T\*C\_G\*T\*C\_G\*T\*C\_G\*T\*T\*C\_G\*G\*C\*G\*C 3' (SEQ ID NO:113) wherein 5' refers to the free 5' end of the oligonucleotide and 3' refers to the free 3' end of the oligonucleotide.

[0139] In other embodiments an oligonucleotide comprising: T<sup>\*</sup>C<sub>n</sub>G<sup>\*</sup>T<sup>\*</sup>T<sup>\*</sup>C<sub>m</sub>G<sup>\*</sup>G, wherein \* represents a stabilized internucleotide linkage and \_ represents phosphodiester or phosphodiester-like internucleotide linkage is provided. Optionally the oligonucleotide may be

5' C G\*T\*C G\*T\*C G\*T\*T\*C G\*G\*C\*G\*C G\*C\*G\*C\*C\*G 3';

(SEQ ID NO: 1115)

-continued

(SEQ ID NO: 116)  
 5' T\*C\_G\*T\*C\_G\*T\*T\*C\_G\_G\*C\_G\*C\_G\_C\_G\*C\*C\_G 3';  
 (SEQ ID NO: 117)  
 5' C\_G\*T\*C\_G\*T\*T\*C\_G\_G\*C\_G\*C\_G\_C\_G\*C\*C\_G 3';  
 (SEQ ID NO: 118)  
 5' G\*T\*C\_G\*T\*T\*C\_G\_G\*C\_G\*C\_G\_C\_G\*C\*C\_G 3';  
 or  
 (SEQ ID NO: 119)  
 5' T\*C\_G\*T\*T\*C\_G\_G\*C\_G\*C\_G\_C\_G\*C\*C\_G 3',

wherein 5' refers to the free 5' end of the oligonucleotide and 3' refers to the free 3' end of the oligonucleotide.

**[0140]** More recently a new class of CpG oligo was identified with the structural feature of two palindromes (vs the single palindrome in the C-class). See, e.g., U.S. Patent Application Pub. 2008/0045473, the entire content of which is incorporated herein by reference. Because of the two palindromes these P-class CpG ODN are able to form higher-order concatamers, which are hypothesized to interact with TLR9 in a different manner from the linear B-class ODN or duplex C-class ODN, with the observed result that the P-class ODN induce higher levels of type I IFN compared to C-class (or B-class), and substantially lower levels of IL-10.

**[0141]** Examples of P-class ODN include:

(SEQ ID NO: 109)

T-C-G-T\*C-G-A\*C-G\*A\*T\*C-G\*G\*C-G\*C-G\*C\*C\*G;

(SEQ ID NO: 120)

T-C-G-T-C-G-A-C-G-A-T\*T\*T-T-A-C-G-A-C-G-T-C-G-T-T\*T\*T;

(SEQ ID NO: 121)

T-C-G-T-C-G-A-C-G-A-T-T-T-A-C-G-A-C-G-T-C-G-T-T-T;

(SEQ ID NO: 122)

T-C-G-T-C-G-A-C-G-A-A-C-G-A-C-G-T-C-G-T;

(SEQ ID NO: 123)

T-C-G-T-C-G-A-C-G-A-T\*T\*T-T-C-G-T-C-G-A-C-G-A-T\*T;

(SEQ ID NO: 553)

T-C-G-T-C-G-A-C-G-A-T-T-T-T-C-G-T-C-G-A-C-G-A-T-T;

(SEQ ID NO: 124)

T-C-G-T-C-G-A-C-G-A-T-C-G-T-C-G-A-C-G-A;

(SEQ ID NO: 125)

C\*G\*C\*G\*C\*G\*C\*G\*C\*G\*C\*G\*C\*G\*C\*G\*C\*G;

(SEQ ID NO: 126)

G\*A\*G\*A\*A\*C\*G\*C\*T\*C\*G\*A\*C\*C\*T\*T\*C\*G\*A\*T\*biot;

(SEQ ID NO: 127)

A\*G\*C\*T\*C\*C\*A\*T\*G\*G\*T\*G\*C\*T\*C\*A\*C\*T\*G;

(SEQ ID NO: 128)

T\*C\*T\*C\*C\*A\*G\*C\*G\*T\*G\*C\*G\*C\*C\*A\*T;

(SEQ ID NO: 129)

T\*C\*C\*A\*T\*G\*A\*C\*G\*T\*T\*C\*C\*T\*G\*A\*G\*G\*T\*T;

(SEQ ID NO: 130)

T\*C\*C\*A\*G\*G\*A\*C\*T\*T\*C\*T\*C\*A\*G\*G\*T\*T;

(SEQ ID NO: 131)

T\*C\*C\*A\*C\*G\*A\*C\*G\*T\*T\*T\*C\*G\*A\*C\*G\*T\*T;

(SEQ ID NO: 132)

T\*C\*G\*T\*C\*G\*T\*T\*T\*G\*A\*C\*G\*T\*T\*T\*G\*A\*C\*G\*T\*T;

(SEQ ID NO: 554)

T\*C\*C\*T\*G\*A\*C\*G\*T\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G\*C\*C;

(SEQ ID NO: 133)

T\*C\*G\*C\*G\*T\*G\*C\*G\*T\*T\*T\*G\*G\*T\*T\*T\*G\*A\*C\*G\*T\*T;

(SEQ ID NO: 134)

T\*C\*G\*C\*G\*A\*C\*G\*T\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G\*C\*C;

(SEQ ID NO: 135)

dig-C\*C\*G\*G\*C\*C\*G\*G\*C\*C\*G\*G\*C\*C\*G\*G\*C\*C\*G;

(SEQ ID NO: 136)

dig-C\*G\*C\*G\*C\*G\*C\*G\*C\*G\*C\*G\*C\*G\*C\*G\*C\*G;

- continued

T*C*C*A*G*G*A*C*T*T*C*T*C*T*C*A*G*G*T*T*T*T*T;	(SEQ ID NO: 137)
G*T*G*C*T*C*G*A*G*G*A*T*G*C*G*C*T*T*C*G*C;	(SEQ ID NO: 138)
G*C*C*G*A*G*G*T*C*C*A*T*G*T*C*G*T*A*C*G*C;	(SEQ ID NO: 139)
T-C-G-C-G-T-G-C-G-T-T-T-G-T-C-G-T-T-T-G-A-C-G-T-T;	(SEQ ID NO: 555)
A*C*C*G*A*T*A*C*C*G*G*T*G*C*C*G*G*T*G*A*C*C*G*C*A*C*C*A*C*G;	(SEQ ID NO: 140)
A*C*C*G*A*T*A*A*C*G*T*T*G*C*C*G*G*T*G*A*C*G*G*C*A*C*C*A*C*G;	(SEQ ID NO: 141)
A*C*C*G*A*T*G*A*C*C*G*T*C*G*C*C*G*G*T*G*A*C*C*G*C*A*C*C*A*C*G;	(SEQ ID NO: 142)
C*G*G*C*G*C*G*C*G*C*C*G*C*G*G*C*G*C*G*C*G*C*G;	(SEQ ID NO: 143)
T*C*G*A*T*C*G*T*T*T*T*C*G*T*G*C*G*T*T*T*T;	(SEQ ID NO: 144)
T*C*G*T*C*C*A*G*G*A*C*T*T*C*T*C*A*G*G*T*T;	(SEQ ID NO: 145)
T*C*G*T*C*G*T*C*C*A*G*G*A*C*T*T*C*T*C*A*G*G*T*T;	(SEQ ID NO: 146)
T*C*G*T*G*A*C*G*G*G*C*G*G*C*G*C*G*C*G*C*C;	(SEQ ID NO: 147)
A*C*G*A*C*G*T*C*G*T*tC*G*G*C*G*C*C*G*C*C*G;	(SEQ ID NO: 148)
G*G*G-G-A-C-G-A-C-G-T-C-G-T-G-C*G*G*C*G*G*C*C*G;	(SEQ ID NO: 149)
G*G*G*A*C*G*A*C*G*T*C*G*T*C*G*T*G*C*G*G*C*C*G*C*C*G;	(SEQ ID NO: 556)
C*C-A-C-G*A-C-G*T*C-G*T*C-G-A-A-G*A-C-G*A-C-G*T*C-G*T-G*G;	(SEQ ID NO: 150)
C*T-G*C*A*G-C*T-G-C*A*G-C*T-G-C*A*G-C*T-G*C*A*G;	(SEQ ID NO: 151)
C*G*G-C*C-G*C*T-G*C*A-G-C*G-G*C*C-G*C*T-G*C*A*G;	(SEQ ID NO: 152)
C*A*T*G*A*C*G*T*T*T*T*T*G*A*T*G*T*T;	(SEQ ID NO: 153)
A*T*G*A*C*G*T*T*T*T*T*G*A*T*G*T*T;	(SEQ ID NO: 154)
T*G*A*C*G*T*T*T*T*T*G*A*T*G*T*T;	(SEQ ID NO: 155)
A*T*G*A*C*G*T*T*T*T*T*G*A*T*G*T*T;	(SEQ ID NO: 156)
T*C*C*A*T*G*A*C-C-G-T*T*T*T*T*G*A*T*G*T*T;	(SEQ ID NO: 157)
T*C*C*A*T*G*A-C-G-T*T*T*T*T*G*A*T*G*T*T;	(SEQ ID NO: 557)
T*C*C*A*T*G*A*C*T*T*T*T*T*G*A*T-G-T*T;	(SEQ ID NO: 558)
T*C*C*A*T*G*A*C-C-G-T*T*T*T*T*G*A*T-G-T*T;	(SEQ ID NO: 559)

- continued

T*C*C*A*T*G*A-C-G-T*T*T*T*T*G*A*T-G*T*T;	(SEQ ID NO: 560)
A*T*G*A*C-G*T*T*T*T*T*G*A*T*G*T*T*G*T;	(SEQ ID NO: 561)
A*T*G*A*C*G*T*T*T*T*T*G*A*T-G*T*T*G*T;	(SEQ ID NO: 562)
A*T*G*A*C-G*T*T*T*T*T*G*A*T-G*T*T*G*T;	(SEQ ID NO: 563)
A*T*G*A-C-G-T*T*T*T*T*G*A-T-G-T*T*G*T;	(SEQ ID NO: 564)
T*C*C*A*T*G*C*G*T*T*T*T*T*G*A*T*G*T*T;	(SEQ ID NO: 158)
T*C*C*A*T*G*A*C*G*T*C*T*T*T*G*A*T*G*T*C;	(SEQ ID NO: 159)
A-C-G-A-C-G-T-C-G-T-T-C-A-C-G-A-C-G-T-C-G-T-chol;	(SEQ ID NO: 160)
A-C-G-A-C-G-T-C-G-T-G-G-C-C-A-C-G-A-C-G-T-C-G-T-D-D-D;	(SEQ ID NO: 161)
A-C-G-A-C-G-T-C-G-T-D-D-D-A-C-G-A-C-G-T-C-G-T-D-D-D;	(SEQ ID NO: 162)
D-D-D-A-C-G-A-C-G-T-C-G-T-D-D-D-A-C-G-A-C-G-T-C-G-T-D-D-D;	(SEQ ID NO: 163)
D-D-D-A-C-G-A-C-G-T-C-G-T-D-D-D-A-C-G-A-C-G-T-C-G-T-chol;	(SEQ ID NO: 164)
G*G*G-A-C-G-A-C-G-T-C-G-T-G*G*C*C-A-C-G-A-C-G-T-C-G-T-C*C*C;	(SEQ ID NO: 165)
C*C*C-A-C-G-A-C-G-T-C-G-T-G*G*G;	(SEQ ID NO: 166)
C*C*C*V-A-C-G-A-C-G-T-C-G-T-G*G*G*G;	(SEQ ID NO: 167)
T*C*C*A*T*C*G*T*T*T*T-T-C-G*T*G*C*C*G*T*T*T*T;	(SEQ ID NO: 565)
T*C*C*A*T*C*G*T*T*T-T-C-G-T*G*C*C*G*T*T*T*T;	(SEQ ID NO: 566)
T*C*C*A*T*C*G*T*T-T-T-C-G-T-G*C*C*G*T*T*T*T;	(SEQ ID NO: 567)
T*C*C*A*T*C*G-T-T-T-C-G*T*G*C*C*G*T*T*T*T;	(SEQ ID NO: 568)
A*T-G*A*C-G*T*T*T*T-T-G*A*C-G*T*T;	(SEQ ID NO: 168)
A*C-G*A*C-G*T*T*T*T-G*A*T-G*T*T;	(SEQ ID NO: 169)
A*C-G*A*C-G*T*T*T*T-C-G*A*C-G*T*T;	(SEQ ID NO: 326)
A*T-G*A*T-G*T*T*T*T-G*A*T-G*T*T;	(SEQ ID NO: 170)
A*T-G*A*C-G*T*T*T*T-G-A*T-G*T*T;	(SEQ ID NO: 171)
A*T-G*A*C-G*T*T*T*T-G*A*T-G*T*T;	(SEQ ID NO: 172)
T*T-G*A*C-G*T*T*T*T-G*A*T-G*T*T;	(SEQ ID NO: 173)

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A*T-G*A*T-G*T*T*T*T-G*A*T-G*T*T;	(SEQ ID NO: 170)
A*T-G*A*G-C*T*T*T*T-G-T*A*T-G*T*T;	(SEQ ID NO: 174)
T*C*G*A*C*G*T*T*T*C*G*G*C*G*C*G*C*G;	(SEQ ID NO: 175)
T*C*C*T*G*A*C*G*T*T*T*C*G*G*C*G*C*G*C*G;	(SEQ ID NO: 176)
T*C*C*T*G*A*C*G*T*T*C*G*G*C*G*C*G*C*G;	(SEQ ID NO: 177)
T*C*C*A*T*G*A*C*G*T*T*C*G*G*C*G*C*G*C*G;	(SEQ ID NO: 178)
T*C*C*T*G*A*C*G*T*T*C*G*G*C*G*C*G*C*G;	(SEQ ID NO: 179)
T*C*G*A*C*G*T*T-T-G-G-C*G*C*G*C*G*C*G;	(SEQ ID NO: 180)
T*C*G*A*C*G*T*T-T-C-G-G-C*G*C*G*C*G*C*G;	(SEQ ID NO: 569)
T*C*G*A*C*G*T*C*G-A-C-G-T-T-A-G-G-G-T-T-A*G*G*G;	(SEQ ID NO: 181)
A*C*G*A*C*G*T*C*G-T-T-A-G-G-G-T-T-A*G*G*G;	(SEQ ID NO: 182)
G*T*C-G*G*C-G*T*T-G*A*C;	(SEQ ID NO: 183)
A-C-G-A-C-G-T-C-G-T-C-G-D-D-D-C-G-G-C-C-G-C-C-G;	(SEQ ID NO: 184)
A-C-G-A-C-G-T-C-G-T-C-G-D-D-D-C*G*G*C*C*G*C*G;	(SEQ ID NO: 570)
T-C-G-T-C-G-A*C*G*A*C*G*T*C*G*T*C*G;	(SEQ ID NO: 185)
T-C-G-T-C-G-A-C-G-A-C-G-T-C-G-D-D-D;	(SEQ ID NO: 186)
A-C-G-A-C-G-T-C-G-T-T*T*T-A-C-G-A-C-G-T-C-G-T-teg;	(SEQ ID NO: 187)
A*C*G*A*C*G*T*C*G*T*D*D*D*A*C*G*A*C*G*T*C*G*T*D*D;	(SEQ ID NO: 571)
D*D*D*A*C*G*A*C*G*T*C*G*T*D*D*D*D*A*C*G*A*C*G*T*C*G*T*D*D;	(SEQ ID NO: 572)
A-C-G-A-C-G-T-C-G-T-T*T*T-A-C-G-A-C-G-T-C-G-T-D-D-D;	(SEQ ID NO: 188)
A-C-G-A-C-G-T-C-G-T-T*T*T-A-C-G-A-C-G-T-C-G-T-T*T*T;	(SEQ ID NO: 189)
A*C-G-A-C-G-T-C-G-T-T*T*T-A-C-G-A-C-G-T-C-G-T-T*T*T;	(SEQ ID NO: 573)
A*C-G-A-C-G-T-C-G-T-T*T*T-A-C-G-A-C-G-T-C-G*T;	(SEQ ID NO: 190)
A-C-G-A-C-G-T-C-G-T-D-D-D-A-C-G-A-C-G-T-C-G-T-L;	(SEQ ID NO: 191)
A-C-G-A-C-G-T-C-G-T-L-A-C-G-A-C-G-T-C-G-T-L;	(SEQ ID NO: 192)
A-C-G-A-C-G-T-C-G-T-teg-teg-A-C-G-A-C-G-T-C-G-T-teg;	(SEQ ID NO: 193)

-continued

C-G-A-C-G-T-C-G-T-D-D-D-D-A-C-G-A-C-G-T-C-G-D-D-D;	(SEQ ID NO: 194)
A-C-G-A-C-G-T-C-G-D-D-D-D-C-G-A-C-G-T-C-G-T-D-D-D;	(SEQ ID NO: 195)
C-G-A-C-G-T-C-G-D-D-D-D-C-G-A-C-G-T-C-G-D-D-D;	(SEQ ID NO: 196)
T-C-G-A-C-G-T-C-G-T-D-D-D-D-A-C-G-A-C-G-T-C-G-A-D-D-D;	(SEQ ID NO: 197)
A-C-G-T-C-G-T-D-D-D-D-A-C-G-A-C-G-A-C-G-T-D-D-D;	(SEQ ID NO: 198)
T-C-G-T-C-G-A-C-G-T-D-D-D-D-A-C-G-T-C-G-A-C-G-A-D-D-D;	(SEQ ID NO: 199)
T-C-G-A-C-G-T-C-G-T-D-D-D-D-A-C-G-A-C-G-T-C-G-T-D-D-D;	(SEQ ID NO: 200)
A-C-G-A-C-G-T-C-G-T-D-D-D-D-A-C-G-T-C-G-T-D-D-D;	(SEQ ID NO: 201)
A-C-G-A-C-G-T-T-D-D-D-D-A-C-G-T-C-G-T-D-D-D;	(SEQ ID NO: 202)
A-C-G-T-C-G-T-D-D-D-D-A-C-G-A-C-G-T-D-D-D;	(SEQ ID NO: 203)
G-G-C-G-C-C-G-D-D-D-D-C-G-G-C-C-G-C-C-D-D-D;	(SEQ ID NO: 204)
G-C-G-G-C-C-G-G-D-D-D-D-C-C-G-G-C-C-G-C-D-D-D;	(SEQ ID NO: 205)
A-C-G-T-C-G-T-D-D-D-D-A-C-G-A-C-G-T-C-G-T-D-D-D;	(SEQ ID NO: 206)
D-A-C-G-A-C-G-T-C-G-T-D-D-D-D-A-C-G-A-C-G-T-C-G-T-D;	(SEQ ID NO: 207)
A*C-G-A-C-G-T-C-G-T-C-G-A-A-G-A-C-G-AC-G-T-C-G-T-D-D-T;	(SEQ ID NO: 208)
T*C-G-A-C-G-T-C-G-T-C-G-A-A-G-A-C-G-T-C-G-T-D-D-T;	(SEQ ID NO: 209)
C*C*A-C-G-A-C-G-T-C-G-A-A-G-A-C-G-A-C-G-T-C-G-T*G*G;	(SEQ ID NO: 574)
T*C*C*A*D*G*A*C*G*T*T*T*T*G*A*T*G*T*T;	(SEQ ID NO: 210)
T*C*C*A*T*G*A*C*G*T*T*D*T*T*G*A*T*G*T*T;	(SEQ ID NO: 211)
T*C*C*A*J*G*A*C*G*T*T*T*T*G*A*T*G*T*T;	(SEQ ID NO: 212)
T*C*C*A*T*G*A*C*G*T*T*T*T*G*A*T*G*T*T;	(SEQ ID NO: 213)
T*C*C*A*T*G*A*C*G*T*T*T*T*G*A*T*G*T*T; Cy3;	(SEQ ID NO: 214)
J*J*J*J*J*G*A*C*G*T*T*T*T*G*A*T*G*T*T;	(SEQ ID NO: 215)
T*C*C*A*J*G*A*C*G*T*T*T*T*G*A*T*G*T*T;	(SEQ ID NO: 216)
T*C*C*A*D*G*A*C*G*T*T*D*T*T*G*A*T*G*T*T;	(SEQ ID NO: 217)
A-C-G-A-C-G-T-C-G-T-D-D-D-D-A-C-G-A-C-G-T-C-G-T-D-D-D-rU;	(SEQ ID NO: 218)

-continued

A-C-G-A-C-G-T-C-G-T-D-D-D-A-C-G-A-C-G-T-C-G-T-D-D-D-rG; (SEQ ID NO: 219)  
A-C-G-A-C-G-T-C-G-T-D-D-D-A-C-G-A-C-G-T-C-G-T-D-D-DrA; (SEQ ID NO: 220)  
D-D-D-A-C-G-A-C-G-T-C-G-T-D-D-D-A-C-G-A-C-G-T-C-G-T-D-D-rU; (SEQ ID NO: 221)  
A-C-G-A-C-G-T-C-G-T-D-D-D-A-C-G-A-C-G-T-C-G-T-D-D-D-rA-rA-rA; (SEQ ID NO: 222)  
T\*C\*G\*A\*T\*G\*A\*C\*G\*T\*T\*C\*C\*T\*G\*A\*C\*G\*T\*T; (SEQ ID NO: 223)  
T-T-T-A-C-G-A-C-G-T-C-G-T-D-D-D-A-C-G-A-C-G-T-C-G-T-D-D-DrU; (SEQ ID NO: 224)  
(T\*C-G-A-C-G-T-C-G-T-) (vitE-) double-teg; (SEQ ID NO: 677)  
T\*C\*G\*A\*C-G\*T\*T\*T\*C-G\*G\*C\*G\*G\*C\*C-G\*C\*C\*G; (SEQ ID NO: 575)  
T\*C\*G\*A\*C-G\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C-G\*C\*C\*G; (SEQ ID NO: 576)  
T\*C-G\*C-G\*A\*C-G\*T\*T\*C-G\*G\*C\*G\*C-G\*C\*G\*C\*C\*G; (SEQ ID NO: 577)  
T\*C\*G\*C-G\*A\*C-G\*T\*T\*C-G\*G\*C\*G\*C-G\*C\*G\*C\*C\*G; (SEQ ID NO: 578)  
T\*C\*G\*C-G\*A\*C-G\*T\*T\*C-G\*G\*C-G\*C\*G\*C\*G\*C\*C\*G; (SEQ ID NO: 579)  
T\*C\*G\*C-G\*A\*C-G\*T\*T\*C-G\*G\*C\*G\*C-G\*C\*G\*C\*C\*G; (SEQ ID NO: 580)  
T\*C\*G\*C-G\*A\*C-G\*T\*T\*C-G\*G\*C\*G\*C-G\*C\*G\*C\*C\*G; (SEQ ID NO: 581)  
T\*C\*G\*C-G\*A\*C-G\*T\*T\*C-G\*G\*C\*G\*C-G\*C\*G\*C\*C\*G; (SEQ ID NO: 582)  
T\*C\*G\*C-G\*A\*C-G\*T\*T\*C-G\*G\*C\*G\*C-G\*C\*G\*C\*C\*G; (SEQ ID NO: 583)  
T\*C\*G\*C-G\*A\*C-G\*T\*T\*C-G\*G\*C\*G\*C-G\*C\*G\*C\*C\*G; (SEQ ID NO: 584)  
T\*C\*G\*C-G\*A\*C-G\*T\*T\*C-G\*G\*C\*G\*C-G\*C\*G\*C\*C\*G; (SEQ ID NO: 225)  
D\*C\*C\*A\*T\*G\*A\*C\*G\*T\*T\*T\*T\*T\*G\*A\*T\*G\*T\*T; (SEQ ID NO: 226)  
T\*D\*C\*A\*T\*G\*A\*C\*G\*T\*T\*T\*T\*T\*G\*A\*T\*G\*T\*T; (SEQ ID NO: 227)  
T\*C\*D\*A\*T\*G\*A\*C\*G\*T\*T\*T\*T\*T\*G\*A\*T\*G\*T\*T; (SEQ ID NO: 228)  
T\*C\*C\*D\*T\*G\*A\*C\*G\*T\*T\*T\*T\*T\*G\*A\*T\*G\*T\*T; (SEQ ID NO: 229)  
T\*C\*C\*A\*T\*G\*A\*C\*G\*T\*T\*T\*T\*D\*G\*A\*T\*G\*T\*T; (SEQ ID NO: 230)  
T\*C\*C\*A\*T\*G\*A\*C\*G\*T\*T\*T\*T\*G\*A\*T\*G\*T\*T; (SEQ ID NO: 231)  
T\*C\*G\*A\*A\*C-G\*T\*T\*C-G\*G\*C\*G\*C-G\*C\*G\*C\*C\*G; (SEQ ID NO: 232)  
T\*C\*G\*T\*C\*G\*A\*A\*C-G\*T\*T\*C-G\*G\*C\*G\*C-G\*C\*G\*C\*C\*G; (SEQ ID NO: 233)

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T\*C\*G\*T\*C\*G\*A\*A\*C-G\*T\*T\*C\*G\*G\*C\*G\*C\*T\*G\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 234)

T\*C\*G\*C\*G\*A\*C-G\*T\*T\*C\*G\*T\*T\*G\*C\*G\*C\*G\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 235)

T\*A\*C\*G\*T\*C-G\*T\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 236)

T\*T\*C\*G\*C\*A\*C-G\*T\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 237)

T\*C\*G\*G\*C\*G\*C\*G\*C\*C-G\*T\*C\*G\*C\*G\*A\*C\*G\*T;  
 (SEQ ID NO: 238)

T\*A\*G\*C-G\*T\*G\*C-G\*T\*T\*T\*G\*A\*C-G\*T\*T\*T\*T\*T\*T\*T;  
 (SEQ ID NO: 239)

T\*A\*G\*C-G\*A\*G\*C-G\*T\*T\*T\*T\*G\*A\*C-G\*T\*T\*T\*T\*T\*T\*T;  
 (SEQ ID NO: 240)

T\*T\*G\*C-G\*A\*G\*C-G\*T\*T\*T\*T\*G\*A\*C-G\*T\*T\*T\*T\*T\*T\*T;  
 (SEQ ID NO: 241)

A\*T\*G\*C-G\*T\*G\*C-G\*T\*T\*T\*T\*G\*A\*C-G\*T\*T\*T\*T\*T\*T\*T;  
 (SEQ ID NO: 242)

T\*T\*A\*C-G\*T\*G\*C-G\*T\*T\*T\*T\*G\*A\*C-G\*T\*T\*T\*T\*T\*T\*T;  
 (SEQ ID NO: 243)

T\*T\*G\*C-A\*T\*G\*C-G\*T\*T\*T\*T\*G\*A\*C-G\*T\*T\*T\*T\*T\*T\*T;  
 (SEQ ID NO: 244)

T\*T\*G\*C-G\*T\*A\*C-G\*T\*T\*T\*T\*G\*A\*C-G\*T\*T\*T\*T\*T\*T\*T;  
 (SEQ ID NO: 245)

T\*T\*G\*C-G\*T\*G\*C-A\*T\*T\*T\*T\*G\*A\*C-G\*T\*T\*T\*T\*T\*T\*T;  
 (SEQ ID NO: 246)

T\*T\*G\*C-G\*T\*T\*G\*A\*C-G\*T\*T\*T\*T\*G\*A\*C-G\*T\*T\*T\*T\*T\*T;  
 (SEQ ID NO: 247)

T\*T\*G\*C-G\*C\*G\*C-G\*T\*T\*T\*T\*G\*A\*C-G\*T\*T\*T\*T\*T\*T\*T;  
 (SEQ ID NO: 248)

T\*T\*G\*C-G\*T\*G\*C-G\*C\*T\*T\*T\*T\*G\*A\*C-G\*T\*T\*T\*T\*T\*T\*T;  
 (SEQ ID NO: 249)

T\*T\*G\*C-G\*T\*G\*C-G\*C\*T\*T\*T\*T\*G\*A\*C-G\*T\*T\*T\*T\*T\*T\*T;  
 (SEQ ID NO: 250)

T\*C\*G\*T\*C-G\*A\*A\*C\*G\*T\*T\*C\*G\*G\*C\*G\*C\*T\*G\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 585)

T\*C\*G\*T\*C-G\*A\*A\*C\*G\*T\*T\*C-G\*G\*C-G\*C\*T\*G\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 586)

T\*C\*G\*T\*C-G\*A\*A\*C\*G\*T\*T\*C-G\*G\*C-G\*C\*T\*G\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 587)

T\*C\*G\*T\*C-G\*A\*A\*C\*G\*T\*T\*C-G\*G\*C-G\*C\*T\*G\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 588)

T\*C\*G\*T\*C-G\*A\*C-G\*T\*T\*C\*G\*G\*C-G\*C\*T\*G\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 251)

T\*C\*G\*T\*C-G\*A\*C-G\*T\*T\*C\*G\*G\*C-G\*C\*T\*G\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 589)

T\*C\*G\*C-G\*A\*C-G\*T\*T\*C\*G\*G\*C-G\*C\*T\*G\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 252)

T\*C\*G\*C-G\*A\*C-G\*T\*T\*C-G\*G\*C-G\*C\*T\*G\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 590)

T\*C\*G\*C-G\*A\*C\*G\*T\*T\*C-G\*T\*T\*G\*C\*G\*C-G\*C\*C\*G;  
 (SEQ ID NO: 253)

T\*C\*G\*C-G\*A\*C-G\*T\*T\*T\*T\*G\*C\*G\*C-G\*C\*C\*G;

- continued

T\*C\*G\*C\*A\*C-G\*T\*C\*G\*T\*T\*G\*C-G\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 254)

T\*C\*G\*C\*A\*C-G\*T\*T\*C\*G\*A\*A\*G\*C-G\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 255)

T\*C\*G\*C\*A\*C-G\*A\*A\*C\*G\*T\*T\*G\*C-G\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 256)

T-C-G-A-C-G-T-C-G-T-D-D-D-T-C-G-A-C-G-T-C-G-T-D-D-D;  
 (SEQ ID NO: 257)

T\*C\*G\*T\*C\*G\*T\*T\*A\*G\*C\*T\*C\*G\*T\*T\*A\*G\*C\*T\*C\*G\*T\*T;  
 (SEQ ID NO: 258)

T\*C\*G\*T\*C\*G\*T\*T\*A\*C\*G\*T\*A\*T\*T\*A\*G\*T\*C\*G\*T\*T;  
 (SEQ ID NO: 259)

T\*C\*G\*T\*C\*G\*T\*T\*A\*C\*G\*T\*C\*G\*T\*T\*A\*C\*G\*T\*A\*A\*T\*T;  
 (SEQ ID NO: 260)

T\*C\*G\*T\*C\*G\*T\*T\*A\*C\*G\*T\*A\*A\*T\*T\*A\*C\*G\*T\*A\*A\*T\*T;  
 (SEQ ID NO: 261)

T\*C\*G\*A\*C\*G\*T\*C\*G-A-C\*G\*T\*G\*A\*C\*G\*G\*G;  
 (SEQ ID NO: 262)

(T-C-G-A-C-G-T-C-G-T-T) 2doub-but;  
 (SEQ ID NO: 678)

(T-C-G-A-C-G-T-C-G-T-T) 2doub-chol;  
 (SEQ ID NO: 679)

(T-C-G-A-C-G-T-C-G-T-T) 2doub-chol;  
 (SEQ ID NO: 680)

T-C-G-A-C-G-T-C-G-T-T-chol-T-T-C-G-A-C-G-T-C-G-T-T-but;  
 (SEQ ID NO: 681)

T\*C\*G\*C-G\*A\*C\*G\*T\*T\*C-G\*G\*C\*G\*C-G\*C\*T\*G\*C\*C\*G;  
 (SEQ ID NO: 263)

T\*C\*G\*C-G\*A\*C\*G\*T\*T\*C-G\*G\*C\*G\*C-G\*T\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 264)

T\*C\*G\*C-G\*A\*C\*G\*T\*T\*C-G\*G\*C\*G\*C-G\*T\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 265)

T\*C\*G\*C-G\*A\*C\*G\*T\*T\*C-G\*G\*C\*G\*C-G\*T\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 591)

T\*C\*G\*C-G-A\*C\*G\*T\*T\*C-G\*G\*C\*G\*C-G\*T\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 592)

T\*C\*G-C\*G\*A\*C\*G\*T\*T\*C-G\*G\*C\*G\*C-G\*T\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 593)

T\*C\*G-C\*G\*A\*C\*G\*T\*T\*C-G\*G\*C\*G\*C-G\*T\*C\*G\*C\*C\*G;  
 (SEQ ID NO: 594)

(T-C-G-A-C-G-T-C-G-T-) (vitE-);  
 (SEQ ID NO: 266)

T\*C-G-A\*C-G\*T\*C-G\*A\*C\*G\*T\*G\*A\*C\*G\*G\*G;  
 (SEQ ID NO: 595)

T\*C\*G\*A\*C\*G\*T\*C\*G\*A\*C\*G\*T\*G\*A\*C\*G\*G\*G;  
 (SEQ ID NO: 596)

T\*C\*G\*A\*C\*G\*T\*C\*G\*A\*C\*G\*T\*G\*A\*C\*G\*G\*G;  
 (SEQ ID NO: 267)

T\*C\*G\*A\*C\*G\*T\*C\*G\*A\*C\*G\*T\*G\*A\*C\*G\*T\*C;  
 (SEQ ID NO: 268)

T\*C\*G\*A\*C\*G\*T\*C\*G\*A\*C\*G\*T\*G\*A\*C\*G;  
 (SEQ ID NO: 269)

(T-C-G-A-C-G-T-C-G-A-) (vitE-);

- continued

T\*C\*G\*T\*C\*G\*T\*T\*A\*C\*G\*T\*A\*A\*C\*T\*A\*C\*G\*T\*C\*G\*T\*T;  
 (SEQ ID NO: 270)

T\*C\*G\*T\*C\*G\*T\*T\*A\*C\*G\*T\*A\*A\*C\*G\*A\*C\*G\*T\*C\*G\*T\*T;  
 (SEQ ID NO: 550)

T\*C\*G\*T\*C\*G\*T\*T\*A\*C\*G\*T\*A\*A\*C\*G\*A\*C\*G\*T\*C\*G\*T\*T;  
 (SEQ ID NO: 271)

T\*C\*G\*T\*C\*G\*T\*T\*A\*G\*C\*T\*A\*A\*T\*T\*A\*G\*C\*T\*C\*G\*T\*T;  
 (SEQ ID NO: 272)

T\*C\*G\*T\*C\*G\*T\*T\*A\*C\*G\*T\*A\*A\*T\*T\*A\*G\*C\*T\*C\*G\*T\*T;  
 (SEQ ID NO: 273)

C\*C\*C\*A\*T\*G\*A\*C\*G\*T\*T\*C\*C\*T\*G\*A\*C\*G\*T\*T;  
 (SEQ ID NO: 274)

G\*C\*C\*A\*T\*G\*A\*C\*G\*T\*T\*C\*C\*T\*G\*A\*C\*G\*T\*T;  
 (SEQ ID NO: 275)

A\*C\*C\*A\*T\*G\*A\*C\*G\*T\*T\*C\*C\*T\*G\*A\*C\*G\*T\*T;  
 (SEQ ID NO: 276)

T\*G\*G\*A\*T\*G\*A\*C\*G\*T\*T\*C\*C\*T\*G\*A\*C\*G\*T\*T;  
 (SEQ ID NO: 277)

T\*T\*T\*A\*T\*G\*A\*C\*G\*T\*T\*C\*C\*T\*G\*A\*C\*G\*T\*T;  
 (SEQ ID NO: 278)

T\*A\*A\*A\*T\*G\*A\*C\*G\*T\*T\*C\*C\*T\*G\*A\*C\*G\*T\*T;  
 (SEQ ID NO: 279)

C\*C\*A\*T\*G\*A\*C\*G\*T\*T\*C\*C\*T\*G\*A\*C\*G\*T\*T;  
 (SEQ ID NO: 280)

C\*A\*T\*G\*A\*C\*G\*T\*T\*C\*C\*T\*G\*A\*C\*G\*T\*T;  
 (SEQ ID NO: 281)

A\*T\*G\*A\*C\*G\*T\*T\*C\*C\*T\*G\*A\*C\*G\*T\*T;  
 (SEQ ID NO: 282)

T\*G\*A\*C\*G\*T\*T\*C\*C\*T\*G\*A\*C\*G\*T\*T;  
 (SEQ ID NO: 283)

T-C-G-A-C-G-T-C-G-A-D-D-D-T-C-G-A-C-G-T-C-G-A-chol;  
 (SEQ ID NO: 284)

teg-iA-iG-iC-iT-iG-iC-iA-iG-iC-iT-D-D-D-T-C-G-A-C-G-A-chol;  
 (SEQ ID NO: 285)

T\*C-G\*C-G\*A\*C-G\*T\*T\*C-G\*G\*G\*C-G\*C-G\*C-C-G;  
 (SEQ ID NO: 286)

T\*C-G\*T\*C-G\*A\*C-G\*T\*T\*C-G\*G\*C-G\*C-G\*C-C-G;  
 (SEQ ID NO: 287)

T\*C-G\*G\*A\*C-G\*T\*T\*C-G\*G\*C-G\*C-G\*C-C-G;  
 (SEQ ID NO: 288)

T\*C-G\*G\*A\*C-G\*T\*T\*C-G\*G\*C-G\*C-G\*C-C-G;  
 (SEQ ID NO: 289)

T\*C-G\*C-G\*A\*C-G\*T\*T\*C-G\*G\*C-G\*C-G\*C-C-G;  
 (SEQ ID NO: 290)

T\*C-G\*C-G\*A\*C-G\*T\*T\*C-G\*G\*C-G\*C-G\*C-C-G;  
 (SEQ ID NO: 597)

T\*C-G\*C-G\*AC-G\*T\*T\*C-G\*C-G\*C-G\*C-C-G;  
 (SEQ ID NO: 291)

T\*C-G\*A\*C-G\*T\*T\*C-G\*G\*C-G\*C-G\*C-C-G;  
 (SEQ ID NO: 292)

T\*C-G\*A\*C-G\*T\*T\*C-G\*G\*C-G\*C-G\*C-C-G;  
 (SEQ ID NO: 293)

T\*C-G\*C-G\*A\*C-G\*T\*T\*C-G\*G\*C-G\*C-C-G;

- continued

T*C-G*C-G*A*C-G*T*T*C-G*G*C*C*G;	(SEQ ID NO: 294)
T*C-G*A*C-G*T*T*C-G*G*C*C*G;	(SEQ ID NO: 295)
T*C-G*T*C-G*A*C-G*T*T*C-G*G*C*G-G*G*C*C*G;	(SEQ ID NO: 296)
T*C-G*T*C-G*A*C-G*T*T*C-G*G*C-C-G*C*C*G;	(SEQ ID NO: 297)
T*C-G*A*C-G*A*C-G*T*T*C-G*G*C*G-C-G*C*C*G;	(SEQ ID NO: 298)
T*C-G*A*C-G*T*C-G*T*T*C-G*G*C*G*C-G*C*C*G;	(SEQ ID NO: 299)
T*C-G*T*C-G*A*C-G*A*T*C-G*G*C*G*C-G-C-G*C*C*G;	(SEQ ID NO: 598)
T*C-G*T*C-G*A*C-G*A*T*C-G*G*C*G*C-G*C*C*G;	(SEQ ID NO: 599)
T*C-G*T*C-G*A*C-G*T*T*C-G*C*C*G-C-G*C*G*C*G;	(SEQ ID NO: 300)
T*C-G*T*C-G*A*C-G*T*T*C-G*G*C*G-C-G*C*G*C*G;	(SEQ ID NO: 301)
T*C-G*T*C-G*A*C-G*T*T*C-G*G*C*G*C-C-G*T*G*C*C*G;	(SEQ ID NO: 302)
T*C-G*T*C-G*T*T*A*C-G*T*A*A*C-G*A*C*G*A*C-G*T*T;	(SEQ ID NO: 600)
T*C-G*T*C-G*T*T*A*C-G*T*A*A*C-G*A*C*G*A*C-G*T*T;	(SEQ ID NO: 601)
T*C-G*T*C-G*T*T*A*C-G*T*A*A*C-G*A*C*G*A*C-G*T*T;	(SEQ ID NO: 602)
T*C-G*T*C-G*A*C*G*A*T*C-G*G*C*G*C-G*C*C*G;	(SEQ ID NO: 603)
A-C-G-A-C-G-T-C-G-T-D-D-D-A-C-G-A-C-G-T-C-G-T-D-D-D-irU;	(SEQ ID NO: 305)
T*C-G*T*C-G*A*C-G*A*T*C-G*G*C*C*G*C-C-G*T*G*C*C*G;	(SEQ ID NO: 306)
T*C-G*T*C-G*A*C-G*A*T*C-G*G*C*G*C-C-G*T*G*C*C*G;	(SEQ ID NO: 307)
T*C-G*T*C-G*A*C-G*A*T*C-G*G*C*G*C-C-G*T*G*C*C*G;	(SEQ ID NO: 308)
T*C-G*T*C-G*A*C-G*A*T*C-G*G*C*G*C-C-G*T*G*C*C*G;	(SEQ ID NO: 642)
T*C-G*T*C-G*A*C-G*A*T*C-G*G*C*G*C-C-G*T*G*C*C*G;	(SEQ ID NO: 603)
T*C-G*T*C-G*A*C-G*A*T*C-G*G*C*G*C-C-G*T*G*C*C*G;	(SEQ ID NO: 604)
T*C-G*T*C-G*A*C-G*A*T*C-G*G*C*G*C-C-G*T*G*C*C*G;	(SEQ ID NO: 605)
T*C-G*T*C-G*A*C-G*A*T*C-G*G*C*G*C-C-G*T*G*C*C*G;	(SEQ ID NO: 606)
T*C-G*T*C-G*A*C-G*A*T*C-G*G*C*G*C-C-G*T*G*C*C*G;	(SEQ ID NO: 607)

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T*C*G*T*C*G*A*C*G*A-T-C*G*G*C*G*C*G*C*G;	(SEQ ID NO: 608)
T*C*G*A*C*G*T*C*G-A-C*G*T*G*A*C*G*T*T;	(SEQ ID NO: 609)
T*C*G*A*C-G*T*C*G*A*C-G*T*G*A*C*G*T*T;	(SEQ ID NO: 610)
T*C*G*A*C-G*T*C*G*A*C*G*TG*A*C*G*T*T;	(SEQ ID NO: 611)
T*C*G*T*C-G*A*C*G*A*C-G*T*G*T*C*G*A*T;	(SEQ ID NO: 612)
T*C*G*A*C-G-T*C*G*A*C*G-T*G*A*C*G*T*T;	(SEQ ID NO: 613)
T*C*G*A-C*G*T*C*G-A*C*G*T*G-A*C*G*T*T;	(SEQ ID NO: 614)
T*C*G*T*C*G*A-C*G*A*T*C*G*G*C*G-C*C*G*T*G*C*C*G;	(SEQ ID NO: 307)
T*C*G*T*C*G*A-C*G*A*C*G*G*C*G-C*G*T*G*C*C*G*T;	(SEQ ID NO: 310)
T*C*G*T*C*G*A*C*G*C*G*C*C-G*T*G*C*C*G*T;	(SEQ ID NO: 615)
T*C*G*T*C-G*A*C-G*A*T*C-G*G*C*G*G*C-G*T*G*C*C*G*T;	(SEQ ID NO: 311)
T*C-G*T*C-G*A*C-G*T*T*C-G*G*C*G*C-C-G*T*G*C*C*G*T;	(SEQ ID NO: 312)
T*C-G*T*C-G*T*C-G*G*C*C*-G*T*G*C*C*G*T;	(SEQ ID NO: 313)
T*C-G*T*C-G*A*C-G*G*C*G*C-C-G*T*G*C*C*G*T;	(SEQ ID NO: 314)
T*C*G*T*C*G*A-C*G*C*G*G*C-G-C*C*G*T*G*C*C*G*T;	(SEQ ID NO: 616)
T*C*G*T*C-G*A-C*G*A-T*C-G*G*C*G*A-A*G*T*C-G*A*C*G*A*T;	(SEQ ID NO: 315)
T*C*G*T*C-G*A*C*G*A-A*T*C*G*T*C-G*A*C*G*A*T;	(SEQ ID NO: 316)
T*C*G*T*C-G*T*A*C-G*G*C*G*C-C-G*T*G*C*C*G*T;	(SEQ ID NO: 317)
T*C*G*T*C*G*A-C*G*A*T*C*G*G*C-G-C*C*G*T*G*C*C*G;	(SEQ ID NO: 617)
T*C*G*T*C*G*A-C*G*A*T*C*G*G*C-G-C*G*T*G*C*C*G;	(SEQ ID NO: 307)
T*C*G*T*C*G*A-C*G*A*T*C*G*G*C-G-C*G*T*G*C*C*G;	(SEQ ID NO: 618)
T*C*G*T*C*G*A-C*G*A*T*C*G-G*C*G-C*G*T*G*C*C*G;	(SEQ ID NO: 310)
T*C*G*T*C*G*A-C*G*A*C*G*G*C*G-C*G*T*G*C*C*G*T;	(SEQ ID NO: 318)
T*C*G*T*C-G*A*C-G*A*T*C-G*G*C*G*C-G*T*G*C*C*G*T;	(SEQ ID NO: 619)
T*C*G*T*C*G*A-C*G*A*T*C*G*G*C-G-C*C*G*T*G*C*C*G*T;	(SEQ ID NO: 620)
T*C*G*T*C*G*A-C*G*A*C*G*G*C*G-C*G*T*G*C*C*G*T;	(SEQ ID NO: 312)
T*C-G*T*C-G*A*C-G*T*T*C-G*G*C*G*C-C-G*T*G*C*C*G*T;	

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T*C-G*T*C-G*A*C-G*T*C-G*G*C*G*C-C-G*T*G*C*C*G*T;	(SEQ ID NO: 621)
T*C*G*T*C-G*A*C*G*A-A*G*T*C-G*A*C*G*A*T;	(SEQ ID NO: 315)
T*C*G*T*C-G*A*C*G*A-G*A-A*T*C*G*T*C-G*A*C*G*A*T;	(SEQ ID NO: 316)
T*C*G*T*C-G*A*C*G*A-C-G*T*G*T*C*G*A*T;	(SEQ ID NO: 319)
T*C*G*A*C-G*T*C*G*A-A*G*A*C-G*T*C*G*A*T;	(SEQ ID NO: 320)
T*C*G*A*C-G*T*C*G*A-A*T*C*G*A*C-G*T*C*G*A*T;	(SEQ ID NO: 321)
T*C*G*T*C-G*A*C-G*A*C*G*G*C*G-A*A*G*C*C*G;	(SEQ ID NO: 322)
T*C*G*T*C-G*A*C-G*A*C*G*G*C-G-A*A*G*C*C*G*T;	(SEQ ID NO: 323)
T*C*G*T*C-G-A*C*G*A*C*G-T*G*T*C*G*A*T;	(SEQ ID NO: 309)
T*C*G*T*C*G*A*C*G*A*C*G*T*G*T*C*G*A*T;	(SEQ ID NO: 622)
T*C*G*A*C-G*T*C*G*A*C-G*T*G*A*C*G-T*T*G*T;	(SEQ ID NO: 324)
T*C<G*T*C-G*A*C-G*A*T*C-G*G*C*G*C-G*C*G*C*G-but;	(SEQ ID NO: 325)
T*C-G*T*C<G*A*C-G*A*T*C-G*G*C*G*C-G*C*G*C*G-but;	(SEQ ID NO: 623)
T*C-G*T*C-G*A*C*G*A*T*C-G*G*C*G*C-G*C*G*C*G-iT;	(SEQ ID NO: 327)
iT-T*C-G*T*C-G*A*C*G*A*T*C-G*G*C*G*C-G*C*G*C*G-iT;	(SEQ ID NO: 328)
T*C-G*T*C-G*A*C-G*A*T*C-G*A*C*G*C-G*C*G*T*C*G;	(SEQ ID NO: 329)
T*C-G*T*C-G*A*C-G*A*T*C-A*A*C*G*C-G*C*G*T*T*G;	(SEQ ID NO: 330)
T*C-G*T*C-G*A*C-G*A*T*C-G*G*C*G*C-G*T*G*C*C*G	(SEQ ID NO: 331)
T*C-G*T*C-G*A*C-G*A*T*C-G*G*C*A*T-A*T*G*C*C*G;	(SEQ ID NO: 332)
T*C-G*T*C-G*A*C-G*A*T*G-C*C*G*C*G-C*G*C*G*G*C;	(SEQ ID NO: 333)
T*C-G*T*C-G*A*C-G*A*T*G*G*C*C*G*C*G*C*G*G*C;	(SEQ ID NO: 624)
T*C-G*T*C-G*A*C*G*A*T*G*G*C*C*G*C*G*C*G*G*C;	(SEQ ID NO: 625)
T*C-G*T*C-G*A*C*G*A*T*G*C*C*G*C*G*C*G*G*C;	(SEQ ID NO: 626)
T*C-G*T*C-G*A*C*G*A*T*G*C*C*G*C*G*C*G*G*C;	(SEQ ID NO: 334)
T*C-G*T*C-G*A*C*G*A*T*G*C*C*G*C*G*C*G*G*C;	(SEQ ID NO: 335)
T*C-G*T*C-G*T*A*C*G*A*T*G*C*C*G*C*G*C*G*G*C;	(SEQ ID NO: 336)

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T*C*G*T*C*G*A*C*G*A*T-G*C*C*G*C*G*C*G*G*C;	(SEQ ID NO: 627)
T*C*G*T*C*G*A*C*G*A*T-G-C*C*G*C*G*C*G*G*C;	(SEQ ID NO: 628)
T*C*G*T*C-G*A*C*G*A*T*C*G*G*C*G*C*G*C*G*C*G-iT;	(SEQ ID NO: 337)
T*C-G*T*C*G*A*C*G*A*T*C*G*G*C*G*C*G*C*G*C*G-iT;	(SEQ ID NO: 629)
T*C*G*T*C*G*A*C*G*A*T*C-G*G*C*G*C*G*C*G*C*G-iT;	(SEQ ID NO: 630)
T*C-G*T*G-C*A*C-G*A*T*C-G*G*C*G*C-G*C*G*C*G;	(SEQ ID NO: 338)
T*Z-G*T*C-G*A*C-G*A*T*C-G*G*C*G*C-G*C*G*C*G;	(SEQ ID NO: 339)
T*C-G*T*Z-G*A*C-G*A*T*C-G*G*C*G*C-G*C*G*C*G;	(SEQ ID NO: 340)
T*C-G*T*C-G*A*Z-G*A*T*C-G*G*C*G*C-G*C*G*C*G;	(SEQ ID NO: 341)
T*C-G*T*C-G*A*C-G*A*T*Z-G*G*C*G*C-G*C*G*C*G;	(SEQ ID NO: 342)
T*C-G*A*C*G*T*C-G*A*C*G*T*C-G*A*C*G;	(SEQ ID NO: 343)
T-C-G-A-C-G-T-C-G-A-C-G-T-C-G-A-C-G;	(SEQ ID NO: 631)
T*C*G*A*C*G*T*C*G*A*C*G*T*C*G*A*C*G;	(SEQ ID NO: 632)
T*C-G*T*C*G*A*C*G*T*T*C*G*G*C*G*C*G*T*G*C*C*G-iT;	(SEQ ID NO: 344)
T*C*G*T*C-G*A*C*G*T*T*C*G*G*C*G*C*G*T*G*C*C*G-iT;	(SEQ ID NO: 633)
T*C*G*T*C-G*A*C*G*T*T-C-G*G*C*G*C*G*T*G*C*C*G-iT;	(SEQ ID NO: 634)
G*C*C*G*C*G-C*G*C*G*G-C*iT*1A*1G-iC*IA*IG-iC*IT*IG-iC*iT;	(SEQ ID NO: 345)
C*G*G*C*G-C*G*C*G*C-G*iT*1A*1G-iC*IA*IG-iC*IT*IG-iC*iT;	(SEQ ID NO: 346)
G*C*C*G*C*G*C*G*G*C*G*C*iT*1A*iG*IC*IA*IG-iC*IT*IG*IC*iT;	(SEQ ID NO: 635)
C*G*G*C*G*C*G*C*G*C*iT*1A*iG*IC*IA*IG-iC*IT*IG*IC*iT;	(SEQ ID NO: 636)
C*G*G*C*G*C-G*T*G*C*C*iT*iT*IG*IC*IA*IG-iC*IT*IG*IC*iT;	(SEQ ID NO: 347)
G*C*C*G*T*G-C*C*G*C*G-C*iT*iT*IG*IC*IA*IG-iC*IT*IG*IC*iT;	(SEQ ID NO: 348)
C*G*G*C*G*C*G*T*G*C*C*iT*iT*IG*IC*IA*IG-iC*IT*IG*IC*iT;	(SEQ ID NO: 637)
G*C*C*G*T*G*C*G*C*G*G*C*iT*iT*IG*IC*IA*IG-iC*IT*IG*IC*iT;	(SEQ ID NO: 638)
T*C*G*G*C*G-C*G*C*G*C-G*A*iT*IA*IG-iC*IA*IG-iC*IT*IG-iC*iT;	(SEQ ID NO: 349)
T*C*G*G*C*G*C*G*C*G*A*iT*IA*IG*IC*IA*IG-iC*IT*IG*IC*iT;	(SEQ ID NO: 639)

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T*C*G*G*C*G*C-C-G*T*G*C*C*G*iT*IT*IG*IC*IA*IG-iC*IT*IG*IC*iT;	(SEQ ID NO: 350)
T*C*G*G*C*G*C*C*G*T*G*C*C*G*iT*IT*IG*IC*IA*IG-iC*IT*IG*IC*iT;	(SEQ ID NO: 350)
CGGCGCXGCGCCG;	(SEQ ID NO: 351)
T-C_G*T*C_G*A*C_G*T*T*C_G*G*C*G_C_G*C*G*C*G;	(SEQ ID NO: 640)
T*C*G*T*C*G*A*C*G*A*C*G*G*C*G*C*G*C*G*C*G;	(SEQ ID NO: 352)
T*C*G*T*C*G*A*C*G*A*J*C*G*G*C*G*C*G*C*G;	(SEQ ID NO: 353)
T*C*G*T*C*G*A*C*G*A*L*C*G*G*C*G*C*G*C*G;	(SEQ ID NO: 354)
T*C*G*T*C*G*A*D*C*G*G*C*G*C*G*C*G;	(SEQ ID NO: 355)
G*G*G-G-A-C-G-A-C-G-T-C-G-T-G-G*G*G*G*G;	(SEQ ID NO: 641)
T*C-G-A-C-G-T-C-G-T-G-G*G*G;	(SEQ ID NO: 356)
T*C*C*A*G*G*A*C*T*T*C*T*C*T*C*A;	(SEQ ID NO: 357)
T*C*G*T*C*G*T*T*T*C*G*G*C*G*C*G*C*G*C*G;	(SEQ ID NO: 644)
T*C*G*T*C-mG*mA*C*mG*mA*T*C*mG*mG*C*mG*C*mG*C*mG*C*mG;	(SEQ ID NO: 358)
T*C*mG*T*C*mG*mA*C*mG*mA*T*C*mG*mG*C*mG*C*mG*C*mG;	(SEQ ID NO: 359)
T*C*G*T*C-mG*mA*C-mG*mA*T*C-mG*mG*C*mG*C*mG*C*mG;	(SEQ ID NO: 645)
and	
T*C-mG*T*C-mG*mA*C-mG*mA*T*C-mG*mG*C*mG*C*mG*C*mG,	(SEQ ID NO: 646)

wherein: - represents phosphodiester linkage; \* represents stabilized internucleotide linkage; biot represents Biotin; but represents butyrate; chol represents Cholesterol; Cy3 represents Bis-hydroxypropyl-3,3',3'-tetramethyl-4,5-benzindocarbocyanine chloride (Glen Research); D represents D spacer (1'2'-dideoxyribose, Glen Research, Sterling, VA); dig represents Digoxigenin; doub-represents doubler; iN represents Inverse nucleotide (inverse orientation: 3' and 5' switched); J represents 1,3-propane-diol; L represents hexaethylene glycol; mN represents 2'-O-methyl nucleoside; rN represents ribonucleoside; teg represents Triethylene glycol; vitE represents Vitamin E; and Z represents 5-methyl-deoxycytidine.

**[0142]** Another recently-discovered class of CpG ODN is the E-class, in which halogen-modified nucleotides are placed immediately 5' to the CpG motif as described in U.S. Pat. No. 8,580,268 and U.S. Published Application 2014/0163213, the entire contents of both of which are incorporated herein by reference. These ODN also induce much higher levels of type I IFN relative to the modest IL-10 production.

**[0143]** Examples of E-class ODN include:

T*G*FF*C-G*T*T*T*T*T*T*T*T*T*T*T*T*T;	(SEQ ID NO: 360)
T*G*T*C-G*FF*T*T*T*T*T*T*T*T*T*T*T*T;	(SEQ ID NO: 361)
T*G*FF*C-G*FF*T*T*T*T*T*T*T*T*T*T*T;	(SEQ ID NO: 362)
T*G*T*FF-G*T*T*T*T*T*T*T*T*T*T*T*T;	(SEQ ID NO: 363)
T*G*T*C-FF*T*T*T*T*T*T*T*T*T*T*T*T;	(SEQ ID NO: 364)
T*FF*C-G*T*T*T*T*T*T*T*T*T*T*T*T;	(SEQ ID NO: 365)
T*G*T*C-G*T*FF*T*T*T*T*T*T*T*T*T*T;	(SEQ ID NO: 366)
T*G*BU*C-G*T*T*T*T*T*T*T*T*T*T*T*T;	(SEQ ID NO: 367)

-continued

(SEQ ID NO: 368)  
T\*G\*T\*C-G\*BU\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 369)  
T\*G\*BU\*C-G\*BU\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 370)  
T\*G\*JU\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 371)  
T\*G\*T\*C-G\*JU\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 372)  
T\*G\*JU\*C-G\*JU\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 373)  
T\*G\*U\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 374)  
T\*G\*T\*C-G\*U\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 375)  
T\*G\*U\*C-G\*U\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 376)  
JU\*C\*G\*T\*C\*G\*T\*T\*T\*T\*C\*G\*G\*T\*C\*G\*T\*T\*T;

(SEQ ID NO: 377)  
T\*C\*G\*JU\*C\*G\*T\*T\*T\*T\*C\*G\*G\*T\*C\*G\*T\*T\*T;

(SEQ ID NO: 378)  
T\*C\*G\*T\*C\*G\*T\*T\*T\*T\*C\*G\*G\*JU\*C\*G\*T\*T\*T;

(SEQ ID NO: 379)  
JU\*C\*G\*JU\*C\*G\*T\*T\*T\*T\*C\*G\*G\*T\*C\*G\*T\*T\*T;

(SEQ ID NO: 380)  
T\*C\*G\*JU\*C\*G\*JU\*T\*T\*T\*T\*C\*G\*G\*T\*C\*G\*T\*T\*T;

(SEQ ID NO: 381)  
T\*C\*G\*T\*C\*G\*T\*T\*T\*T\*C\*G\*G\*JU\*C\*G\*JU\*T\*T\*T;

(SEQ ID NO: 382)  
JU\*C-G\*T\*C\*G\*T\*T\*T\*T\*A\*C\*G\*G\*C\*G\*C\*G\*T\*G\*C\*G;

(SEQ ID NO: 383)  
T\*C\*G\*JU\*C-G\*T\*T\*T\*T\*A\*C\*G\*G\*C\*G\*C\*G\*T\*G\*C\*G;

(SEQ ID NO: 384)  
T\*G\*T\*C-G\*EU\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 385)  
T\*G\*EU\*C-G\*EU\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 386)  
JU\*C-G\*T\*C\*G\*A\*C\*G\*A\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G;

(SEQ ID NO: 387)  
T\*C\*G\*JU\*C-G\*A\*C\*G\*A\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G;

(SEQ ID NO: 388)  
JU\*C-G\*T\*C\*G\*A\*C\*G\*A\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G;

(SEQ ID NO: 389)  
JU\*C-G-A-C-G-T-C-G-T-G-G\*G\*G;

(SEQ ID NO: 390)  
T\*C-G-A-C-G-JU-C-G-T-G-G\*G\*G;

(SEQ ID NO: 391)  
T\*C-G-A-C-G-JU-C-G-JU-G-G\*G\*G;

G\*JU\*C-G\*T;

G\*JU\*C-G\*JU\*T;

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(SEQ ID NO: 392)  
T\*G\*CU\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 393)  
T\*G\*EU\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 394)  
JU\*C-G\*JU\*C-G\*T\*T\*T\*A\*C\*G\*G\*C\*G\*C\*G\*T\*G\*C\*G;

(SEQ ID NO: 395)  
T\*C-G\*JU\*C-G\*JU\*T\*T\*T\*A\*C\*G\*G\*C\*G\*C\*G\*T\*G\*C\*G;

(SEQ ID NO: 396)  
T\*C\*T\*T\*T\*T\*T\*T\*G\*JU\*C-G\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 397)  
T\*C\*T\*T\*T\*T\*T\*T\*G\*JU\*C-G\*JU\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 398)  
JU\*C\*T\*T\*T\*T\*T\*T\*T\*G\*T\*C-G\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 399)  
T\*C\*T\*T\*T\*T\*T\*T\*G\*U\*C-G\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 400)  
JU\*C-G\*A\*C\*G\*T\*C\*G\*A\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G;

(SEQ ID NO: 400)  
JU\*C\*G\*A\*C\*G\*T\*C\*G\*A\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G;

(SEQ ID NO: 401)  
JU\*C-G\*A\*C\*G\*T\*C\*G\*A\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G;

(SEQ ID NO: 401)  
JU\*C\*G\*A\*C\*G\*T\*C\*G\*A\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G;

(SEQ ID NO: 402)  
EU\*C-G\*A\*C\*G\*T\*C\*G\*A\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G;

(SEQ ID NO: 402)  
EU\*C\*G\*A\*C\*G\*T\*C\*G\*A\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G;

(SEQ ID NO: 403)  
JU\*C-G\*T\*C\*G\*A\*C\*G\*A\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G;

(SEQ ID NO: 403)  
JU\*C-G\*T\*C\*G\*A\*C\*G\*A\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G;

(SEQ ID NO: 404)  
EU\*C-G\*T\*C\*G\*A\*C\*G\*A\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G;

(SEQ ID NO: 405)  
JU\*C-G\*T\*C\*G\*A\*C\*G\*A\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G;

(SEQ ID NO: 406)  
T\*G\*T\*C-G\*FU\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 407)  
T\*G\*FU\*C-G\*FU\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 408)  
T\*G\*U\*C-G\*UT\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 409)  
T\*G\*T\*C-6NB\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 410)  
T\*G\*T\*6NB-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 410)  
T\*G\*T\*6NB-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 411)  
JU\*G\*T\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

-continued

(SEQ ID NO: 412)  
JU\*G\*JU\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 413)  
T\*G\*T\*C-G\*T\*JU\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 414)  
T\*G\*FT\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 415)  
T\*G\*T\*C-G\*FT\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 416)  
T\*G\*FT\*C-G\*FT\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 392)  
T\*G\*CU\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 417)  
T\*G\*T\*C-G\*CU\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 418)  
T\*G\*CU\*C-G\*CU\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 419)  
T\*JU\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
T\*G\*JU\*C-G\*T\*T\*T;  
  
(SEQ ID NO: 420)  
T\*G\*JU\*C-G\*T\*T\*T\*T\*T\*C-G\*T\*T;  
(T\*G\*JU\*C-G\*T\*T\*L\*) 2doub-3mG;  
(JU\*C-G\*T\*T\*C\*G\*L\*) 2doub-3mG;  
  
(SEQ ID NO: 421)  
T\*T\*JU\*C-G\*T\*C-G\*T\*T\*T\*C-G\*T\*C-G\*T\*T;  
  
(SEQ ID NO: 422)  
BU\*C-G-A-C-G-T-C-G-T-G-G\*G\*G;  
  
(SEQ ID NO: 423)  
T\*G\*JU\*G-C\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
(T\*G\*JU\*C-G\*T\*T\*L\*) 2doub-teg;  
(JU\*C-G\*T\*T\*C\*G\*L\*) 2doub-teg;  
  
(SEQ ID NO: 424)  
JU\*C-G\*T\*C-G\*T\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*G\*C\*G;  
  
(SEQ ID NO: 425)  
T\*C\*G\*JU\*C-G\*T\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*G\*C\*G;  
  
(SEQ ID NO: 426)  
T\*C\*G\*T\*C-G\*T\*T\*T\*JU\*C-G\*G\*C\*G\*C\*G\*C\*G\*C\*G;  
  
(SEQ ID NO: 427)  
JU\*C-G\*T\*C-G\*T\*T\*T\*T\*C-G\*G\*JU\*C-G\*T\*T\*T\*T;  
  
(SEQ ID NO: 428)  
T\*C\*G\*JU\*C-G\*T\*T\*T\*T\*T\*C-G\*G\*JU\*C-G\*T\*T\*T\*T;  
  
(SEQ ID NO: 429)  
T\*G\*JU\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 430)  
T\*G\*JU\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 431)  
JU\*C-G-A-C-G-T-C-G-T-G-G\*E\*G\*G;  
  
(SEQ ID NO: 432)  
T\*mG\*JU\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

-continued

(SEQ ID NO: 433)  
T\*G\*JU\*C-mG\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 434)  
T\*mG\*JU\*C-mG\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 379)  
JU\*C-G\*JU\*C-G\*T\*T\*T\*T\*C-G\*G\*T\*C\*G\*T\*T\*T;  
  
(SEQ ID NO: 379)  
JU\*C-G\*JU\*C-G\*T\*T\*T\*T\*C-G\*G\*T\*C\*G\*T\*T\*T;  
  
(SEQ ID NO: 435)  
T\*G\*PU\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 436)  
T\*G\*T\*C-G\*PU\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 422)  
BU\*C-G-A-C-G-T-C-G-T-G-G\*G\*G;  
  
(SEQ ID NO: 437)  
T\*G\*JU\*C-G\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*G\*C\*G;  
  
(SEQ ID NO: 438)  
T\*JU\*C-G\*T\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*G\*C\*G\*T;  
  
(SEQ ID NO: 439)  
T\*EU\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 440)  
T\*G\*EU\*G-C\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 376)  
JU\*C-G\*T\*C-G\*T\*T\*T\*T\*T\*C-G\*G\*T\*C-G\*T\*T\*T;  
  
(SEQ ID NO: 441)  
EU\*C-G\*T\*C-G\*T\*T\*T\*T\*C-G\*G\*T\*C-G\*T\*T\*T\*T;  
G\*JU\*C-G\*T-hex;  
G\*JU\*C-G\*JU\*T-hex;  
G\*EU\*C-G\*EU\*T-hex;  
  
(SEQ ID NO: 442)  
EU\*C-G\*T\*C-G\*T\*T\*T\*A\*C-G\*G\*C\*G\*C\*G\*T\*G\*C\*G;  
  
(SEQ ID NO: 443)  
T\*C\*G\*EU\*C-G\*T\*T\*T\*A\*C-G\*G\*C\*G\*C\*G\*T\*G\*C\*G;  
  
(SEQ ID NO: 444)  
EU\*C-G\*T\*C-G\*A\*C-G\*A\*T\*C-G\*G\*C\*G\*C\*G\*C\*G;  
  
(SEQ ID NO: 445)  
JU\*C\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 446)  
JU\*C\*T\*T\*T\*T\*T\*T\*T\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 447)  
T\*C\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 448)  
JU\*C\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 449)  
JU\*C-G\*T\*C-G\*T\*T\*C-G\*T\*C-G\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 450)  
T\*C\*G\*T\*C-G\*T\*T\*T\*C-G\*T\*C-G\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 451)  
JU\*C-G\*T\*C-G\*T\*T\*T\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;  
  
(SEQ ID NO: 452)  
T\*G\*JU\*C-E\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

-continued

(SEQ ID NO: 453)  
T\*G\*JU\*C-I\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 454)  
T\*G\*JU\*Z-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 455)  
T\*G\*T\*C-G\*T\*T\*JU\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 456)  
T\*G\*T\*C-G\*T\*T\*JU\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 457)  
JU\*C-G\*T\*C-G\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*G\*T;

(SEQ ID NO: 458)  
EU\*C-G\*T\*C-G\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*G\*C\*G\*T;

(SEQ ID NO: 459)  
T\*C-G\*EU\*C-G\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*G\*C\*G\*T;

(SEQ ID NO: 460)  
T\*C-G\*T\*C-G\*T\*T\*JU\*C-G\*G\*C\*G\*C\*G\*C\*G\*C\*G\*T;

(SEQ ID NO: 461)  
T\*C-G\*T\*C-G\*T\*T\*EU\*C-G\*G\*C\*G\*C\*G\*C\*G\*C\*G\*T;

(SEQ ID NO: 462)  
EU\*C-G\*T\*C-G\*T\*T\*EU\*C-G\*G\*C\*G\*C\*G\*C\*G\*C\*G\*T;

(SEQ ID NO: 463)  
EU\*C-G\*EU\*C-G\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*G\*C\*G\*T;

(SEQ ID NO: 464)  
JU\*C-G\*EU\*C-G\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*G\*T;

(SEQ ID NO: 465)  
JU\*C-G\*T\*C-G\*T\*T\*T\*T\*T\*C-G\*T\*T\*T\*T\*C-G\*T;

(SEQ ID NO: 466)  
EU\*C-G\*T\*C-G\*T\*T\*T\*T\*T\*C-G\*T\*T\*T\*T\*C-G\*T;

(SEQ ID NO: 467)  
T\*G\*BVU\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 468)  
T\*T\*C-G\*BVU\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 469)  
JU\*C-G\*G\*C\*G\*G\*C\*G\*C\*G\*C\*G;

(SEQ ID NO: 470)  
JU\*C-G\*T\*C-G\*T\*T\*T\*T\*A\*C\*G\*G\*C\*G\*C\*G\*T\*G\*C\*

C\*3mG;

(SEQ ID NO: 471)  
EU\*C-G\*T\*C-G\*T\*T\*T\*T\*A\*C\*G\*G\*C\*G\*C\*G\*T\*G\*C\*

C\*3mG;

(SEQ ID NO: 472)  
EU\*C-G\*EU\*C-G\*T\*T\*T\*T\*A\*C\*G\*G\*C\*G\*C\*G\*T\*G\*C\*

C\*3mG;

(SEQ ID NO: 472)  
EU\*C-G\*EU\*C-G\*T\*T\*T\*T\*A\*C\*G\*G\*C\*G\*C\*G\*T\*G\*C\*

C\*3mG;

(SEQ ID NO: 473)  
EU\*C-G\*T\*C-G\*T\*T\*T\*T\*A\*C\*G\*G\*C\*G\*C\*G\*T\*G\*C\*

C\*G\*iT;

-continued

(SEQ ID NO: 474)  
JU\*C-G\*T\*C-G\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*3mG;

(SEQ ID NO: 475)  
EU\*C-G\*T\*C-G\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*3mG;

(SEQ ID NO: 475)  
EU\*C-G\*T\*C-G\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*3mG;

(SEQ ID NO: 476)  
EU\*C-G\*EU\*C-G\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*3mG;

(SEQ ID NO: 476)  
EU\*C-G\*T\*C-G\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*3mG;

(SEQ ID NO: 477)  
EU\*C-G\*T\*C-G\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*3mG;

(SEQ ID NO: 478)  
JU\*C-G\*T\*C-G\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*3mG;

(SEQ ID NO: 479)  
EU\*C-G\*T\*C-G\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*G\*iT;

(SEQ ID NO: 480)  
JU\*C-G\*T\*C-G\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*G\*iT;

(SEQ ID NO: 481)  
EU\*C-G\*T\*C-G\*A\*C\*G\*T\*T\*C-G\*G\*C\*G\*C\*G\*T\*G\*C\*

C\*3mG;

(SEQ ID NO: 482)  
JU\*C-G\*T\*C-G\*A\*C\*G\*T\*T\*C-G\*G\*C\*G\*C\*G\*T\*G\*C\*

C\*3mG;

(SEQ ID NO: 483)  
JU\*C-G\*T\*C-G\*A\*C\*G\*A\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*3mG;

(SEQ ID NO: 484)  
EU\*C-G\*T\*C-G\*A\*C\*G\*A\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*3mG;

(SEQ ID NO: 485)  
EU\*C-G\*T\*C-G\*A\*C\*G\*T\*T\*C-G\*G\*C\*G\*C\*G\*T\*G\*C\*

C\*G\*iT;

(SEQ ID NO: 486)  
EU\*C-G\*T\*C-G\*A\*C\*G\*A\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*G\*iT;

(SEQ ID NO: 487)  
T\*G\*NI\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 488)  
T\*G\*NP\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 489)  
T\*G\*6NB\*C-G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 441)  
EU\*C-G\*T\*C-G\*T\*T\*T\*T\*C-G\*G\*T\*T\*C-G\*T\*T\*T;

(SEQ ID NO: 490)  
JU\*C-G\*T\*C-G\*A\*C\*G\*A\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*G\*C;

(SEQ ID NO: 491)  
EU\*C-G\*T\*C-G\*A\*C\*G\*A\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*G\*C;

(SEQ ID NO: 492)  
T\*T\*C-G\*T\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*G\*C\*G\*T;

(SEQ ID NO: 493)  
T\*EU\*C-G\*T\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*G\*C\*G\*T;

(SEQ ID NO: 494)  
JU\*C-G\*T\*T\*T\*T\*C-G\*G\*C\*G\*C\*G\*C\*G\*T;

-continued

(SEQ ID NO: 495)  
JU\*JU\*C-G\*T\*T\*T\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G\*C\*G\*T;

(SEQ ID NO: 438)  
T\*JU\*C\*G\*T\*T\*T\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G\*C\*G\*T;

(SEQ ID NO: 496)  
EU\*C\*G\*T\*T\*C\*G\*T\*T\*T\*A\*C\*G\*G\*C\*G\*C\*G\*T\*G\*C\*G\*T;

G\*T;

(SEQ ID NO: 497)  
T\*EU\*C\*G\*T\*T\*T\*T\*A\*C\*G\*G\*C\*G\*C\*G\*T\*G\*C\*G\*T;

(SEQ ID NO: 498)  
T\*JU\*C\*G\*T\*T\*T\*T\*A\*C\*G\*G\*C\*G\*C\*G\*T\*G\*C\*G\*T;

(SEQ ID NO: 499)  
JU\*C\*G\*T\*C\*G\*T\*T\*T\*rG\*rU\*rU\*rG\*rU;rG\*rU;

(SEQ ID NO: 500)  
EU\*C-G\*T\*C\*G\*A\*C\*G\*A\*T\*C\*G\*G\*C\*G\*G\*C\*G\*C\*G\*T;

(SEQ ID NO: 500)  
EU\*C\*G\*T\*C\*G\*A\*C\*G\*A\*T\*C\*G\*G\*C\*G\*G\*C\*G\*C\*G\*T;

(SEQ ID NO: 402)  
EU-C-G\*A\*C\*G\*T\*C\*G\*A\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G\*C\*G;

(SEQ ID NO: 402)  
EU-C-G\*A\*C\*G\*T\*C\*G\*A\*T\*C\*G\*G\*C\*G\*C\*G\*C\*G\*C\*G;

(SEQ ID NO:) (SEQ ID NO: 373)  
T\*G\*U\*C\*G\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

(SEQ ID NO: 374)  
T\*G\*T\*C-G\*U\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T\*T;

wherein: - represents phosphodiester internucleotide linkage; \* represents phosphorothioate internucleotide linkage; 2doub represents Doubler2 (Chemgenes); 3 mG represents 3'-O-Methyl-rG; 6NB represents 6-nitro-benzimidazol; BU represents 5-bromo-2'-deoxyuridine; BVU represents 5-(d-bromo-vinyl)-uridine; CU represents 5-chloro-2'-deoxyuridine; E represents 7-deaza-dG; EU represents 5-ethyl-2'-deoxyuridine; F represents 5-fluoro-dU; FF represents 2,4-difluorotoluene; FT represents a,a,a-trifluoro-dT; FU represents 5-fluoro-dU; hex represents hexadecylglycerol; I represents inosine; iT represents inverse nucleotide (3' and 5' switched); JU represents 5-iodo-2'-deoxyuridine; L represents Spacer 18 (hexaethylenglycol phosphate); NI represents nitroindol; NP represents nitropyrrol; PU represents 5-proynyl-dU; teg represents Spacer 9 (triethylenglycol phosphate); U represents Uridine; and Z represents 5-methyl-dC.

**[0144]** Methods to reduce the amount of B cell activation with CpG ODN and increase or maintain the amount of IFN- $\alpha$  induction are not well known to those skilled in the art, but without committing to a particular mechanism of action underlying the invention, it has now been discovered in accordance with the invention that B cell proliferation and IL-10 secretion appear to require a more sustained TLR9 signal compared to that required to induce plasmacytoid dendritic cells (pDC) to secrete IFN- $\alpha$ . Such a sustained TLR9 signal is provided by the B-class CpG ODN to a greater degree than the other CpG ODN classes mentioned above. In addition, the duration of the TLR9 signal can be shortened by positioning phosphodiester (PO) linkages at the CpG ("semi-soft" designs) and/or at other positions within the ODN. The "softest" CpG ODN with the least

sustained B cell activation are those with completely phosphodiester backbones, but these are so rapidly degraded in vivo that the IFN- $\alpha$  response is also compromised, unless the ODN is circular (to protect against exonucleases), or is delivered in a formulation such as virus-like particles (VLP), nanoparticles (NP), immune stimulating complexes (ISCOMs), or the like, which also protects against nucleases.

**[0145]** The immunostimulatory oligonucleotide molecules may have a homogeneous backbone (e.g., entirely phosphodiester (PO) or entirely phosphorothioate (PS)) or a chimeric backbone. An exception to this is the A-class CpG design (and A/E-class) in which the central portion of the ODN including at least 8 nucleotides and preferably 10 or more nucleotides must be phosphodiester for optimal activity. For purposes of the instant invention, a chimeric backbone refers to a partially stabilized backbone, wherein at least one internucleotide linkage is phosphodiester or phosphodiester-like, and wherein at least one other internucleotide linkage is a stabilized internucleotide linkage, wherein the at least one phosphodiester or phosphodiester-like linkage and the at least one stabilized linkage are different. The stabilized linkage(s) is/are preferentially placed at the 5' and 3' ends of the oligonucleotide in order to protect the ends from exonucleases; the phosphodiester linkages are placed in the middle and contribute to inducing a stronger IFN- $\alpha$  response than can easily be achieved with PS alone.

**[0146]** Since boranophosphonate linkages have been reported to be stabilized relative to phosphodiester linkages, for purposes of the chimeric nature of the backbone, boranophosphonate linkages can be classified either as phosphodiester-like or as stabilized, depending on the context. For example, a chimeric backbone according to the instant invention could, in one embodiment, include at least one phosphodiester (phosphodiester or phosphodiester-like) linkage and at least one boranophosphonate (stabilized) linkage. In another embodiment, a chimeric backbone according to the instant invention could include boranophosphonate (phosphodiester or phosphodiester-like) and phosphorothioate (stabilized) linkages. A "stabilized internucleotide linkage" shall mean an internucleotide linkage that is relatively resistant to in vivo degradation (e.g., via an exo- or endo-nuclease), compared to a phosphodiester internucleotide linkage. Preferred stabilized internucleotide linkages include, without limitation, phosphorothioate, phosphorodithioate, methylphosphonate and methylphosphorothioate. Other stabilized internucleotide linkages include, without limitation, peptide, alkyl, diphospho type linkages, and others as described above.

**[0147]** Modified backbones such as phosphorothioates may be synthesized using automated techniques employing either phosphoramidite or H-phosphonate chemistries. Aryl- and alkyl-phosphonates can be made, e.g., as described in U.S. Pat. No. 4,469,863; and alkylphosphotriesters (in which the charged oxygen moiety is alkylated), e.g., as described in U.S. Pat. No. 5,023,243 and European Patent No. 092,574, can be prepared by automated solid phase synthesis using commercially available reagents. Methods for making other DNA backbone modifications and substitutions have been described. Uhlmann E et al. (1990) Chem Rev 90:544; Goodchild J (1990) Bioconjugate Chem 1:165. Methods for preparing chimeric oligonucleotides are also known. For instance patents issued to Uhlmann et al.

have described such techniques, including, for example, U.S. Pat. Nos. 7,566,703, 7,795,235, 8,283,328, and 8,304,396.

[0148] Mixed backbone modified ODN may be synthesized using a commercially available DNA synthesizer and standard phosphoramidite chemistry. F. E. Eckstein, "Oligonucleotides and Analogues—A Practical Approach", IRL Press, Oxford, U K, 1991; and M. D. Matteucci and M. H. Caruthers, Tetrahedron Lett. 21, 719 (1980). After coupling, phosphorothioate (PS) linkages are introduced by sulfurization using the Beaucage reagent (R. P. Iyer, W. Egan, J. B. Regan and S. L. Beaucage, J. Am. Chem. Soc. 112, 1253 (1990)) (0.075 M in acetonitrile) or phenyl acetyl disulfide (PADS) followed by capping with acetic anhydride, 2,6-lutidine in tetrahydrofuran (1:1:8; v: v: v) and N-methylimidazole (16% in tetrahydrofuran). This capping step is performed after the sulfurization reaction to minimize formation of undesired phosphodiester (PO) linkages at positions where a phosphorothioate linkage should be located. In the case of the introduction of a phosphodiester linkage, e.g. at a CpG dinucleotide, the intermediate phosphorous-III is oxidized by treatment with a solution of iodine in water/pyridine. After cleavage from the solid support and final deprotection by treatment with concentrated ammonia (15 hrs at 50° C.), the ODN are analyzed by HPLC on a Gen-Pak Fax column (Millipore-Waters) using a NaCl-gradient (e.g. buffer A: 10 mM NaH<sub>2</sub>PO<sub>4</sub> in acetonitrile/water=1: 4/v: v pH 6.8; buffer B: 10 mM NaH<sub>2</sub>PO<sub>4</sub>, 1.5 M NaCl in acetonitrile/water=1: 4/v: v; 5 to 60% B in 30 minutes at 1 ml/min) or by capillary gel electrophoresis. The ODN can be purified by HPLC or by FPLC on a Source High Performance column (Amersham Pharmacia). HPLC-homogeneous fractions are combined and desalts via a C18 column or by ultrafiltration. The ODN was analyzed by MALDI-TOF mass spectrometry to confirm the calculated mass.

[0149] The oligonucleotides of the invention can also include other modifications. These include nonionic DNA analogs, such as alkyl- and aryl-phosphates (in which the charged phosphonate oxygen is replaced by an alkyl or aryl group), phosphodiester and alkylphosphotriesters, in which the charged oxygen moiety is alkylated. Oligonucleotides which contain diol, such as tetraethyleneglycol or hexaethyleneglycol, at either or both termini have also been shown to be substantially resistant to nuclease degradation.

[0150] In some embodiments the oligonucleotides may be "soft" or "semi-soft" oligonucleotides. A soft oligonucleotide is an immunostimulatory oligonucleotide having a partially stabilized backbone, in which phosphodiester or phosphodiester-like internucleotide linkages occur only within and immediately adjacent to at least one internal pyrimidine-purine dinucleotide (YZ). Preferably YZ is YG, a pyrimidine-guanosine (YG) dinucleotide. The at least one internal YZ dinucleotide itself has a phosphodiester or phosphodiester-like internucleotide linkage. A phosphodiester or phosphodiester-like internucleotide linkage occurring immediately adjacent to the at least one internal YZ dinucleotide can be 5', 3', or both 5' and 3' to the at least one internal YZ dinucleotide.

[0151] In particular, phosphodiester or phosphodiester-like internucleotide linkages involve "internal dinucleotides". An internal dinucleotide in general shall mean any pair of adjacent nucleotides connected by an internucleotide linkage, in which neither nucleotide in the pair of nucleotides is a terminal nucleotide, i.e., neither nucleotide in the

pair of nucleotides is a nucleotide defining the 5' or 3' end of the oligonucleotide. Thus a linear oligonucleotide that is n nucleotides long has a total of n-1 dinucleotides and only n-3 internal dinucleotides. Each internucleotide linkage in an internal dinucleotide is an internal internucleotide linkage. Thus a linear oligonucleotide that is n nucleotides long has a total of n-1 internucleotide linkages and only n-3 internal internucleotide linkages. The strategically placed phosphodiester or phosphodiester-like internucleotide linkages, therefore, refer to phosphodiester or phosphodiester-like internucleotide linkages positioned between any pair of nucleotides in the oligonucleotide sequence. In some embodiments the phosphodiester or phosphodiester-like internucleotide linkages are not positioned between either pair of nucleotides closest to the 5' or 3' end.

[0152] Preferably a phosphodiester or phosphodiester-like internucleotide linkage occurring immediately adjacent to the at least one internal YZ dinucleotide is itself an internal internucleotide linkage. Thus for a sequence N<sub>1</sub> YZ N<sub>2</sub>, wherein N<sub>1</sub> and N<sub>2</sub> are each, independent of the other, any single nucleotide, the YZ dinucleotide has a phosphodiester or phosphodiester-like internucleotide linkage, and in addition (a) N<sub>1</sub> and Y are linked by a phosphodiester or phosphodiester-like internucleotide linkage when N<sub>1</sub> is an internal nucleotide, (b) Z and N<sub>2</sub> are linked by a phosphodiester or phosphodiester-like internucleotide linkage when N<sub>2</sub> is an internal nucleotide, or (c) N<sub>1</sub> and Y are linked by a phosphodiester or phosphodiester-like internucleotide linkage when N<sub>1</sub> is an internal nucleotide and Z and N<sub>2</sub> are linked by a phosphodiester or phosphodiester-like internucleotide linkage when N<sub>2</sub> is an internal nucleotide.

[0153] Soft oligonucleotides according to the instant invention are believed to be relatively susceptible to nuclease cleavage compared to completely stabilized oligonucleotides. Without intending to be bound to a particular theory or mechanism, it is believed that soft oligonucleotides of the invention are susceptible to cleavable resulting in fragments with reduced or no immunostimulatory activity relative to full-length soft oligonucleotides. Incorporation of at least one nuclease-sensitive internucleotide linkage, particularly near the middle of the oligonucleotide, is believed to provide an "off switch" which alters the pharmacokinetics and pharmacodynamics of the oligonucleotide so as to reduce the duration of maximal immunostimulatory activity of the oligonucleotide. In particular, the nuclease-sensitive linkage may reduce the magnitude of NF-κB induction while increasing the magnitude of the IRF3 and/or IRF7 induction. TLR9 activation can lead to strong activation of either or both of the NF-κB pathway (leading to expression of cytokines such as IL-6 and expression of costimulatory molecules) and the IRF3/7 pathways leading to IFN-α secretion. There generally seems to be some antagonism between these pathways. For example, B-class CpG ODN predominantly activate the former, whereas the A-class CpG ODN activate the latter. Strong NF-κB induction is associated with B-class CpG oligos and may lead to increased IL-10 secretion. While this may be useful for systemic CpG oligo therapy, it is not desirable for intratumoral therapy. The increased IRF3/7 induction provided by the nuclease-sensitive internucleotide linkage leads to great production of IFN-α in the tumor microenvironment, which improves the chances for a productive and therapeutic anti-tumor immune response following intratumoral therapy without increasing the production of undesirable IL-10. This reduced half-life of CpG

oligos containing nuclease-sensitive linkages can be of particular value in tissues and in clinical applications in which it is desirable to avoid injury related to chronic local inflammation or immunostimulation, e.g., the kidney, since the oligos are less likely to accumulate in the tissue to high concentrations.

[0154] A semi-soft oligonucleotide is an immunostimulatory oligonucleotide having a partially stabilized backbone, in which phosphodiester or phosphodiester-like internucleotide linkages occur only within at least one internal pyrimidine-purine (YZ) dinucleotide. Semi-soft oligonucleotides generally possess increased immunostimulatory potency relative to corresponding fully stabilized immunostimulatory oligonucleotides. Due to the greater potency of semi-soft oligonucleotides, semi-soft oligonucleotides may be used, in some instances, at lower effective concentrations and have lower effective doses than conventional fully stabilized immunostimulatory oligonucleotides in order to achieve a desired biological effect.

[0155] It is believed that the foregoing properties of semi-soft oligonucleotides generally increase with increasing "dose" of phosphodiester or phosphodiester-like internucleotide linkages involving internal YZ dinucleotides. Thus it is believed, for example, that generally for a given oligonucleotide sequence with four internal YZ dinucleotides, an oligonucleotide with four internal phosphodiester or phosphodiester-like YZ internucleotide linkages is more immunostimulatory than an oligonucleotide with three internal phosphodiester or phosphodiester-like YZ internucleotide linkages, which in turn is more immunostimulatory than an oligonucleotide with two internal phosphodiester or phosphodiester-like YZ internucleotide linkages, which in turn is more immunostimulatory than an oligonucleotide with one internal phosphodiester or phosphodiester-like YZ internucleotide linkage. Importantly, inclusion of even one internal phosphodiester or phosphodiester-like YZ internucleotide linkage often can be advantageous over no internal phosphodiester or phosphodiester-like YZ internucleotide linkage. In addition to the number of phosphodiester or phosphodiester-like internucleotide linkages, the position along the length of the oligonucleotide can also affect potency.

[0156] The soft and semi-soft oligonucleotides will generally include, in addition to the phosphodiester or phosphodiester-like internucleotide linkages at preferred internal positions, 5' and 3' ends that are resistant to degradation. Such degradation-resistant ends can involve any suitable modification that results in an increased resistance against exonuclease digestion over corresponding unmodified ends. For instance, the 5' and 3' ends can be stabilized by the inclusion thereof of at least one phosphate modification of the backbone. In a preferred embodiment, the at least one phosphate modification of the backbone at each end is independently a phosphorothioate, phosphorodithioate, methylphosphonate, or methylphosphorothioate internucleotide linkage. In another embodiment, the degradation-resistant end includes one or more nucleotide units connected by peptide or amide linkages at the 3' end.

[0157] A phosphodiester internucleotide linkage is the type of linkage characteristic of oligonucleotides found in nature. The phosphodiester internucleotide linkage includes a phosphorus atom flanked by two bridging oxygen atoms and bound also by two additional oxygen atoms, one charged and the other uncharged. Phosphodiester internucle-

otide linkage is particularly preferred when it is important to reduce the tissue half-life of the oligonucleotide or to get the strongest possible induction of type I IFN secretion from pDC.

[0158] A phosphodiester-like internucleotide linkage is a phosphorus-containing bridging group that is chemically and/or diastereomerically similar to phosphodiester. Measures of similarity to phosphodiester include susceptibility to nuclease digestion and ability to activate RNase H. Thus, for example phosphodiester, but not phosphorothioate, oligonucleotides are susceptible to nuclease digestion, while both phosphodiester and phosphorothioate oligonucleotides activate RNase H. In a preferred embodiment the phosphodiester-like internucleotide linkage is boranophosphate (or equivalently, boranophosphonate) linkage. U.S. Pat. Nos. 5,177,198; 5,859,231; 6,160,109; 6,207,819; Sergueev et al., (1998) J Am Chem Soc 120:9417-27. In another preferred embodiment the phosphodiester-like internucleotide linkage is diastereomerically pure Rp phosphorothioate. It is believed that diastereomerically pure Rp phosphorothioate is more susceptible to nuclease digestion and is better at activating RNase H than mixed or diastereomerically pure Sp phosphorothioate. Stereoisomers of CpG oligonucleotides are the subject of published PCT application PCT/US99/17100 (WO 00/06588). It is to be noted that for purposes of the instant invention, the term "phosphodiester-like internucleotide linkage" specifically excludes phosphorodithioate and methylphosphonate internucleotide linkages.

[0159] As described above the soft and semi-soft oligonucleotides of the invention may have phosphodiester like linkages between C and G. One example of a phosphodiester-like linkage is a phosphorothioate linkage in an Rp conformation. Oligonucleotide p-chirality can have apparently opposite effects on the immune activity of a CpG oligonucleotide, depending upon the time point at which activity is measured. Krieg et al., Oligonucleotides 2003 13 (6): 491-499. At an early time point of 40 minutes, the Rp but not the Sp stereoisomer of phosphorothioate CpG oligonucleotide induces JNK phosphorylation in mouse spleen cells. In contrast, when assayed at a late time point of 44 hr, the Sp but not the Rp stereoisomer is active in stimulating spleen cell proliferation. This difference in the kinetics and bioactivity of the Rp and Sp stereoisomers does not result from any difference in cell uptake, but rather most likely is due to two opposing biologic roles of the p-chirality. First, the enhanced activity of the Rp stereoisomer compared to the Sp for stimulating immune cells at early time points indicates that the Rp may be more effective at interacting with the CpG receptor, TLR9, or inducing the downstream signaling pathways. On the other hand, the faster degradation of the Rp PS-oligonucleotides compared to the Sp results in a much shorter duration of signaling, so that the Sp PS-oligonucleotides appear to be more biologically active when tested at later time points probably because of the greater nuclease-resistance of the Sp linkage, which provided a more sustained signal through TLR9 for B cell proliferation.

[0160] Thus the oligonucleotides may be heterogeneous in backbone composition thereby containing any possible combination of polymer units linked together.

[0161] The term "oligonucleotide" also encompasses oligonucleotides with substitutions or modifications, such as in the sugars. For example, they include oligonucleotides 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 oligonucleotides may include a 2'-O-alkylated ribose group. In addition, modified oligonucleotides may include sugars such as arabinose or 2'-fluoroarabinose instead of ribose.

[0162] The immunostimulatory oligonucleotides of the instant invention can encompass various chemical modifications and substitutions, in comparison to natural RNA and DNA, involving a phosphodiester internucleotide bridge, or a 13-D-ribose unit. Examples of chemical modifications are known to the skilled person and are described, for example, in Uhlmann E et al. (1990) *Chem Rev* 90:543; "Protocols for Oligonucleotides and Analogs" Synthesis and Properties & Synthesis and Analytical Techniques, S. Agrawal, Ed., Humana Press, Totowa, USA 1993; Crooke S T et al. (1996) *Annu Rev Pharmacol Toxicol* 36:107-129; and Hunziker J et al. (1995) *Mod Synth Methods* 7:331-417. An oligonucleotide according to the invention may have one or more modifications, wherein each modification is located at a particular phosphodiester internucleotide bridge and/or at a particular β-D-ribose unit in comparison to an oligonucleotide of the same sequence which is composed of natural DNA or RNA.

[0163] For example, the invention relates to an oligonucleotide which may comprise one or more modifications and wherein each modification is independently selected from: a) the replacement of a phosphodiester internucleotide bridge located at the 3' and/or the 5' end of a nucleotide by a modified internucleotide bridge; b) the replacement of phosphodiester bridge located at the 3' and/or the 5' end of a nucleotide by a dephospho bridge; c) the replacement of a sugar phosphate unit from the sugar phosphate backbone by another unit; and d) the replacement of a β-D-ribose unit by a modified sugar unit.

[0164] More detailed examples for the chemical modification of an oligonucleotide are as follows:

[0165] A phosphodiester internucleotide bridge located at the 3' and/or the 5' end of a nucleotide can be replaced by a modified internucleotide bridge, wherein the modified internucleotide bridge is for example selected from phosphorothioate, phosphorodithioate, NR<sup>1</sup>R<sup>2</sup>-phosphoramidate, boranophosphate, α-hydroxybenzyl phosphonate, phosphate-(C<sub>1</sub>-C<sub>21</sub>)—O-alkyl ester, phosphate-[(C<sub>6</sub>-C<sub>12</sub>)aryl-(C<sub>1</sub>-C<sub>21</sub>)]—O-alkylJester, (C<sub>1</sub>-C<sub>8</sub>)alkylphosphonate and/or (C<sub>6</sub>-C<sub>12</sub>) arylphosphonate bridges, (C<sub>7</sub>-C<sub>12</sub>)-α-hydroxymethyl-aryl (e.g., disclosed in WO 95/01363), wherein (C<sub>6</sub>-C<sub>12</sub>)aryl, (C<sub>6</sub>-C<sub>20</sub>)aryl and (C<sub>6</sub>-C<sub>14</sub>)aryl are optionally substituted by halogen, alkyl, alkoxy, nitro, cyano, and where R<sup>1</sup> and R<sup>2</sup> are, independently of each other, hydrogen, (C<sub>1</sub>-C<sub>18</sub>)-alkyl, (C<sub>6</sub>-C<sub>20</sub>)-aryl, (C<sub>6</sub>-C<sub>14</sub>)-aryl-(C<sub>1</sub>-C<sub>5</sub>)-alkyl, preferably hydrogen, (C<sub>1</sub>-C<sub>8</sub>)-alkyl, preferably (C<sub>1</sub>-C<sub>4</sub>)-alkyl and/or methoxyethyl, or R<sup>1</sup> and R<sup>2</sup> form, together with the nitrogen atom carrying them, a 5-6-membered heterocyclic ring which can additionally contain a further heteroatom from the group O, S and N.

[0166] The replacement of a phosphodiester bridge located at the 3' and/or the 5' end of a nucleotide by a dephospho bridge (dephospho bridges are described, for example, in Uhlmann E and Peyman A in "Methods in Molecular Biology", Vol. 20, "Protocols for Oligonucleotides and Analogs", S. Agrawal, Ed., Humana Press,

Totowa 1993, Chapter 16, pp. 355 ff), wherein a dephospho bridge is for example selected from the dephospho bridges formacetal, 3'-thioformacetal, methylhydroxylamine, oxime, methylenedimethyl-hydrazone, dimethylenesulfone and/or silyl groups.

[0167] A sugar phosphate unit (i.e., a β-D-ribose and phosphodiester internucleotide bridge together forming a sugar phosphate unit) from the sugar phosphate backbone (i.e., a sugar phosphate backbone is composed of sugar phosphate units) can be replaced by another unit, wherein the other unit is for example suitable to build up a "morpholino-derivative" oligomer (as described, for example, in Stirchak E P et al. (1989) *Oligonucleotides Res* 17:6129-41), that is, e.g., the replacement by a morpholino-derivative unit; or to build up a polyamide oligonucleotide ("PNA"; as described for example, in Nielsen P E et al. (1994) *Bioconjug Chem* 5:3-7), that is, e.g., the replacement by a PNA backbone unit, e.g., by 2-aminoethylglycine.

[0168] A 3-ribose unit or a β-D-2'-deoxyribose unit can be replaced by a modified sugar unit, wherein the modified sugar unit is for example selected from β-D-ribose, α-D-2'-deoxyribose, L-2'-deoxyribose, 2'-F-2'-deoxyribose, 2'-F-arabinose, 2'-O-(C<sub>1</sub>-C<sub>6</sub>)alkyl-ribose, preferably 2'-O-(C<sub>1</sub>-C<sub>6</sub>)alkyl-ribose is 2'-O-methylribose, 2'-O-(C<sub>2</sub>-C<sub>6</sub>) alkenyl-ribose, 2'-[O-(C<sub>1</sub>-C<sub>6</sub>) alkyl-O-(C<sub>1</sub>-C<sub>6</sub>)alkyl]-ribose, 2'-NH<sub>2</sub>-2'-deoxyribose, β-D-xylo-furanose, α-arabinofuranose, 2,4-dideoxy-β-D-erythro-hexo-pyranose, and carbocyclic (described, for example, in Froehler J (1992) *J Am Chem Soc* 114:8320) and/or open-chain sugar analogs (described, for example, in Vandendriessche et al. (1993) *Tetrahedron* 49:7223) and/or bicyclosugar analogs (described, for example, in Tarkov M et al. (1993) *Helv Chim Acta* 76:481).

[0169] In some embodiments the sugar is 2'-O-methylribose, particularly for one or both nucleotides linked by a phosphodiester or phosphodiester-like internucleotide linkage.

[0170] In particular sequences described herein a set of modified bases is defined. For instance the letter Y is used to refer to a nucleotide containing a cytosine or a modified cytosine. A modified cytosine as used herein is a naturally occurring or non-naturally occurring pyrimidine base analog of cytosine which can replace this base without impairing the immunostimulatory activity of the oligonucleotide. Modified cytosines include but are not limited to 5-substituted cytosines (e.g., 5-methyl-cytosine, 5-fluoro-cytosine, 5-chloro-cytosine, 5-bromo-cytosine, 5-iodo-cytosine, 5-hydroxy-cytosine, 5-hydroxymethyl-cytosine, 5-difluoromethyl-cytosine, and unsubstituted or substituted 5-alkynyl-cytosine), 6-substituted cytosines, N4-substituted cytosines (e.g., N4-ethyl-cytosine), 5-aza-cytosine, 2-mercaptop-cytosine, isocytosine, pseudo-isocytosine, cytosine analogs with condensed ring systems (e.g., N,N'-propylene cytosine or phenoxazine), and uracil and its derivatives (e.g., 5-fluoro-uracil, 5-bromo-uracil, 5-bromovinyl-uracil, 4-thio-uracil, 5-hydroxy-uracil, 5-propynyl-uracil). Some of the preferred cytosines include 5-methyl-cytosine, 5-fluoro-cytosine, 5-hydroxy-cytosine, 5-hydroxymethyl-cytosine, and N4-ethyl-cytosine. In another embodiment of the invention, the cytosine base is substituted by a universal base (e.g., 3-nitropyrrole, P-base), an aromatic ring system (e.g., fluorobenzene or difluorobenzene) or a hydrogen atom (dSpacer).

**[0171]** The letter Z is used to refer to guanine or a modified guanine base. A modified guanine as used herein is a naturally occurring or non-naturally occurring purine base analog of guanine which can replace this base without impairing the immunostimulatory activity of the oligonucleotide. Modified guanines include but are not limited to 7-deazaguanine, 7-deaza-7-substituted guanine (such as 7-deaza-7-(C2-C6) alkynylguanine), 7-deaza-8-substituted guanine, hypoxanthine, N2-substituted guanines (e.g., N2-methyl-guanine), 5-amino-3-methyl-3H,6H-thiazolo[4,5-d]pyrimidine-2,7-dione, 2,6-diaminopurine, 2-aminopurine, purine, indole, adenine, substituted adenines (e.g., N6-methyladenine, 8-oxo-adenine) 8-substituted guanine (e.g., 8-hydroxyguanine and 8-bromoguanine), and 6-thioguanine. In another embodiment of the invention, the guanine base is substituted by a universal base (e.g., 4-methyl-indole, 5-nitro-indole, and K-base), an aromatic ring system (e.g. benzimidazole or dichloro-benzimidazole, 1-methyl-1H-[1,2,4]triazole-3-carboxylic acid amide) or a hydrogen atom (dSpacer).

**[0172]** The oligonucleotides may have one or more accessible 5' ends. It is possible to create modified oligonucleotides having two such 5' ends. This may be achieved, for instance by attaching two oligonucleotides through a 3'-3' linkage to generate an oligonucleotide having one or two accessible 5' ends. The 3'3'-linkage may be a phosphodiester, phosphorothioate or any other modified internucleotide bridge. Methods for accomplishing such linkages are known in the art. For instance, such linkages have been described in Seliger, H. et al., Oligonucleotide analogs with terminal 3'-3' and 5'-5'-internucleotidic linkages as antisense inhibitors of viral gene expression, *Nucleosides & Nucleotides* (1991), 10 (1-3), 469-77; and Jiang, et al., Pseudo-cyclic oligonucleotides: *in vitro* and *in vivo* properties, *Bioorganic & Medicinal Chemistry* (1999), 7 (12), 2727-2735.

**[0173]** Additionally, 3'3'-linked oligonucleotides where the linkage between the 3'-terminal nucleotides is not a phosphodiester, phosphorothioate or other modified bridge, can be prepared using an additional spacer, such as tri- or tetra-ethyleneglycol phosphate moiety (Durand, M. et al., Triple-helix formation by an oligonucleotide containing one (dA) 12 and two (dT) 12 sequences bridged by two hexaethylene glycol chains, *Biochemistry* (1992), 31 (38), 9197-204, U.S. Pat. Nos. 5,658,738, and 5,668,265). Alternatively, the non-nucleotidic linker may be derived from ethanediol, propanediol, or from an abasic deoxyribose (dSpacer) unit (Fontanel, Marie Laurence et al., Sterical recognition by T4 polynucleotide kinase of non-nucleosidic moieties 5'-attached to oligonucleotides; *Oligonucleotides Research* (1994), 22 (11), 2022-7) using standard phosphoramidite chemistry. The non-nucleotidic linkers can be incorporated once or multiple times, or combined with each other allowing for any desirable distance between the 3'-ends of the two ODNs to be linked.

**[0174]** The oligonucleotides may be partially resistant to degradation (e.g., are stabilized). A "stabilized oligonucleotide molecule" shall mean an oligonucleotide that is relatively resistant to *in vivo* degradation (e.g. via an exo- or endo-nuclease). Oligonucleotide stabilization can be accomplished via backbone modifications. Oligonucleotides having phosphorothioate linkages provide maximal protection for the oligonucleotide from degradation by intracellular exo- and endo-nucleases. Other modified oligonucleotides include phosphodiester modified oligonucleotides, combi-

nations of phosphodiester and phosphorothioate oligonucleotide, methylphosphonate, methylphosphorothioate, phosphorodithioate, p-ethoxy, and combinations thereof. Oligonucleotides which contain diol, such as tetraethylenglycol or hexaethylenglycol, at either or both termini have also been shown to be substantially resistant to nucleic acid degradation. Circular ODN are protected against exonuclease degradation. For example, the Mologen double stem-loop immunomodulator MGN1703 (formerly dSLIM-30L1) is a covalently closed 116-nucleotide dumbbell-shaped CpG-containing phosphodiester backbone oligonucleotide having the sequence 5'-AGGTGGTAACCCCTAGGGGTTACCACCTTCAT-TGGAAAACGTTCTCGGGGC GTTCT-TAGGTGGTAACCCCTAGGGGTTACCACCTTCATTG-GAAAACGTTCTCG GGGCCTT-3' (SEQ ID NO:501). Schmidt M et al., *Allergy* 2006 61:56-63; Kapp, K et al., *Mol Ther Nucleic Acids* 2014 3: e170.

**[0175]** The immunostimulatory oligonucleotides may also contain one or more unusual linkages between the nucleotide or nucleotide-analogous moieties. The usual internucleoside linkage is a 3'5'-linkage. All other linkages are considered to be unusual internucleoside linkages, such as 2'5', 5'5', 3'3', 2'2', 2'3'-linkages. The nomenclature 2' to 5' is chosen according to the carbon atom of ribose. However, if unnatural sugar moieties are employed, such as ring-expanded sugar analogs (e.g. hexanose, cyclohexene or pyranose) or bi- or tricyclic sugar analogs, then this nomenclature changes according to the nomenclature of the monomer. In 3'-deoxy- $\beta$ -D-ribopyranose analogs (also called p-DNA), the mononucleotides are e.g. connected via a 4'2'-linkage.

**[0176]** If the oligonucleotide contains one 3'3'-linkage, then this oligonucleotide may have two unlinked 5'-ends. Similarly, if the oligonucleotide contains one 5'5'-linkage, then this oligonucleotide may have two unlinked 3'-ends. The accessibility of unlinked ends of nucleotides may be better accessible by their receptors. Both types of unusual linkages (3'3' and 5'5') were described by Ramalho Ortigao et al. (*Antisense Research and Development* (1992) 2, 129-46), whereby oligonucleotides having a 3'3'-linkage were reported to show enhanced stability towards cleavage by nucleases.

**[0177]** Different types of linkages can also be combined in one molecule which may lead to branching of the oligomer. If one part of the oligonucleotide is connected at the 3'-end via a 3'3'-linkage to a second oligonucleotide part and at the 2'-end via a 2'3'-linkage to a third part of the molecule, this results e.g. in a branched oligonucleotide with three 5'-ends (3'3', 2'3'-branched).

**[0178]** In certain embodiments of the invention, a sustained release delivery system, including for example nanoparticles, ISCOMS, VLP, and dendrimers may be used to formulate and deliver a CpG-ODN. In one embodiment, a VLP as described in U.S. Pat. Nos. 9,518,095, 7,888,098, 9,404,126 (each incorporated by reference in their entireties) is contemplated for use in the methods of the present disclosure. (See also, e.g., Manolova et al., *Eur. J. Immunol.*, 2008, 38:1404-1413; Gomes et al., *Vaccines*, 2017, 5,6; Gomes et al., *Front. Immunol.*, 2017; 8:226; and Mohsen et al., *J. Controlled Release*, 251, 2017, 92-100).

### III. Checkpoint Inhibitors

#### A. PD-1

**[0179]** Programmed death-1 receptor (PD-1), also known as CD279, is a type 1 membrane protein expressed on activated T cells (including CD8<sup>+</sup> T cells), B cells, and macrophages. Its cognate ligands are PD-L1 and PD-L2, and binding of PD-1 particularly by PD-L1 blocks “Signal 3” in T cells and potently inhibits the effector arm of an adaptive immune response, for example by leading to the death of T cells expressing PD-1.

**[0180]** In humans, PD-1 is a 268-amino acid polypeptide having an amino acid sequence published as GenBank Accession No. NP\_005009. The protein includes an extracellular IgV domain, transmembrane domain, and intracellular domain having two phosphorylation sites.

**[0181]** The  $K_D$  for interaction between PD-1 and PD-L1 is 770 nM.

**[0182]** In preferred embodiments of the invention, the antibody inhibits binding between PD-1 and PD-L1. Preferably, the antibody can inhibit binding with PD-L1 with an  $IC_{50}$  of about 100 nM or lower; more preferably, about 10 nM or lower, for example about 5 nM or lower; yet more preferably, about 2 nM or lower; or even more preferably, for example, about 1 nM or lower.

**[0183]** Further, in another embodiment, the anti-PD-1 antibody has a binding affinity for PD-1 that is at least as strong as that of PD-L1. In certain embodiments, the anti-PD-1 antibody has a binding affinity for PD-1 that is at least 10 times as strong as that of PD-L1. In certain embodiments, the anti-PD-1 antibody has a binding affinity for PD-1 that is at least 100 times as strong as that of PD-L1. In certain embodiments, the anti-PD-1 antibody has a binding affinity for PD-1 that is at least 1000 times as strong as that of PD-L1.

**[0184]** Anti-PD-1 antibodies are known in the art and include, for example, those disclosed in U.S. Pat. No. 6,808,710 to Wood et al., U.S. Pat. No. 7,488,802 to Collins et al., and U.S. Pat. No. 8,728,474 to Honjo et al. Anti-PD-1 antibodies are commercially available as pembrolizumab (formerly known as lambrolizumab and MK-3475, KEYTRUDA®, Merck,  $K_D$  29 pM) and nivolumab (OPDIVO®, Bristol-Myers Squibb,  $K_D$  2.6 nM). Additional anti-PD-1 antibodies currently under development include pidilizumab (CT-011, Cure Tech).

#### B. PD-L1

**[0185]** Programmed death-ligand 1 receptor (PD-L1), also known as CD274 and B7 homolog 1 (B7-H1), is a type 1 membrane protein expressed on activated T cells (including CD8<sup>+</sup> T cells and so-called tumor-infiltrating lymphocytes (TIL cells)), B cells, macrophages, and dendritic cells, as well as on many types of tumor cells. Its cognate ligands are PD-1 and B7.1 (CD80), and binding of PD-1 by PD-L1 blocks “Signal 3” in T cells and can potently inhibit the T cell effector functions mediating an adaptive immune response, for example by leading to the death of T cells expressing PD-1.

**[0186]** PD-L1 expression is upregulated on T cells, NK cells, macrophages, myeloid dendritic cells, B cells, epithelial cells, and vascular endothelial cells in response to

interferon gamma (IFN- $\gamma$ ). PD-L1 expression is also upregulated on tumors, e.g., renal cell carcinoma and ovarian cancer, in response to IFN- $\gamma$ .

**[0187]** In humans, PD-L1 is expressed in either of two isoforms, a longer isoform a or a shorter isoform b. Isoform a is a 290-amino acid polypeptide having an amino acid sequence published as GenBank Accession No. NP\_054862; the mature peptide comprises amino acid residues 19-290, with residues 239-259 representing the transmembrane domain. Isoform b is a 176-amino acid polypeptide having an amino acid sequence published as GenBank NP\_001254635; the mature peptide comprises amino acid residues 19-259.

**[0188]** As mentioned above, the  $K_D$  for interaction between PD-1 and PD-L1 is 770 nM.

**[0189]** In preferred embodiments of the invention, the antibody inhibits binding between PD-1 and PD-L1. Preferably, the antibody can inhibit binding with PD-1 with an  $IC_{50}$  of about 100 nM or lower; more preferably, about 10 nM or lower, for example about 5 nM or lower; yet more preferably, about 2 nM or lower; or even more preferably, for example, about 1 nM or lower.

**[0190]** Further, in another embodiment, the anti-PD-L1 antibody has a binding affinity for PD-L1 that is at least as strong as that of PD-1. In certain embodiments, the anti-PD-L1 antibody has a binding affinity for PD-L1 that is at least 10 times as strong as that of PD-1. In certain embodiments, the anti-PD-L1 antibody has a binding affinity for PD-L1 that is at least 100 times as strong as that of PD-1. In certain embodiments, the anti-PD-L1 antibody has a binding affinity for PD-L1 that is at least 1000 times as strong as that of PD-1.

**[0191]** Anti-PD-L1 antibodies are known in the art and include, for example, those disclosed in U.S. Pat. No. 7,943,743 to Korman et al. While no anti-PD-L1 antibodies are yet approved by the FDA for commercialization in the United States, several anti-PD-L1 antibodies are currently under development in human clinical trials, including MPDL3280A (Genetech/Roche,  $K_D$  0.4 nM), BMS-936559 (Bristol-Myers Squibb), and MEDI-4736 (AstraZeneca).

#### C. CTLA-4

**[0192]** Cytotoxic T-lymphocyte-associated protein 4 (CTLA-4), also known as CTIA4 or CD152, is a membrane protein expressed on T cells and regulatory T cells (Treg). Its cognate ligands include B7-1 (CD80) and B7-2 (CD86) on antigen-presenting cells (APC). Binding of B7-1 or B7-2 by CTLA-4 blocks “Signal 2” in T cells and inhibits the initiation of an adaptive immune response.

**[0193]** In humans, CTLA-4 is encoded in various isoforms, including one with an amino acid sequence published as GenBank Accession No. NP\_001032720.

**[0194]** A preferred anti-CTLA-4 antibody is an antibody that specifically binds to human CTLA-4. More particularly, the anti-CTLA-4 antibody specifically binds to an epitope in the extracellular domain of human CTLA-4 and inhibits binding between CTLA-4 and one or both of its cognate ligands B7-1 and B7-2.

**[0195]** A preferred anti-CTLA-4 antibody is a human antibody that specifically binds to human CTLA-4. More particularly, the anti-CTLA-4 antibody specifically binds to an epitope in the extracellular domain of human CTLA-4 and inhibits binding between CTLA-4 and one or both of its cognate ligands B7-1 and B7-2. Exemplary human anti-

CTLA-4 antibodies are described in detail in International Application No. PCT/US99/30895, published on Jun. 29, 2000 as WO 00/37504; European Patent Appl. No. EP 1262193 A1, published Apr. 12, 2002; U.S. patent application Ser. No. 09/472,087, now issued as U.S. Pat. No. 6,682,736, to Hanson et al.; U.S. patent application Ser. No. 09/948,939, published as US 2002/0086014; U.S. patent application Ser. No. 11/988,396, published as US 2009/0117132; and U.S. patent application Ser. No. 13/168,206, published as US 2012/0003179, the entire disclosures of which are incorporated herein by reference. Such antibodies include, but are not limited to, 3.1.1, 4.1.1, 4.8.1, 4.10.2, 4.13.1, 4.14.3, 6.1.1, 11.2.1, 11.6.1, 11.7.1, 12.3.1.1, and 12.9.1.1, as well as MDX-010. Human antibodies provide a substantial advantage in the treatment methods of the present disclosure, as they are expected to minimize the immunogenic and allergic responses that are associated with use of non-human antibodies in human patients.

[0196] Anti-CTLA-4 antibodies specifically include ipilimumab (YERVOY®, Bristol-Myers Squibb).

[0197] Characteristics of useful human anti-CTLA-4 antibodies of the invention are extensively discussed in WO 00/37504, EP 1262193, and U.S. Pat. No. 6,682,736 as well as U.S. Patent Application Publication Nos. US2002/0086014 and US2003/0086930, and the amino and nucleic acid sequences set forth therein are incorporated by reference herein in their entirety. Briefly, the antibodies of the invention include antibodies having amino acid sequences of an antibody such as, but not limited to, antibody 3.1.1, 4.1.1, 4.8.1, 4.10.2, 4.13.1, 4.14.3, 6.1.1, 11.2.1, 11.6.1, 11.7.1, 12.3.1.1, 12.9.1.1, and MDX-010. The invention also relates to antibodies having the amino acid sequences of the CDRs of the heavy and light chains of these antibodies, as well as those having changes in the CDR regions, as described in the above-cited applications and patent. The invention also concerns antibodies having the variable regions of the heavy and light chains of those antibodies. In another embodiment, the antibody is selected from an antibody having the full length, variable region, or CDR, amino acid sequences of the heavy and light chains of antibodies 3.1.1, 4.1.1, 4.8.1, 4.10.2, 4.13.1, 4.14.3, 6.1.1, 11.2.1, 11.6.1, 11.7.1, 12.3.1.1, and 12.9.1.1, and MDX-010.

[0198] Methods of administering anti-CTLA-4 antibodies are well known in the art. Most commonly the antibodies are given by systemic administration, generally IV. In animal models but not humans, intra-tumoral administration also has been explored as a way to reduce doses and toxicity (Fransen M F et al., *Oncoimmunology* 2013 Nov. 1; 2 (11): e26493).

[0199] In one embodiment, the invention comprises an antibody-therapeutic agent combination comprising a human anti-CTLA-4 antibody disclosed in U.S. patent application Ser. No. 09/948,939, published as U.S. Patent Application Publication No. 2002/0086014 and No. 2003/0086930, and references cited therein, including, but not limited to, MAAb 10D1 (MDX-010, Medarex, Princeton, N.J.). Even more preferably, the anti-CTLA-4 antibody is MDX-010. Alternatively, the anti-CTLA-4 antibody is 11.2.1 (Ticilimumab; CP-675,206).

[0200] In preferred embodiments of the invention, the antibody inhibits binding between CTLA-4 and B7-1, B7-2, or both. Preferably, the antibody can inhibit binding with B7-1 with an  $IC_{50}$  of about 100 nM or lower; more preferably, about 10 nM or lower, for example about 5 nM or

lower; yet more preferably, about 2 nM or lower; or even more preferably, for example, about 1 nM or lower. Likewise, the antibody can inhibit binding with B7-2 with an  $IC_{50}$  of about 100 nM or lower; more preferably, 10 nM or lower, for example, even more preferably, about 5 nM or lower; yet more preferably, about 2 nM or lower; or even more preferably, about 1 nM or lower.

[0201] Further, in another embodiment, the anti-CTLA-4 antibody has a binding affinity for CTLA-4 that is at least as strong as that of B7-1. In certain embodiments, the anti-CTLA-4 antibody has a binding affinity for CTLA-4 that is at least 10 times as strong as that of B7-1. In certain embodiments, the anti-CTLA-4 antibody has a binding affinity for CTLA-4 that is at least 100 times as strong as that of B7-1. In certain embodiments, the anti-CTLA-4 antibody has a binding affinity for CTLA-4 that is at least 1000 times as strong as that of B7-1.

[0202] Further, in another embodiment, the anti-CTLA-4 antibody has a binding affinity for CTLA-4 that is at least as strong as that of B7-2. In certain embodiments, the anti-CTLA-4 antibody has a binding affinity for CTLA-4 that is at least 10 times as strong as that of B7-2. In certain embodiments, the anti-CTLA-4 antibody has a binding affinity for CTLA-4 that is at least 100 times as strong as that of B7-2. In certain embodiments, the anti-CTLA-4 antibody has a binding affinity for CTLA-4 that is at least 1000 times as strong as that of B7-2.

[0203] Further, in another embodiment, the anti-CTLA-4 antibody has a binding affinity for CTLA-4 of about  $10^{-8}$  M, or greater affinity, more preferably, about  $10^{-9}$  M or greater affinity, more preferably, about  $10^{-10}$  M or greater affinity, and even more preferably, about  $10^{-11}$  M or greater affinity.

[0204] In certain embodiments, the anti-CTLA-4 antibody can compete for binding with an antibody having heavy and light chain amino acid sequences of an antibody selected from the group consisting of 4.1.1, 6.1.1, 11.2.1, 4.13.1 and 4.14.3. Further, in certain embodiments, the anti-CTLA-4 antibody can compete for binding with an MDX-010 antibody.

[0205] In another embodiment, the anti-CTLA-4 antibody preferably cross-competes with an antibody having a heavy and light chain sequence, a variable heavy and a variable light chain sequence, and/or the heavy and light CDR sequences of antibody 4.1.1, 4.13.1, 4.14.3, 6.1.1 or 11.2.1. For example, the antibody can bind to the epitope to which an antibody that has heavy and light chain amino acid sequences, variable sequences and/or CDR sequences, of an antibody selected from the group consisting of 4.1.1, 4.13.1, 4.14.3, 6.1.1, or 11.2.1 binds. In another embodiment, the anti-CTLA-4 antibody cross-competes with an antibody having heavy and light chain sequences, or antigen-binding sequences, of MDX-010.

[0206] In another embodiment, the invention is practiced using an anti-CTLA-4 antibody that comprises a heavy chain comprising the amino acid sequences of CDR1, CDR2, and CDR3, and a light chain comprising the amino acid sequences of CDR1, CDR2, and CDR3, of an antibody selected from the group consisting of 3.1.1, 4.1.1, 4.8.1, 4.10.2, 4.13.1, 4.14.3, 6.1.1, 11.2.1, 11.6.1, 11.7.1, 12.3.1.1, and 12.9.1.1, or sequences having changes from said CDR sequences selected from the group consisting of conservative changes, wherein the conservative changes are selected from the group consisting of replacement of nonpolar residues by other nonpolar residues, replacement of polar

charged residues other polar uncharged residues, replacement of polar charged residues by other polar charged residues, and substitution of structurally similar residues; non-conservative substitutions, wherein the non-conservative substitutions are selected from the group consisting of substitution of polar charged residue for polar uncharged residues and substitution of nonpolar residues for polar residues, additions and deletions.

[0207] In a further embodiment of the invention, the antibody contains fewer than 10, 7, 5, or 3 amino acid changes from the germline sequence in the framework or CDR regions. In another embodiment, the antibody contains fewer than 5 amino acid changes in the framework regions and fewer than 10 changes in the CDR regions. In one preferred embodiment, the antibody contains fewer than 3 amino acid changes in the framework regions and fewer than 7 changes in the CDR regions. In a preferred embodiment, the changes in the framework regions are conservative and those in the CDR regions are somatic mutations.

[0208] In another embodiment, the antibody has at least 80%, more preferably, at least 85%, even more preferably, at least 90%, yet more preferably, at least 95%, more preferably, at least 99%, sequence identity over the heavy and light chain CDR1, CDR2 and CDR3 sequences with the CDR sequences of antibody 3.1.1, 4.1.1, 4.8.1, 4.10.2, 4.13.1, 4.14.3, 6.1.1, 11.2.1, 11.6.1, 11.7.1, 12.3.1.1, and 12.9.1.1. Even more preferably, the antibody shares 100% sequence identity over the heavy and light chain CDR1, CDR2 and CDR3 with the sequence of antibody 3.1.1, 4.1.1, 4.8.1, 4.10.2, 4.13.1, 4.14.3, 6.1.1, 11.2.1, 11.6.1, 11.7.1, 12.3.1.1, and 12.9.1.1.

[0209] In yet another embodiment, the antibody has at least 80%, more preferably, at least 85%, even more preferably, at least 90%, yet more preferably, at least 95%, more preferably, at least 99%, sequence identity over the heavy and light chain variable region sequences with the variable region sequences of antibody 3.1.1, 4.1.1, 4.8.1, 4.10.2, 4.13.1, 4.14.3, 6.1.1, 11.2.1, 11.6.1, 11.7.1, 12.3.1.1, and 12.9.1.1. Even more preferably, the antibody shares 100% sequence identity over the heavy and light chain variable region sequences with the sequences of antibody 3.1.1, 4.1.1, 4.8.1, 4.10.2, 4.13.1, 4.14.3, 6.1.1, 11.2.1, 11.6.1, 11.7.1, 12.3.1.1, and 12.9.1.1.

#### D. Other Checkpoint Inhibitors

[0210] In addition to those listed above, other checkpoints are known in the art and their inhibitors are included in the invention. For example, BTLA provides a negative signal in response to HVEM, and TIM3 provides a negative signal in response to Gal9. Adenosine can trigger suppressive effects through the adenosine A2a receptor, and IDO and TDO are well known immunosuppressive pathways thought to be involved in anti-tumor immunity. LAG3 binds to MHC class II with higher affinity than CD4. LAG3 negatively regulates cellular proliferation, activation, and homeostasis of T cells, in a fashion similar to CTLA-4 and PD-1, and it has been reported to play a role in Treg suppressive function. LAG3 also helps maintain CD8<sup>+</sup> T cells in a tolerogenic state and, working with PD-1, helps maintain CD8 exhaustion during chronic viral infection. LAG3 is known to be involved in the maturation and activation of dendritic cells. Additional checkpoint inhibitors for use in the invention include, without limitation, antibodies and antigen-binding fragments thereof, capable of binding specifically to any one or more

of BTLA, TIM3, and LAG3. Also contemplated by the invention are bispecific antibodies and bispecific antigen-binding fragments thereof which are capable of binding specifically to any one or more of BTLA, TIM3, and LAG3. [0211] The invention contemplates combinations of a TLR9 agonist and a checkpoint inhibitor, where the checkpoint inhibitor can be a single CPI or any combination of two or more CPI. While it is likely that in clinical use only one or only a pair of CPI will be used, the invention contemplates using any one, any two, any three, or any four or more CPI selected from, for example, inhibitors of CTLA-4, PD-1, PD-L1, TIM3, LAG3, or BTLA.

#### E. Origin of Antibodies

[0212] While the anti-PD-1, anti-PD-L1, and anti-CTLA-4 antibodies discussed previously herein may be preferred, the skilled artisan, based upon the disclosure provided herein, would appreciate that the invention encompasses a wide variety of anti-PD-1, anti-PD-L1, and anti-CTLA-4 antibodies and is not limited to these particular antibodies. More particularly, while human antibodies are preferred for use in humans, the invention is in no way limited to human antibodies; rather, the invention encompasses useful antibodies regardless of species origin, and includes, among others, chimeric humanized and/or primatized antibodies. Also, although certain of the antibodies exemplified herein were obtained using a transgenic mammal, e.g., a mouse comprising a human immune repertoire, the skilled artisan, based upon the disclosure provided herein, would understand that the present disclosure is not limited to an antibody produced by this or by any other particular method. Instead, the invention includes an anti-PD-1, anti-PD-L1, or anti-CTLA-4 antibody produced by any method, including, but not limited to, a method known in the art (e.g., screening phage display libraries, and the like) or to be developed in the future for producing an anti-PD-1, anti-PD-L1, or anti-CTLA-4 antibody of the invention. Based upon the extensive disclosure provided herein and in, e.g., U.S. Pat. No. 6,682,736 to Bedian et al., and U.S. Pat. App. Pub. No. 2002/0088014, one skilled in the art can readily produce and identify an anti-PD-1, anti-PD-L1, or anti-CTLA-4 antibody useful for treatment of cancer in combination with a CpG ODN using the novel methods disclosed herein.

[0213] The present disclosure encompasses human antibodies produced using a transgenic non-human mammal, i.e., XenoMouse<sup>TM</sup> (Abgenix, Inc., Fremont, Calif.) as disclosed in the U.S. Pat. No. 6,682,736, to Hanson et al.

[0214] Another transgenic mouse system for production of "human" antibodies is referred to as "HuMAb-Mouse<sup>TM</sup>" (Medarex, Princeton, N.J.), which contain human immunoglobulin gene miniloci that encode unrearranged human heavy (mu and gamma) and kappa light chain immunoglobulin sequences, together with targeted mutations that inactivate the endogenous mu and kappa chain loci (Lonberg et al. Nature 368:856-859 (1994), and U.S. Pat. No. 5,770,429).

[0215] However, the invention uses human anti-PD-1, anti-PD-L1, or anti-CTLA-4 antibodies produced using any transgenic mammal such as, but not limited to, the Kirin TC Mouse<sup>TM</sup> (Kirin Beer Kabushiki Kaisha, Tokyo, Japan) as described in, e.g., Tomizuka et al., Proc Natl Acad Sci USA 97:722 (2000); Kuroiwa et al., Nature Biotechnol 18:1086 (2000); U.S. Patent Application Publication No. 2004/

0120948, to Mikayama et al.; and the HuMAB-Mouse™ (Medarex, Princeton, N.J.) and XenoMouse™ (Abgenix, Inc., Fremont, Calif.), supra. Thus, the invention encompasses using an anti-PD-1, anti-PD-L1, or anti-CTLA-4 antibody produced using any transgenic or other non-human animal.

[0216] Moreover, while the preferred method of producing a human anti-PD-1, anti-PD-L1, or anti-CTLA-4 antibody comprises generation of the antibodies using a non-human transgenic mammal comprising a human immune repertoire, the present disclosure is in no way limited to this approach. Rather, as would be appreciated by one skilled in the art once armed with the disclosure provided herein, the invention encompasses using any method for production of a human, or any other antibody specific for PD-1, PD-L1, or CTLA-4 produced according to any method known in the art or to be developed in the future for production of antibodies that specifically bind an antigen of interest.

[0217] Human antibodies can be developed by methods that include, but are not limited to, use of phage display antibody libraries. For example, using these techniques, antibodies can be generated to CTLA-4-expressing cells, CTLA-4 itself, forms of CTLA-4, epitopes or peptides thereof, and expression libraries thereto (see e.g. U.S. Pat. No. 5,703,057), which can thereafter be screened for the activities described above.

[0218] In another embodiment, the antibodies employed in methods of the invention are not fully human, but "humanized". In particular, murine antibodies or antibodies from other species can be "humanized" or "primatized" using techniques well known in the art. See, e.g., Winter and Harris Immunol. Today 14:43-46 (1993), Wright et al. Crit. Reviews in Immunol. 12:125-168 (1992), and U.S. Pat. No. 4,816,567, to Cabilly et al., and Mage and Lamoyi in Monoclonal Antibody Production Techniques and Applications pp. 79-97, Marcel Dekker, Inc., New York, N.Y. (1987).

[0219] As will be appreciated based upon the disclosure provided herein, antibodies for use in the invention can be obtained from a transgenic non-human mammal, and hybridomas derived therefrom, but can also be expressed in cell lines other than hybridomas.

[0220] Mammalian cell lines available as hosts for expression are well known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to Chinese hamster ovary (CHO) cells, NSO, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), and human hepatocellular carcinoma cells (e.g., Hep G2). Non-mammalian prokaryotic and eukaryotic cells can also be employed, including bacterial, yeast, insect, and plant cells.

[0221] Various expression systems can be used as well known in the art, such as, but not limited to, those described in e.g., Sambrook and Russell, Molecular Cloning, A Laboratory Approach, Cold Spring Harbor Press, Cold Spring Harbor, N.Y. (2001), and Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons, NY (2002). These expression systems include dihydrofolate reductase (DHFR)-based systems, among many others. The glutamine synthetase system of expression is discussed in whole or part in connection with European Patents Nos. EP 216 846, EP 256 055, and EP 323 997 and European Patent Application 89303964. In one embodiment, the antibody used is made in NSO cells using a glutamine synthetase system (GS-NSO).

In another embodiment, the antibody is made in CHO cells using a DHFR system. Both systems are well-known in the art and are described in, among others, Barnes et al. Biotech & Bioengineering 73:261-270 (2001), and references cited therein.

[0222] Site-directed mutagenesis of the antibody CH2 domain to eliminate glycosylation may be preferred in order to prevent changes in either the immunogenicity, pharmacokinetic, and/or effector functions resulting from non-human glycosylation. Further, the antibody can be deglycosylated by enzymatic (see, e.g., Thotakura et al. Meth. Enzymol. 138:350 (1987)) and/or chemical methods (see, e.g., Hakimuddin et al., Arch. Biochem. Biophys. 259:52 (1987)).

[0223] Further, the invention encompasses using an anti-PD-1 antibody, anti-PD-L1 antibody, or anti-CTLA-4 antibody comprising an altered glycosylation pattern. The skilled artisan would appreciate, based upon the disclosure provided herein, that an anti-PD-1 antibody, anti-PD-L1 antibody, or anti-CTLA-4 antibody can be modified to comprise additional, fewer, or different glycosylation sites compared with the corresponding unaltered antibody. Such modifications are described in, e.g., U.S. Patent Application Publication Nos. 2003/0207336, and 2003/0157108, and International Patent Publication Nos. WO 01/81405 and 00/24893.

[0224] Additionally, the invention comprises using an anti-PD-1 antibody, anti-PD-L1 antibody, or anti-CTLA-4 antibody regardless of the glycoform, if any, present on the antibody. Moreover, methods for extensively remodeling the glycoform present on a glycoprotein are well-known in the art and include, e.g., those described in International Patent Publication Nos. WO 03/031464, WO 98/58964, and WO 99/22764, and US Patent Application Publication Nos. 2004/0063911, 2004/0132640, 2004/0142856, 2004/0072290, and U.S. Pat. No. 6,602,684 to Umana et al.

[0225] Further, the invention encompasses using an anti-PD-1 antibody, anti-PD-L1 antibody, or anti-CTLA-4 antibody with any art-known covalent and non-covalent modification, including, but not limited to, linking the polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxalkylenes, in the manner set forth in, for example, U.S. Patent Application Publication Nos. 2003/0207346 and 2004/0132640, and U.S. Pat. Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192; and 4,179,337.

[0226] Additionally, the invention encompasses using an anti-PD-1 antibody, anti-PD-L1 antibody, or anti-CTLA-4 antibody, or antigen-binding portion thereof, chimeric protein comprising, e.g., a human serum albumin polypeptide, or fragment thereof. Whether the chimeric protein is produced using recombinant methods by, e.g., cloning of a chimeric nucleic acid encoding the chimeric protein, or by chemical linkage of the two peptide portions, the skilled artisan would understand once armed with the teachings provided herein that such chimeric proteins are well-known in the art and can confer desirable biological properties such as, but not limited to, increased stability and serum half-life to the antibody of the invention and such molecules are therefore included herein.

[0227] Antibodies that are generated for use in the invention need not initially possess a particular desired isotype. Rather, the antibody as generated can possess any isotype and can be isotype switched thereafter using conventional

techniques. These include direct recombinant techniques (see, e.g., U.S. Pat. No. 4,816,397), and cell-cell fusion techniques (see e.g., U.S. Pat. No. 5,916,771).

[0228] The effector function of the antibodies of the invention may be changed by isotype switching to an IgG1, IgG2, IgG3, IgG4, IgD, IgA, IgE, or IgM for various therapeutic uses. Furthermore, dependence on complement for cell killing can be avoided through the use of bispecifics, immunotoxins, or radiolabels, for example.

[0229] Therefore, while the preferred anti-CTLA-4 antibodies used in the invention are exemplified by antibodies having the amino acid sequences of 3.1.1, 4.1.1, 4.8.1, 4.10.2, 4.13.1, 4.14.3, 6.1.1, 11.2.1, 11.6.1, 11.7.1, 12.3.1.1, 12.9.1.1, and MDX-010, or, e.g., the sequences of the V regions or CDRs thereof, the present disclosure is not limited in any way to using these, or any other, particular anti-CTLA-4 antibodies. Preferably, the antibody is 4.1.1, 4.13.1, 11.2.1, and/or MDX-010. However, any anti-CTLA-4 antibody, or antigen-binding portion thereof, as described elsewhere herein, or as known in the art or developed in the future, can be used in a method of the invention. More particularly, humanized chimeric antibodies, anti-CTLA-4 antibodies derived from any species (including single chain antibodies obtained from camelids as described in, e.g., U.S. Pat. Nos. 5,759,808 and 6,765,087, to Casterman and Hamers), as well as any human antibody, can be combined with a CpG ODN to practice the novel methods disclosed herein.

[0230] The invention also encompasses such antibodies as disclosed in, *inter alia*, International Patent Publication Nos. WO 00/37504 (published Jun. 29, 2000); WO 01/14424 (published Mar. 1, 2001); WO 93/00431 (published Jan. 7, 1993); and WO 00/32231 (published Jun. 8, 2000), among many others.

[0231] Thus, the skilled artisan, once provided with the teachings provided herein, would readily appreciate that the anti-CTLA-4 antibody-therapeutic agent combination of the invention can comprise a wide plethora of anti-CTLA-4 antibodies.

[0232] Further, one skilled in the art, based upon the disclosure provided herein, would understand that the invention is not limited to administration of only a single antibody; rather, the invention encompasses administering at least one anti-CTLA-4 antibody, e.g., 4.1.1, 4.13.1 and 11.2.1, in combination with a CpG ODN. Moreover, the invention encompasses administering any combination of any known anti-CTLA-4 antibody, including, but not limited to, administering a CpG ODN in combination with, e.g., 4.1.1, 4.13.1, 11.2.1 and MDX-010. Thus, any combination of anti-CTLA-4 antibodies can be combined with at least one therapeutic agent and the present disclosure encompasses any such combination and permutation thereof.

#### IV. CpG DNA and Checkpoint Inhibitor Combination Immunotherapy

[0233] The present disclosure relates to combination tumor immunotherapy comprising locally administering CpG ODN into or in proximity to a cancerous tumor, and systemically administering a checkpoint inhibitor, such as an anti-PD-1 antibody, an anti-PD-L1 antibody, or an anti-CTLA-4 antibody, to treat cancer. A single human clinical trial has been reported in which patients were treated with a combination of a CpG ODN (B-class, dosed subcutaneously up to 0.15 mg/kg/wk) and an anti-CTLA-4 antibody (Mill-

ward M et al., Br. J. Cancer 2013 108 (10): 1998-2004). This study established an MTD for a weekly combination of IV anti-CTLA-4 and subcutaneous CpG over 12 weeks of therapy in 21 patients with stage IV melanoma. Although the results of the study were not considered encouraging enough to warrant continued development of TLR9 agonists in oncology (all immune-oncology drug development by the sponsor was terminated), several interesting findings from the study support the utility of the present disclosure. First, the combination of a TLR9 agonist and a checkpoint inhibitor is relatively well tolerated—there was no observed systemic autoimmune disease, and only three patients developed dose-limiting toxicities during the pre-specified initial 6 week period, two of whom were in the highest dose group of the anti-CTLA-4 antibody. Second, there was no induction of antibody response against the anti-CTLA-4 antibody from the combination regimen. Third, two patients achieved partial responses to the treatment, and several others had unusually prolonged stable disease.

[0234] Combination of high IFN-inducing CpG ODN and anti-PD-1, anti-PD-L1, or anti-CTLA-4 is useful for treatment of primary and secondary (i.e., metastatic) cancers. More specifically, among many potential treatment options, CpG ODN and anti-checkpoint combination therapy can be used to treat cancer. In certain embodiments, the cancer to be treated is or includes a cancerous tumor. A “cancerous tumor” as used herein refers to an abnormal swelling or macroscopic collection of cells comprising abnormal cells characterized by their growth or proliferation without regulation by normal external signals. In certain embodiments, a cancerous tumor is a carcinoma, sarcoma, or adenocarcinoma; these are sometimes referred to as solid tumors. In certain embodiments, a cancerous tumor excludes hematologic malignancies. In certain embodiments, a cancerous tumor includes certain hematologic malignancies, e.g., lymphomas.

[0235] Representative cancers treatable by the methods of the present disclosure (e.g., methods of treating cancer by administration of one or more CpG-ODN alone or in combination with one or more CPI) specifically include, without limitation, cancers of skin, head and neck, esophagus, stomach, liver, colon, rectum, pancreas, lung, breast, cervix, ovary, kidney, bladder, prostate, thyroid, brain, muscle, and bone. Also specifically included among cancers treatable by the methods of the invention are melanoma, renal cell carcinoma, and non-small cell lung cancer (NSCLC). Also specifically included among cancers treatable by the methods of the invention are lymphoma, cancer of the bone marrow, carcinoid tumor, and neuroblastoma.

[0236] While in some embodiments the foregoing cancers are preferred, the present disclosure relates to treatment of a wide variety of malignant cell proliferative disorders, including, but not limited to Kaposi's sarcoma, synovial sarcoma, mesothelioma, hepatobiliary (hepatic and biliary duct), a primary or secondary brain tumor, lung cancer (NSCLC and SCLC), bone cancer, skin cancer, cancer of the head or neck, cutaneous or intraocular melanoma, cancer of the anal region, stomach (gastric) cancer, gastrointestinal (gastric, colorectal, and duodenal) cancer, colon cancers, uterine cancer, carcinoma of the fallopian tubes, carcinoma of the endometrium, carcinoma of the cervix, carcinoma of the vagina, carcinoma of the vulva, cancer of the esophagus, cancer of the small intestine, cancer of the endocrine system, cancer of the thyroid gland, cancer of the parathyroid gland,

cancer of the adrenal gland, sarcoma of soft tissue, cancer of the urethra, prostate cancer, cancer of the penis, testicular cancer, cancer of the bladder, cancer of the kidney or ureter, carcinoma of the renal pelvis, pancreatic cancers, neoplasms of the central nervous system (CNS) including primary or secondary CNS tumor, spinal axis tumors, brain stem glioma, glioblastoma, meningioma, myoblastoma, astrocytoma, pituitary adenoma, adrenocortical cancer, gall bladder cancer, cholangiocarcinoma, fibrosarcoma, neuroblastoma, and retinoblastoma; as well as, in some embodiments, non-Hodgkin's lymphoma (NHL, including indolent and aggressive), Hodgkin's lymphoma, cutaneous T-cell lymphoma, lymphocytic lymphomas, primary CNS lymphoma, chronic or acute myeloid leukemia, chronic or acute lymphocytic leukemia, erythroblastoma, and multiple myeloma; or a combination of two or more of the foregoing cancers.

[0237] The cancers to be treated may be refractory cancers. A refractory cancer as used herein is a cancer that is resistant to the ordinary standard of care prescribed. These cancers may appear initially responsive to a treatment (and then recur), or they may be completely non-responsive to the treatment. The ordinary standard of care will vary depending upon the cancer type, and the degree of progression in the subject. It may be a chemotherapy, an immunotherapy, surgery, radiation, or a combination thereof. Those of ordinary skill in the art are aware of such standards of care. Subjects being treated according to the invention for a refractory cancer therefore may have already been exposed to another treatment for their cancer. Alternatively, if the cancer is likely to be refractory (e.g., given an analysis of the cancer cells or history of the subject), then the subject may not have already been exposed to another treatment.

[0238] In certain embodiments, refractory cancers include cancers which are refractory to treatment with a checkpoint inhibitor. Cancers of this type are sometimes referred to as "cold". Methods of the instant invention can be used to treat such "cold" cancers or tumors to convert them into "hot" ones, i.e., cancers or tumors which respond to treatment, including treatment with a checkpoint inhibitor, even the same checkpoint inhibitor.

[0239] Examples of refractory cancers include but are not limited to melanomas, renal cell carcinomas, colon cancer, liver (hepatic) cancers, pancreatic cancer, non-Hodgkin's lymphoma, lung cancer, and leukemias.

[0240] The methods of the invention in certain instances may be useful for replacing existing surgical procedures or drug therapies, although in other instances the present disclosure is useful in improving the efficacy of existing therapies for treating such conditions. Accordingly combination therapy may be used to treat subjects that are undergoing or that will undergo a treatment for cancer. For example, the agents may be administered to a subject in combination with another anti-proliferative (e.g., an anti-cancer) therapy. Suitable anti-cancer therapies include surgical procedures to remove the tumor mass, chemotherapy, or localized radiation. The other anti-proliferative therapy may be administered before, concurrent with, or after treatment with the CpG ODN/CPI combination of the invention. There may also be a delay of several hours, days, and in some instances weeks between the administration of the different treatments, such that the CpG ODN/CPI combination may be administered before or after the other treatment. The invention further contemplates the use of the CpG ODN/CPI combination in cancer subjects prior to and following surgery, radiation or chemotherapy.

[0241] In one embodiment, the invention provides compositions and methods of producing or increasing an anti-

tumor response using a CpG ODN-CPI combination, wherein CpG ODN enhances an anti-tumor response by an amount of CPI which is otherwise sub-optimal for inducing the same level of anti-tumor response when used alone. In certain embodiments, when the CpG ODN is not used in conjunction with a CPI to elicit an anti-tumor response, administering CpG ODN alone does not produce or increase the anti-tumor response. In alternate embodiments, both the CpG ODN and the CPI can elicit an anti-tumor response alone and/or when administered in combination.

[0242] In one embodiment, the invention provides compositions and methods of producing or increasing an anti-tumor response using a CpG ODN-CPI antibody combination, wherein CpG ODN enhances an anti-tumor response by an amount of antibody which is otherwise sub-optimal for inducing the same level of anti-tumor response when used alone. In certain embodiments, when the CpG ODN is not used in conjunction with a CPI antibody to elicit an anti-tumor response, administering CpG ODN alone does not produce or increase the anti-tumor response. In alternate embodiments, both the CpG ODN and the CPI antibody can elicit an anti-tumor response alone and/or when administered in combination.

[0243] In certain embodiments, the CpG ODN may enhance the effects of the CPI (or vice-versa) in an additive manner. In a preferred embodiment, the CpG ODN enhances the effects of the CPI (or vice versa) in a synergistic manner. In another embodiment, the CPI enhances the effect of a CpG ODN in an additive manner. Preferably, the effects are enhanced in a synergistic manner. Thus, in certain embodiments, the invention encompasses methods of disease treatment or prevention that provide better therapeutic profiles than expected based on administration of CpG ODN alone and CPI alone.

[0244] In certain embodiments, the CpG ODN may enhance the effects of the CPI antibody (or vice-versa) in an additive manner. In a preferred embodiment, the CpG ODN enhances the effects of the CPI antibody (or vice versa) in a synergistic manner. In another embodiment, the CPI antibody enhances the effect of a CpG ODN in an additive manner. Preferably, the effects are enhanced in a synergistic manner. Thus, in certain embodiments, the invention encompasses methods of disease treatment or prevention that provide better therapeutic profiles than expected based on administration of CpG ODN alone and CPI antibody alone.

[0245] In certain embodiments, the CpG ODN is administered with CPI (with or without other modalities such as radiotherapy) as a part of a neoadjuvant therapeutic regimen to achieve an anti-tumor effect that will make possible curative surgery.

[0246] In certain embodiments, the CpG ODN is administered together with CPI (with or without other modalities such as radiotherapy) following surgical resection of a primary or metastatic tumor or in the setting of minimal residual disease in order to prevent tumor recurrence.

[0247] Also encompassed by the invention are combination therapies that have additive potency or an additive therapeutic effect while reducing or avoiding unwanted or adverse effects. The invention also encompasses synergistic combinations where the therapeutic efficacy is greater than additive, while unwanted or adverse effects are reduced or avoided. In certain embodiments, the methods of the invention permit treatment or prevention of diseases and disorders wherein treatment is improved by an enhanced anti-tumor response using lower and/or less frequent doses of CpG ODN and/or CPI to reduce the incidence of unwanted or

adverse effects caused by the administration of CpG ODN alone and/or CPI alone, while maintaining or enhancing efficacy of treatment, preferably increasing patient compliance, improving therapy, and/or reducing unwanted or adverse effects.

#### V. Additional Combination Therapy

**[0248]** Methods of the invention can be used in conjunction with other anti-cancer therapies, including chemotherapy, other immunotherapy, radiotherapy, hormone therapy, and the like. Conventional chemotherapeutics and targeted antineoplastic agents have been developed based on the simplistic notion that cancer constitutes a cell-autonomous genetic or epigenetic disease. However, it is becoming clear that many of the available anticancer drugs that have collectively saved millions of life-years mediate therapeutic effects by eliciting de novo or reactivating pre-existing tumor-specific immune responses. Accumulating evidence indicates that the therapeutic efficacy of several antineoplastic agents relies on their capacity to influence the tumor-host interaction, tipping the balance toward the activation of an immune response specific for malignant cells.

**[0249]** For example, Table 1 lists certain FDA-approved anticancer agents whose efficacy is reduced by immune deficiencies (Zitvogel L. et al., *Immunity* 2013 39 (1): 74-88).

TABLE 1

Agent	Tumor	Immune Defects
5-fluorouracil anthracyclines	EL4 lymphomas CT26 colorectal carcinomas, MCA205 fibrosarcomas, MCA-induced tumors	Nu/Nu genotype Nu/Nu genotype, depletion of CD8 <sup>+</sup> or γδ T cells, blockade of CD11b, neutralization of IL-1, IL-17, or IFN-γ
ATRA ± arsenic trioxide arsenic trioxide cisplatin + digoxin cyclophosphamide	murine APLs CT26 colorectal cancers MCA205 fibrosarcomas AB1-HA mesotheliomas	SCID phenotype Nu/Nu genotype Nu/Nu genotype Ifngr2 <sup>-/-</sup> , Tnfsf10 <sup>-/-</sup> , depletion of CD8 <sup>+</sup> T cells or NK cells
dasatinib	P815 mastocytomas	depletion of CD4 <sup>+</sup> or CD8 <sup>+</sup> T cells
gemcitabine	AB12 mesotheliomas, EJ-6-2 fibrosarcomas, EL4 lymphomas, TC1 insulinomas	Nu/Nu genotype
imatinib	AK7 mesotheliomas, B16 melanomas, RMA-S lymphomas GISTs developing in Kit <sup>V558I</sup> mice	depletion of NK cells Rag1 <sup>-/-</sup> , depletion of CD8 <sup>+</sup> T cells
mitomycin C + digoxin oxaliplatin	MCA205 fibrosarcomas CT26 colorectal carcinomas, MCA205 fibrosarcomas	Nu/Nu genotype Nu/Nu genotype
paclitaxel PLX4720 (BRAF inhibitor)	Ret-driven melanomas SM1WT1 melanomas	depletion of CD8 <sup>+</sup> T cells Ccr2 <sup>-/-</sup> , Ifng <sup>-/-</sup> , Prf1 <sup>-/-</sup> , depletion of CD8 <sup>+</sup> T cells

Table 1 Abbreviations:

APL, acute promyelocytic leukemia;

ATRA, all-trans retinoic acid;

BRAF, B-Raf;

GIST, gastrointestinal stromal tumor;

IFN, interferon;

IL, interleukin;

MCA, 3-methylcholanthrene;

NK, natural killer;

SCID, severe combined immunodeficient

#### VI. Dosage Regimens

**[0250]** Dosage regimens can be adjusted to provide the optimum desired response. For example, a single bolus can be administered, several divided doses can be administered over time, or the dose may be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the mammalian subjects to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on (a) the unique characteristics of the active compound and the particular therapeutic or prophylactic effect to be achieved, and (b) the limitations inherent in the art of compounding such an active compound for the treatment of sensitivity in individuals.

**[0251]** Thus, the skilled artisan would appreciate, based upon the disclosure provided herein, that the dose and dosing regimen is adjusted in accordance with methods well-known in the therapeutic arts. That is, the maximum tolerable dose can be readily established, and the effective

amount providing a detectable therapeutic benefit to a patient can also be determined, as can the temporal requirements for administering each agent to provide a detectable therapeutic benefit to the patient. Accordingly, while certain dose and administration regimens are exemplified herein, these examples in no way limit the dose and administration regimen that can be provided to a patient in practicing the present disclosure. Further, one skilled in the art would understand, once armed with the teachings provided herein, that a therapeutic benefit, such as, but not limited to, detectable decrease in tumor size and/or metastasis, and increased time to recurrence, among many other parameters, can be assessed by a wide variety of methods known in the art for assessing the efficacy of treatment of cancer, and these methods are encompassed herein, as well as methods to be developed in the future.

[0252] It is to be noted that dosage values may vary with the type and severity of the condition to be alleviated, and may include single or multiple doses. It is to be further understood that for any particular subject, specific dosage regimens should be adjusted over time according to the individual need and the professional judgment of the person administering or supervising the administration of the compositions, and that dosage ranges set forth herein are exemplary only and are not intended to limit the scope or practice of the claimed composition. For example, doses may be adjusted based on pharmacokinetic or pharmacodynamic parameters, which may include clinical effects such as toxic effects and/or laboratory values. Thus, the present disclosure encompasses intra-patient dose-escalation as determined by the skilled artisan. Determining appropriate dosages and regimens for administration of the active compound or compounds are well-known in the relevant art and would be understood to be encompassed by the skilled artisan once provided the teachings disclosed herein.

[0253] In various embodiments of the present disclosure, a prime-boost dosing regimen is employed that includes one or multiple administrations of a specific volume of a first composition comprising one or more CpG-ODN (e.g., a CpG-A ODN, optionally where one or more of the ODN are formulated in a VLP) via a specific route (i.e., a "prime"), followed by one or multiple administrations of a specific volume of a second composition comprising either one or more CpG-ODN (e.g., a CpG-A ODN, optionally where one or more of the ODN are formulated in a VLP) or one or more CPI via a specific route (i.e., a "boost").

[0254] In various embodiments of the present disclosure, where the CpG-A ODN is formulated with a VLP, the first dose of VLP induces an antibody response to the VLP coat protein. For example, if the CpG-A G10 is formulated with the Qb bacteriophage coat protein to produce CMP-001 (formerly known as CYT003 or QbG10), then human dosing results in the production of antibodies to the VLP protein, Qb.

[0255] CpG-A ODN that are not encapsulated in a VLP can be taken up directly by pDC through ODN receptors. This approach to therapy is effective if the ODN has one or more phosphorothioate linkages protecting the 5' and/or the 3' ends of the ODN against degradation. Preferred embodiments of CpG-A ODN for direct injection without a VLP have at least 1, and preferably 2 phosphorothioate linkages at the 5' and 3' ends, and especially preferred embodiments have 3, 4, or 5 phosphorothioate linkages at the 3' end of the ODN.

[0256] However, CpG-A ODN that have no phosphorothioate linkages at all can still be used quite effectively for therapy, especially if they are packed into a VLP, or otherwise protected against degradation using any of the many formulations and delivery systems known to those expert in the art of oligonucleotide therapeutics. Some CpG-A ODN delivery systems can be taken up directly by pDC, but the Qb VLP delivery system used e.g., in CMP-001, requires the presence of anti-Qb antibodies to opsonize the VLP so that it may be taken up by the pDC via the Fc receptor that is expressed on the pDC, FcgrIIa. Because the VLP is extremely immunogenic, the initial injection of CMP-001 through intratumoral, SC or other route of administration, induces the production of high titer opsonizing antibodies as early as 1 week after the initial injection (the "priming" dose). This priming dose simply needs to be large enough in a human to induce the antibody response, which can be achieved with a dose of at least 100 ug, and more preferably at least 300 ug. In some embodiments the priming dose is 1 mg and in other embodiments is more than 1 mg, including most preferably doses up to 10 mg. Following the priming dose, the 2<sup>nd</sup>, 3<sup>rd</sup>, and subsequent injections of the VLP containing the CpG-A are rapidly opsonized by the pre-existing anti-Qb antibody in the serum and tissues, leading to the uptake of the VLP into pDC (in which TLR9 is activated, inducing type I IFN production). These subsequent injections may be given at a frequency of daily, weekly, monthly, or any intermediate frequency of administration, and for durations of weeks, months, or years of therapy, as needed for the treatment of a patient.

[0257] It will be appreciated by those of ordinary skill in the art that prime-boost methods and compositions thereof and described herein may be accomplished by employing a variety of different regimens. In various embodiments, certain regimens may include multiple (i.e., one, two, three, four, or five) priming administrations, and/or multiple (i.e., one, two, three, four, or five) boosting administrations, and/or multiple (i.e., one, two, three, four, or five) secondary boosting administrations.

[0258] In some embodiments, methods contemplated herein comprise administering the compositions (e.g., composition comprising CpG and/or CPI) more than once to the subject. In particular embodiments, a composition is administered at least two, at least three, at least four, at least five, or more times (e.g., twice (two times), three times, four times, five times, or more) to the subject. Stated another way, multiple doses (i.e., 2, 3, 4, 5, 6, or more doses) of a composition are administered to the subject. When a first composition is administered multiple times (i.e., twice (two times), three times, four times, five times, or more), each administration of the first composition may be sequential and each and all administrations of the composition are prior to administration of a second composition.

[0259] As described herein, in other embodiments, compositions (e.g., composition comprising CpG and/or CPI) may be administered concurrently at least once. In one such embodiment, methods are provided herein that comprise administering (1) a composition comprising a first CpG and sequentially administering, in either order, (2) a second dose of the composition comprising the CpG concurrently with a composition comprising a second CpG.

[0260] With respect to the methods described herein that include sequential administration of compositions (e.g., composition comprising CpG and/or CPI), the time interval

between doses can be readily determined by a person skilled in the art practicing clinical trials. The dosing regimen for human subjects may also be informed by results from pre-clinical studies and knowledge in the art. In certain embodiments, time interval between administration of doses (e.g., a priming, first boost, second boost, third boost, etc.) of the compositions may be at least one, two, three, four, five, six, or seven days or one, two, three, four, five, six, seven, or eight weeks, or may be at least one, two, three, four, five, six, seven, eight, nine, ten, or eleven months, or at least one, two, three, or four years. The time intervals as described herein between administrations of the same or different compositions pertain to any of the administration regimens described herein.

#### CpG ODN Dosing

[0261] In accordance with the methods of the present disclosure, CpG ODN is administered locally to the cancerous tumor, i.e., by intratumoral or peritumoral administration. Alternatively or in addition, in certain embodiments CpG ODN is administered locally to the cancerous tumor by, for example, intraperitoneal injection or infusion or intravesicular instillation.

[0262] Most of the prior art with CpG used subcutaneous administration, not intratumoral or peritumoral. Intratumoral therapy in oncology is generally preferred only for the treatment of primary lesions, not in the situation of metastatic disease. The reason for this is that most intratumoral therapies have only a local effect. In some unusual cases, intratumoral therapies can lead to regression of distant tumor masses as a result of the induction of a specific immune response against tumor antigens present not only in the injected lesion, but also in distant metastases. In the case of radiotherapy (XRT), this has been termed an "abscopal effect" as described above. Some authors have noted cases in which abscopal effects have been induced by TLR agonists, including intratumoral TLR9 (Brody et al, J. Clin. Oncol. 2010 28 (28): 4324-4332; Kim et al., Blood 2012 119 (2): 355-363), but these responses have been uncommon and generally of brief duration.

[0263] The immune effects of XRT given prior to CpG ODN administration will disrupt the inhibitory mechanisms that normally limit the efficacy of the CpG-induced response, increasing the potential for clinical response. In addition, the production of IFN- $\alpha$  in the tumor has been associated with and is required for an improved response to XRT (Burnette et al, Cancer Res. 2011 71:2488-2496), providing further evidence for benefit from the use of intratumoral high IFN CpG following XRT.

[0264] In one form, the present disclosure comprises a method for improving the induction of abscopal responses from XRT by administering XRT, preferably hypofractionated XRT (as described in Prasanna et al.), to a cancer patient and then administering an intratumoral or peritumoral high IFN-inducing CpG ODN in the same region or lymphatic drainage. Preferred peritumoral injections are in the same lymphatic drainage as the tumor, in order to facilitate that the same APC are exposed both to the tumor Ag released following XRT to the tumor, and to the TLR ligand.

[0265] Methods of intratumoral or peritumoral delivery of CpG ODN include not only direct injection, but also can include topical delivery intraperitoneal delivery for abdominal tumors such as ovarian, pancreatic, colon, or gastric), intraocular for eye malignancies, oral for gastric and intes-

tinal cancer, and intravesicular administration for bladder cancer. Also contemplated for intratumoral administration of CpG ODN is systemic delivery using tumor delivery vehicles such as tumor-targeted aptamers, antibody conjugates, nanoparticles, ISCOMS, VLP, multilaminar vesicles, pH-sensitive peptides, and cationic peptides.

[0266] For systemic therapy, CpG ODN can be variably dosed based on weight, body surface area, or using a fixed dose. For intratumoral or peritumoral administration, the CpG ODN dose typically is fixed. Doses of CpG ODN for parenteral (including intratumoral and peritumoral) delivery for inducing an immune response when CpG ODN is administered in combination with other therapeutic agents, such as the CPI of the invention, typically range from about 1  $\mu$ g to 100 mg per administration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween.

[0267] In certain embodiments, subject doses of CpG ODN for intratumoral and peritumoral delivery typically range from about 10  $\mu$ g to about 100 mg per administration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween. In certain embodiments, subject doses of CpG ODN for intratumoral and peritumoral delivery typically range from about 100  $\mu$ g to about 100 mg per administration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween. In certain embodiments, subject doses of CpG ODN for intratumoral and peritumoral delivery typically range from about 1 mg to about 100 mg per administration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween. In certain embodiments, subject doses of CpG ODN for intratumoral and peritumoral delivery typically range from about 10 mg to about 100 mg per administration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween.

[0268] In yet other embodiments, doses of CpG ODN for parenteral (including intratumoral and peritumoral) delivery for inducing an immune response when CpG ODN is administered in combination with other therapeutic agents, such as the CPI of the invention, typically range from about 1  $\mu$ g to about 50 mg per administration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween. In certain embodiments, subject doses of CpG ODN for intratumoral and peritumoral delivery typically range from about 10  $\mu$ g to about 50 mg per administration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween. In certain embodiments, subject doses of CpG ODN for intratumoral and peritumoral delivery typically range from about 100  $\mu$ g to about 50 mg per administration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween. In certain embodiments, subject doses of CpG ODN for intratumoral and peritumoral delivery typically range from about 1 mg to about 50 mg per administration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween. In certain embodiments, subject doses of CpG ODN for intratumoral and peritumoral delivery typically range from about 10 mg to about 50 mg per administration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween.

tration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween.

[0269] In yet other embodiments, doses of CpG ODN for parenteral (including intratumoral and peritumoral) delivery for inducing an immune response when CpG ODN is administered in combination with other therapeutic agents, such as the CPI of the invention, typically range from about 1 µg to about 10 mg per administration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween. In certain embodiments, subject doses of CpG ODN for intratumoral and peritumoral delivery typically range from about 10 µg to about 10 mg per administration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween. In certain embodiments, subject doses of CpG ODN for intratumoral and peritumoral delivery typically range from about 100 µg to about 10 mg per administration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween. In certain embodiments, subject doses of CpG ODN for intratumoral and peritumoral delivery typically range from about 1 mg to about 10 mg per administration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween.

[0270] In yet other embodiments, doses of CpG ODN for parenteral (including intratumoral and peritumoral) delivery for inducing an immune response when CpG ODN is administered in combination with other therapeutic agents, such as the CPI of the invention, typically range from about 1 µg to about 1 mg per administration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween. In certain embodiments, subject doses of CpG ODN for intratumoral and peritumoral delivery typically range from about 10 µg to about 1 mg per administration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween. In certain embodiments, subject doses of CpG ODN for intratumoral and peritumoral delivery typically range from about 100 µg to about 1 mg per administration, which depending on the application could be given daily, weekly, or monthly and any other amount of time therebetween.

[0271] For each of the fixed doses described above, in certain embodiments the dose of CpG-ODN will be administered in a total volume of greater than 4 mL. In certain embodiments, the dose will be administered in a volume 4.5, 5, 5, 5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 mL. In various embodiments, the injection may be into a single site, or into multiple and/or different sites. In some embodiments all of the injection volume is administered intratumorally into a single tumor. In other embodiments the injection volume is divided up between 2 or more tumors, equally, or in varying volumes depending on the size of the tumor. In some embodiments the volume is split between 1 or more tumors and 1 or more peritumoral or subcutaneous sites. In various embodiments, where multiple doses of a CpG-ODN are administered to a subject (e.g., as part of a prime-boost regimen), each and every dose of the CpG-ODN, including CpG formulated with VLP, is administered in a volume greater than 4 mL.

[0272] As will be appreciated and as described herein, in certain embodiments the “volume” administered can be total volume that is split into multiple different injected tumors, or a single tumor, and can include some volume that is injected intratumorally, and some volume injected peritumorally in the same patient (i.e., the large dose volume of greater than 4 mL may be distributed in appropriate fractions to appropriate multiple sites).

[0273] In other embodiments, the dose to be administered at a given time is 1-50 mL containing a first amount of CpG-ODN and it is administered/distributed to multiple lesions and/or sites (e.g., potentially targeting lymph nodes) via intra- and/or peri-tumoral and/or SC injections, such that the total volume administered is greater than 4 mL.

[0274] In certain embodiments of the invention, a sustained release delivery system, including for example nanoparticles, ISCOMS, VLP, and dendrimers (reviewed in, for example, Gomes Dos Santos A L et al., *Curr Pharm Biotechnol.* 2005 6 (1): 7-15; Joshi V B et al., *AAPSJ.* 2013 15 (1): 85-94; and Arima H et al., *Curr Top Med Chem.* 2014 14 (4): 465-77), may be used to administer a single intratumoral or peritumoral therapeutic dose of the CpG ODN. In certain embodiments of the invention, a sustained release delivery system, including for example nanoparticles, ISCOMS, VLP, and dendrimers, may be used to administer a single intratumoral or peritumoral therapeutic dose of the CpG ODN, with no further CpG ODN required.

[0275] As is well known in the art, individual doses are increased when using a sustained delivery system of any of the types well described in the literature.

[0276] In certain embodiments using a single administration of a sustained release formulation of CpG ODN, the subject dose of CpG ODN for intratumoral and peritumoral delivery typically ranges from about 0.1 mg to about 500 mg per administration, and it is given within one week of XRT; within one week of a checkpoint inhibitor; or within one week of both XRT and a checkpoint inhibitor. In certain embodiments using a single administration of a sustained release formulation of CpG ODN, the subject dose of CpG ODN for intratumoral and peritumoral delivery typically ranges from about 1 mg to about 500 mg per administration, and it is given within one week of XRT; within one week of a checkpoint inhibitor; or within one week of both XRT and a checkpoint inhibitor. In certain embodiments using a single administration of a sustained release formulation of CpG ODN, the subject dose of CpG ODN for intratumoral and peritumoral delivery typically ranges from about 10 mg to about 500 mg per administration, and it is given within one week of XRT; within one week of a checkpoint inhibitor; or within one week of both XRT and a checkpoint inhibitor. In certain embodiments using a single administration of a sustained release formulation of CpG ODN, the subject dose of CpG ODN for intratumoral and peritumoral delivery typically ranges from about 100 mg to about 500 mg per administration, and it is given within one week of XRT; within one week of a checkpoint inhibitor; or within one week of both XRT and a checkpoint inhibitor.

[0277] In certain embodiments using a single administration of a sustained release formulation of CpG ODN, the subject doses of CpG ODN for intratumoral and peritumoral delivery typically range from about 0.1 mg to about 250 mg per administration, and it is given within one week of XRT; within one week of a checkpoint inhibitor; or within one week of both XRT and a checkpoint inhibitor. In certain

embodiments using a single administration of a sustained release formulation of CpG ODN, the subject dose of CpG ODN for intratumoral and peritumoral delivery typically ranges from about 1 mg to about 250 mg per administration, and it is given within one week of XRT; within one week of a checkpoint inhibitor; or within one week of both XRT and a checkpoint inhibitor. In certain embodiments using a single administration of a sustained release formulation of CpG ODN, the subject dose of CpG ODN for intratumoral and peritumoral delivery typically ranges from about 10 mg to about 250 mg per administration, and it is given within one week of XRT; within one week of a checkpoint inhibitor; or within one week of both XRT and a checkpoint inhibitor. In certain embodiments using a single administration of a sustained release formulation of CpG ODN, the subject dose of CpG ODN for intratumoral and peritumoral delivery typically ranges from about 100 mg to about 250 mg per administration, and it is given within one week of XRT; within one week of a checkpoint inhibitor; or within one week of both XRT and a checkpoint inhibitor.

[0278] In certain embodiments using a single administration of a sustained release formulation of CpG ODN, the subject dose of CpG ODN for intratumoral and peritumoral delivery typically ranges from about 0.1 mg to about 100 mg per administration, and it is given within one week of XRT; within one week of a checkpoint inhibitor; or within one week of both XRT and a checkpoint inhibitor. In certain embodiments using a single administration of a sustained release formulation of CpG ODN, the subject dose of CpG ODN for intratumoral and peritumoral delivery typically ranges from about 1 mg to about 100 mg per administration, and it is given within one week of XRT; within one week of a checkpoint inhibitor; or within one week of both XRT and a checkpoint inhibitor. In certain embodiments using a single administration of a sustained release formulation of CpG ODN, the subject dose of CpG ODN for intratumoral and peritumoral delivery typically ranges from about 10 mg to about 100 mg per administration, and it is given within one week of XRT; within one week of a checkpoint inhibitor; or within one week of both XRT and a checkpoint inhibitor.

[0279] The desired clinical effect of the administered dose of CpG ODN can readily be followed using standard assays and methods well known to those skilled in the art. For example, biomarker responses to TLR9 stimulation can be measured as described elsewhere herein.

#### CPI Antibody Dosing

[0280] Certain commercially available anti-PD-1 antibodies are currently approved in the United States for intravenous infusion dosing at 2 mg/kg body weight once every three weeks. Other commercially available anti-PD-1 antibodies are currently approved in the United States for intravenous infusion dosing at 3 mg/kg body weight once every two weeks. Commercially available anti-CTLA-4 antibodies are currently approved in the United States for intravenous infusion dosing at 3 mg/kg body weight once every three weeks.

[0281] In accordance with the methods of the present disclosure, in certain embodiments, CPI antibody is administered, at least in part, systemically, e.g., intravenously.

[0282] Exemplary, non-limiting doses for a therapeutically effective amount of a CPI antibody systemically administered according to the invention are: at least about

0.1 mg/kg body weight, at least about 0.3 mg/kg body weight, at least about 0.5 mg/kg body weight, at least about 1 mg/kg body weight, at least about 2 mg/kg body weight, at least about 3 mg/kg body weight, at least about 4 mg/kg body weight, at least about 5 mg/kg body weight, and at least about 6 mg/kg body weight.

[0283] In certain embodiments, a therapeutically effective amount of systemically administered CPI antibody can range from about 0.1 to about 30 mg/kg body weight, about 0.3 to about 25 mg/kg body weight, about 1 to about 20 mg/kg body weight, about 2 to about 20 mg/kg body weight, about 3 to about 20 mg/kg body weight, about 5 to about 20 mg/kg body weight, about 10 to about 20 mg/kg body weight, about 1 to about 15 mg/kg body weight, about 2 to about 15 mg/kg body weight, about 3 to about 15 mg/kg body weight, about 5 to about 15 mg/kg body weight, about 10 to about 15 mg/kg body weight, about 1 to about 10 mg/kg body weight, about 2 to about 10 mg/kg body weight, about 3 to about 10 mg/kg body weight, or about 5 to about 10 mg/kg body weight.

[0284] In certain embodiments, the CPI antibody is systemically administered at a dose of at least about 0.3 mg/kg body weight, at least about 1 mg/kg body weight, at least about 2 mg/kg body weight, at least about 3 mg/kg body weight, at least about 5 mg/kg body weight, at least about 6 mg/kg body weight, at least 10 mg/kg body weight, at least about 15 mg/kg body weight, or at least about 20 mg/kg body weight.

[0285] In certain embodiments, the CPI antibody is administered by intravenous (i.v.) infusion at a dose ranging from about 0.1 to about 50 mg/kg body weight, from about 0.3 to about 20 mg/kg body weight, from about 1 to about 15 mg/kg body weight, from about 2 to about 15 mg/kg body weight, from about 3 to about 15 mg/kg body weight, or from about 6 to about 15 mg/kg body weight.

[0286] In certain embodiments, the CPI antibody is administered in an intravenous formulation as a sterile aqueous solution containing about 5 to about 20 mg/mL of CPI antibody, in an appropriate buffer system.

[0287] In accordance with the methods of the present disclosure, in certain embodiments, CPI antibody is administered, at least in part, locally to the cancerous tumor, i.e., by intratumoral or peritumoral administration. In certain embodiments, such local administration is by direct injection, while in other embodiments, such administration can be topical delivery, intraperitoneal delivery for abdominal tumors such as ovarian, pancreatic, intraocular delivery for eye malignancies, oral delivery for gastric and intestinal cancer, and intravesicular administration for bladder cancer. Also contemplated for intratumoral administration of CPI antibody is systemic delivery using tumor delivery vehicles such as tumor-targeted aptamers, nanoparticles, ISCOMS, VLP, and cationic peptides.

[0288] For local, i.e., intratumoral or peritumoral, administration, the CPI antibody advantageously can be administered at a dose about 10-fold less to about 20-fold less than the systemic doses just listed above.

[0289] In accordance with the present disclosure, CPI antibody dosing will typically be less frequent than CpG ODN dosing. For example, anti-PD-1 antibody may be administered about once every three weeks to about once every three months. Similarly, anti-PD-L1 antibody may be administered about once every three weeks to about once every three months. Similarly, anti-CTLA-4 antibody may

be administered about once every three weeks to about once every three months. The invention further specifically contemplates CPI antibody dosing that is more frequent than about once every three weeks and less frequent than about once every three months.

[0290] Intratumoral or peritumoral CpG and systemic CPI can be given on the same or different days. For example, intratumoral or peritumoral CpG and the intravenous anti-PD-1 or anti-PD-L1 can be given on the same or different days.

[0291] Further, an exemplary dose escalation protocol with respect to CpG ODN, CPI antibody, or both CpG ODN and CPI antibody can be used to determine the maximum tolerated dose (MTD), to assess dose-limiting toxicity (DLT), if any, associated with administration of CpG ODN-CPI antibody combination therapy. For example, with respect to CPI antibody dose escalation at a given dose of CpG ODN, such protocol can comprise administering increasing doses, such as, but not limited to about 0.1 mg/kg, 0.3 mg/kg, 1 mg/kg, 2 mg/kg, 3 mg/kg, 4 mg/kg, 5 mg/kg, 6 mg/kg, 7 mg/kg, 10 mg/kg, 12 mg/kg, 15 mg/kg, or more than 15 mg/kg, or any combination thereof, more preferably, successive doses of 0.1 mg/kg, 0.3 mg/kg, 1 mg/kg, 2 mg/kg, 3 mg/kg, 6 mg/kg, 10 mg/kg, 15 mg/kg or 20 mg/kg are administered and the patient is assessed for toxicity, if any, as well as for efficacy of treatment, among other parameters. Such studies to determine toxicity and efficacy of dose regimens are well-known in the art. See, for example, Millward M. et al., Br. J. Cancer 2013 108 (10): 1998-2004.

## VII. Pharmaceutical Compositions

[0292] In certain embodiments, the CpG ODN is formulated with a marker, e.g., a radio-opaque marker or dye, that facilitates visualization of the CpG ODN administration into and/or adjacent to the tumor to be treated. Alternatively the CpG ODN is covalently conjugated to or otherwise labeled with a compound that enables the detection of the area of administration. Examples of such labels are well known in the art, and include fluorescent dyes, aptamers, fluorescent RNAs such as spinach and derivatives thereof, quantum dots, gold and other nanoparticles, antibodies, etc.

[0293] CpG ODN may be directly administered to the subject or may be administered in conjunction with a nucleic acid delivery complex. A nucleic acid delivery complex shall mean a nucleic acid molecule associated with (e.g., ionically or covalently bound to; or encapsulated within) a targeting means (e.g., a molecule that results in higher affinity binding to target cell). Examples of nucleic acid delivery complexes include oligonucleotides associated with a sterol (e.g. cholesterol), a lipid (e.g., a cationic lipid, viroosome, or liposome), or a target cell-specific binding agent (e.g., a ligand recognized by target cell specific receptor). Preferred complexes may be sufficiently stable in vivo to prevent significant uncoupling prior to internalization by the target cell. However, the complex can be cleavable under appropriate conditions within the cell so that the nucleic acid is released in a functional form.

[0294] Delivery vehicles or delivery devices for delivering oligonucleotides and/or antigens to surfaces have been described. The CpG ODN and/or the antigen and/or other therapeutics may be administered alone (e.g., in saline or buffer) or using any delivery vehicles known in the art. For instance the following delivery vehicles have been described: Cochleates; Emulsomes, ISCOMs; Liposomes;

Live bacterial vectors (e.g., *Salmonella*, *Escherichia coli*, *Bacillus Calmette-Guerin*, *Shigella*, *Lactobacillus*); Live viral vectors (e.g., Vaccinia, adenovirus, Herpes Simplex); Microspheres; Oligonucleotide vaccines; Polymers; Polymer rings; Proteosomes; Sodium Fluoride; Transgenic plants; Virosomes; Virus-like particles, and cationic lipids, peptides, or other carriers that have a charge interaction with the polyanionic oligonucleotide. Other delivery vehicles are known in the art and some additional examples are provided below in the discussion of vectors.

[0295] In one embodiment, the CPI is administered parenterally (e.g., intravenously) in an aqueous solution while the CpG ODN is administered by intratumoral or peritumoral injection. Preferred formulations and dosage forms of the CpG ODN are described in U.S. Patent Application Publication No. US 2004/0198680, the disclosure of which is incorporated herein by reference in its entirety. However, the skilled artisan would understand, based upon the disclosure provided herein, that the invention is not limited to these, or any other, formulations, doses, routes of administration, and the like. Thus, the following discussion describes various formulations for practicing the methods of the invention comprising administration of any CPI antibody in combination with a CpG ODN, but the invention is not limited to these formulations, but comprises any formulation as can be readily determined by one skilled in the art once armed with the teachings provided herein for use in the methods of the invention.

[0296] The antibodies employed in the invention can be incorporated into pharmaceutical compositions suitable for administration to a subject. Typically, the pharmaceutical composition comprises the antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible. Examples of pharmaceutically acceptable carriers include one or more of water, saline, phosphate buffered saline, dextrose, trehalose, glycerol, ethanol and the like, as well as combinations thereof. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Pharmaceutically acceptable substances such as wetting or minor amounts of auxiliary substances such as wetting or emulsifying agents, preservatives or buffers, which enhance the shelf life or effectiveness of the antibody or antibody portion.

[0297] The antibodies may be in a variety of forms. These include, for example, liquid, semi solid and solid dosage forms, such as liquid solutions (e.g., injectable and infusible solutions), dispersions or suspensions, tablets, pills, powders, liposomes and suppositories. The preferred form depends on the intended mode of administration and therapeutic application. Typical preferred compositions are in the form of injectable or infusible solutions, such as compositions similar to those used for passive immunization of humans with other antibodies. The preferred mode of administration is parenteral (e.g., intravenous, subcutaneous, intra-peritoneal, intramuscular). In a preferred embodiment, the antibody is administered by intravenous infusion or injection. In another preferred embodiment, the antibody is administered by intramuscular or subcutaneous injection.

[0298] Therapeutic compositions typically must be sterile and stable under the conditions of manufacture and storage.

The composition can be formulated as a solution, microemulsion, dispersion, liposome, or other ordered structure suitable to high drug concentration. Sterile injectable solutions can be prepared by incorporating the antibody in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filter sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile filtered solution thereof. The proper fluidity of a solution can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prolonged absorption of injectable compositions can be brought about by including in the composition an agent that delays absorption, for example, monostearate salts and gelatin.

[0299] The CpG ODN can be administered by a variety of methods known in the art, including, without limitation, local injection or infusion into and/or adjacent to a tumor. As used herein, "into a tumor" or "intratumoral" means anywhere generally within the margins of a tumor. As used herein, "adjacent to a tumor" or "peritumoral" means anywhere generally within about a 2.5 cm thick zone surrounding the margins of a tumor. The invention also contemplates local injection or infusion of the CpG ODN into and/or adjacent to a tumor bed following surgical resection of a tumor. Non-needle injection may be employed, if desired. In certain embodiments the CpG ODN can be administered locally to lung by inhalation or bronchoalveolar lavage. As will be appreciated by the skilled artisan, the route and/or mode of administration will vary depending upon the desired results.

[0300] The CPI can be administered by a variety of methods known in the art, including, without limitation, oral, parenteral, mucosal, by-inhalation, topical, buccal, nasal, and rectal. For certain therapeutic applications, the preferred route/mode of administration is subcutaneous, intramuscular, intravenous or infusion. Non-needle injection may be employed, if desired. As will be appreciated by the skilled artisan, the route and/or mode of administration will vary depending upon the desired results.

[0301] Dosage regimens may be adjusted to provide the optimum desired response. For example, a single bolus may be administered, several divided doses may be administered over time, or the dose may be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the mammalian subjects to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on (a) the unique characteristics of the antibody and the particular therapeutic or prophylactic effect to be achieved, and (b) the limitations

inherent in the art of compounding such an active compound for the treatment of sensitivity in individuals.

[0302] It is to be noted that dosage values may vary with the type and severity of the condition to be alleviated, and may include single or multiple doses. It is to be further understood that for any particular subject, specific dosage regimens may be adjusted over time according to the individual need and the professional judgment of the person administering or supervising the administration of the compositions, and that dosage ranges set forth herein are exemplary only and are not intended to limit the scope or practice of the claimed composition.

[0303] In one embodiment, the antibody is administered in an intravenous formulation as a sterile aqueous solution containing 5 or 10 mg/mL of antibody, with sodium acetate, polysorbate 80, and sodium chloride at a pH ranging from about 5 to 6. Preferably, the intravenous formulation is a sterile aqueous solution containing 5 or 10 mg/mL of antibody, with 20 mM sodium acetate, 0.2 mg/ml polysorbate 80, and 140 mM sodium chloride at pH 5.5.

[0304] In one embodiment, part of the dose is administered by an intravenous bolus and the rest by infusion of the antibody formulation. For example, a 0.01 mg/kg intravenous injection of the antibody may be given as a bolus, and the rest of a predetermined antibody dose may be administered by intravenous injection. A predetermined dose of the antibody may be administered, for example, over a period of an hour and a half to two hours to five hours.

[0305] The formulations of the pharmaceutical compositions described herein may be prepared by any method known or hereafter developed in the art of pharmacology. In general, such preparatory methods include the step of bringing the active ingredient into association with a carrier or one or more other accessory ingredients, and then, if necessary or desirable, shaping or packaging the product into a desired single- or multi-dose unit.

[0306] A pharmaceutical composition of the invention may be prepared, packaged, or sold in bulk, as a single unit dose, or as a plurality of single unit doses. As used herein, a "unit dose" is discrete amount of the pharmaceutical composition comprising a predetermined amount of the active ingredient. The amount of the active ingredient is generally equal to the dosage of the active ingredient which would be administered to a subject or a convenient fraction of such a dosage such as, for example, one-half or one-third of such a dosage.

[0307] The relative amounts of the active ingredient, the pharmaceutically acceptable carrier, and any additional ingredients in a pharmaceutical composition of the invention will vary, depending upon the identity, size, and condition of the subject treated and further depending upon the route by which the composition is to be administered. By way of example, the composition may comprise between 0.1% and 100% (w/w) active ingredient.

[0308] In addition to the active ingredient, a pharmaceutical composition of the invention may further comprise one or more additional pharmaceutically active agents. Particularly contemplated additional agents include anti-emetics, anti-diarrheals, chemotherapeutic agents, cytokines, and the like.

[0309] Controlled- or sustained-release formulations of a pharmaceutical composition of the invention may be made using conventional technology.

[0310] As used herein, "parenteral administration" of a pharmaceutical composition includes any route of administration characterized by physical breaching of a tissue of a subject and administration of the pharmaceutical composition through the breach in the tissue. Parenteral administration thus includes, but is not limited to, administration of a pharmaceutical composition by injection of the composition, by application of the composition through a surgical incision, by application of the composition through a tissue-penetrating non-surgical wound, and the like. In particular, parenteral administration is contemplated to include, but is not limited to, intravenous, intraperitoneal, intramuscular, subcutaneous, intracisternal, and kidney dialytic infusion techniques.

[0311] Formulations of a pharmaceutical composition suitable for parenteral administration comprise the active ingredient combined with a pharmaceutically acceptable carrier, such as sterile water or sterile isotonic saline. Such formulations may be prepared, packaged, or sold in a form suitable for bolus administration or for continuous administration. Injectable formulations may be prepared, packaged, or sold in unit dosage form, such as in ampules or in multi-dose containers containing a preservative. Formulations for parenteral administration include, but are not limited to, suspensions, solutions, emulsions in oily or aqueous vehicles, pastes, and implantable sustained-release or biodegradable formulations as discussed below. Such formulations may further comprise one or more additional ingredients including, but not limited to, suspending, stabilizing, or dispersing agents. In one embodiment of a formulation for parenteral administration, the active ingredient is provided in dry (e.g., powder or granular) form for reconstitution with a suitable vehicle (e.g., sterile pyrogen-free water) prior to parenteral administration of the reconstituted composition.

[0312] A composition of the present disclosure can be administered by a variety of methods known in the art. The route and/or mode of administration vary depending upon the desired results. The active compounds can be prepared with carriers that protect the compound against rapid release, such as a controlled release formulation, including implants, transdermal patches, and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Many methods for the preparation of such formulations are described by e.g., Sustained and Controlled Release Drug Delivery Systems, J. R. Robinson, ed., Marcel Dekker, Inc., New York, (1978). Pharmaceutical compositions are preferably manufactured under GMP conditions.

[0313] The pharmaceutical compositions may be prepared, packaged, or sold in the form of a sterile injectable aqueous or oily suspension or solution. This suspension or solution may be formulated according to the known art, and may comprise, in addition to the active ingredient, additional ingredients such as the dispersing agents, wetting agents, or suspending agents described herein. Such sterile injectable formulations may be prepared using a non-toxic parenterally-acceptable diluent or solvent, such as water or 1,3-butane diol, for example. Other acceptable diluents and solvents include, but are not limited to, Ringer's solution,

isotonic sodium chloride solution, and fixed oils such as synthetic mono- or di-glycerides. Other parentally-administrable formulations which are useful include those which comprise the active ingredient in microcrystalline form, in a liposomal preparation, or as a component of a biodegradable polymer system. Compositions for sustained release or implantation may comprise pharmaceutically acceptable polymeric or hydrophobic materials such as an emulsion, an ion exchange resin, a sparingly soluble polymer, or a sparingly soluble salt.

[0314] The CpG ODN and CPI active ingredient components of the invention can be administered to an animal, preferably a mammal, more preferably a human. The precise dosage administered of each active ingredient will vary depending upon any number of factors, including but not limited to, the type of animal and type of disease state being treated, the age of the animal and the route(s) of administration.

[0315] The CpG ODN and CPI active ingredient components of the invention may be co-administered with any of numerous other compounds (antihormonal therapy agents, cytokines, anti-cytokine antibodies, or anti-cytokine receptor antibodies, inhibitors of indoleamine 2,3-dioxygenase (IDO) or tryptophan 2,3-dioxygenase (TDO), chemotherapeutic, antibiotic and/or antiviral drugs, among many others). Alternatively, such other compound(s) may be administered an hour, a day, a week, a month, or even more, in advance of the CpG ODN-CPI combination, or any permutation thereof. Further, such other compound(s) may be administered an hour, a day, a week, or even more, after administration of radiation, stem cell transplant, or administration of any therapeutic agent (e.g., cytokine, chemotherapeutic compound, and the like), or any permutation thereof. The frequency and administration regimen will be readily apparent to the skilled artisan and will depend upon any number of factors such as, but not limited to, the type and severity of the disease being treated, the age and health status of the animal, the identity of the compound or compounds being administered, the route of administration of the various compounds, and the like. Several instructive examples demonstrating methods of co-administering CpG ODN-CPI combination to treat cancer are provided, but the invention is not limited in any way to these examples, which merely serve to illustrate methods encompassed by the invention.

### VIII. Kits

[0316] The invention includes various kits for treatment of cancer. The kits comprise a therapeutically effective amount of CpG ODN and, optionally, a therapeutically effective amount of a CPI, along with instructional materials which describe use of the combination to perform the methods of the invention. In certain embodiments, the kits comprise a therapeutically effective amount of CpG ODN and, optionally, a therapeutically effective amount of a CPI antibody, along with instructional materials which describe use of the combination to perform the methods of the invention. Although exemplary kits are described below, the contents of other useful kits will be apparent to the skilled artisan in light of the present disclosure. Each of these kits is included within the invention.

[0317] In one embodiment, the invention encompasses a kit comprising any combination of CpG ODN and an anti-PD-1 antibody. While such kit is preferred, the inven-

tion is not limited to this particular combination. Further, the kit can comprise a wide plethora of additional agents for treatment of cancer. Such agents are set forth previously and include chemotherapeutic compounds, cancer vaccines, TLR agonists other than a CpG ODN, other CpG ODNs, receptor tyrosine kinase inhibitors (such as, but not limited to, SU11248), agents useful in treating abnormal cell growth or cancer, antibodies or other ligands that inhibit tumor growth by binding to IGF-1R, a chemotherapeutic agent (taxane, *vinca* alkaloid, platinum compound, intercalating antibiotics, among many others), and cytokines, among many others, as well as palliative agents to treat, e.g., any toxicities that arise during treatment such as, but not limited to, an anti-diarrheal, an anti-emetic, and the like.

**[0318]** In one embodiment, the invention encompasses a kit comprising any combination of CpG ODN and an anti-PD-L1 antibody. While such kit is preferred, the invention is not limited to this particular combination. Further, the kit can comprise a wide plethora of additional agents for treatment of cancer. Such agents are set forth previously and include chemotherapeutic compounds, cancer vaccines, TLR agonists other than a CpG ODN, other CpG ODNs, receptor tyrosine kinase inhibitors (such as, but not limited to, SU11248), agents useful in treating abnormal cell growth or cancer, antibodies or other ligands that inhibit tumor growth by binding to IGF-1R, a chemotherapeutic agent (taxane, *vinca* alkaloid, platinum compound, intercalating antibiotics, among many others), and cytokines, among many others, as well as palliative agents to treat, e.g., any toxicities that arise during treatment such as, but not limited to, an anti-diarrheal, an anti-emetic, and the like.

**[0319]** In one embodiment, the invention encompasses a kit comprising any combination of CpG ODN and an anti-CTLA-4 antibody. In one embodiment the kit is used for both agents to be administered together via an intratumoral or peritumoral route, weekly for a course of therapy. When the anti-CTLA-4 antibody is delivered by intratumoral or peritumoral administration instead of systemic, the dose will be adjusted as familiar to those skilled in the art: preferred doses of intratumoral anti-CTLA-4 antibody are given as a fixed dose, generally in the range from 0.1 mg to 10 mg, and most preferably in the range from 1 mg to 5 mg. A course of therapy may vary in duration as is standard in the art, but will typically be at least 12 weeks in duration. As long as patients do not develop serious toxicity, and continue to have measurable tumor, the treatment can be continued, even for a period of several years. Drug holidays and breaks from treatment are encompassed as well. Breaks in treatment may be 1 week, 2 weeks, or longer, and may be provided every month, or less often, or provided depending on patient tolerability. While such kit is preferred, the invention is not limited to this particular combination. Further, the kit can comprise a wide plethora of additional agents for treatment of cancer. Such agents are set forth previously and include chemotherapeutic compounds, cancer vaccines, TLR agonists other than a CpG ODN, other CpG ODNs, receptor tyrosine kinase inhibitors (such as, but not limited to, SU11248), agents useful in treating abnormal cell growth or cancer, antibodies or other ligands that inhibit tumor growth by binding to IGF-1R, a chemotherapeutic agent (taxane, *vinca* alkaloid, platinum compound, intercalating antibiotics, among many others), and cytokines, among many others, as well as palliative agents to treat, e.g., any toxicities

that arise during treatment such as, but not limited to, an anti-diarrheal, an anti-emetic, and the like.

**[0320]** Having now described the present disclosure in detail, the same will be more clearly understood by reference to the following examples, which are included herewith for purposes of illustration only and are not intended to be limiting of the invention.

## EXAMPLES

### Example 1—Exemplary CpG to Induce Maximal Level of Type I IFN and Minimal Level of IL-10

**[0321]** As described in detail in PCT/US2015/067269, examples of preferred A-class CpG ODN are:

(SEQ ID NO: 80)  
ggGGGACGAGCTCGTCggggggG;

(SEQ ID NO: 58)  
ggGGGACGATCGTCGggggggG;

(SEQ ID NO: 81)  
ggGGACGATCGAACGTggggggG;

(SEQ ID NO: 78)  
ggGGTCGACGTCGACGTCGAGggggggG; and

(SEQ ID NO: 79)  
ggGGACGACGTCTGggggggG,

where each lower case letter represents a nucleotide linked to its 3'-adjacent nucleotide by a phosphorothioate (PS) linkage; and each upper case letter represents a nucleotide linked to its 3'-adjacent nucleotide (if present) by a phosphodiester (PO) linkage, except that the 3'-terminal nucleotide is represented by an upper case letter since it has no 3'-adjacent nucleotide.

**[0322]** Examples of preferred novel A-class CpG ODN sequences are:

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### Examples of preferred novel A-class CpG ODN sequences are:

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(SEQ ID NO: 502)  
gGGGACGATCGTCGggggG;

(SEQ ID NO: 503)  
ggGGTCGACGTCGACGTCGAgggggG;

(SEQ ID NO: 504)  
gGGGTCGTCGACGAGggggG;

(SEQ ID NO: 505)  
ggGGACGAGCTCGTCggggggG;

(SEQ ID NO: 506)  
ggGGGACGAGCTCGTCggggggG;

(SEQ ID NO: 507)  
ggGGGACGAGCTCGTCggggggG;

(SEQ ID NO: 508)  
gGGGACGAGCTCGTCggggG;

(SEQ ID NO: 77)  
ggGGACGATCGTCGggggggG;

(SEQ ID NO: 49)  
ggGGGACGATCGTCGggggggG;

-continued

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**Examples of preferred novel A-class CpG ODN sequences are:**


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gGGGACGATCGTCGggggG; (SEQ ID NO: 509)  
 gGGGACGATCGTCGggggG; (SEQ ID NO: 502)  
 gGGGACGATCGAACGTggggggG; (SEQ ID NO: 81)  
 ggGGACGATCGAACGTggggggG; (SEQ ID NO: 510)  
 gGGGACGATCGAACGTggggggG; (SEQ ID NO: 510)  
 gGGGACGATCGAACGTggggggG; (SEQ ID NO: 511)  
 gGGGTCGACGTCGACGTCGAGggggggG; (SEQ ID NO: 78)  
 ggGGTCGACGTCGACGTCGAGggggggG; (SEQ ID NO: 512)  
 gGGGTCGACGTCGACGTCGAGggggggG; (SEQ ID NO: 512)  
 gGGGTCGACGTCGACGTCGAGggggggG; (SEQ ID NO: 513)  
 gGGGACGACGTCGTggggGG; (SEQ ID NO: 514)  
 gGGGACGACGTCGTggggggG; (SEQ ID NO: 79)  
 ggGGACGACGTCGTggggggG; (SEQ ID NO: 514)  
 gGGGACGACGTCGTggggggG; (SEQ ID NO: 514)  
 gGGGACGACGTCGTggggggG; (SEQ ID NO: 515)  
 and  
 ggGTCGTCGACGAggggG, (SEQ ID NO: 516)

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where again each lower case letter represents a nucleotide linked to its 3'-adjacent nucleotide by a phosphorothioate (PS) linkage; and each upper case letter represents a nucleotide linked to its 3'-adjacent nucleotide (if present) by a phosphodiester (PO) linkage, except that the 3'-terminal nucleotide is represented by an upper case letter since it has no 3'-adjacent nucleotide.

**[0323]** Examples of preferred novel A/E-class CpG ODN sequences are:

gGGGACGAICGTCGgggg; (SEQ ID NO: 1)  
 gGGGACGAICGTCGgggg; (SEQ ID NO: 2)  
 gGGGACGAGCIGCTCgggg; (SEQ ID NO: 3)

-continued

ggGGICACCGGTGAgggggG; (SEQ ID NO: 4)  
 ggGGICACGTACGTCGAgggggG; (SEQ ID NO: 5)  
 ggGGICACGIAACGTCGAgggggG; (SEQ ID NO: 6)  
 ggGGICACGTACGICGAgggggG; (SEQ ID NO: 7)  
 ggGGICACGIACGICGAgggggG; (SEQ ID NO: 8)  
 ggGGACGICGACGTggggG; (SEQ ID NO: 9)  
 ggGGICACGTCGACGTCGAGggggG; (SEQ ID NO: 10)  
 ggGGICACGICGACGTCGAGggggG; (SEQ ID NO: 11)  
 ggGGICACGTCGACGICGAGggggG; (SEQ ID NO: 12)  
 ggGGICACGICGACGICGAGggggG; (SEQ ID NO: 13)  
 gGGGACGACGICGIGggggG; (SEQ ID NO: 14)  
 gGGGICGTCGACGAggggG; (SEQ ID NO: 15)  
 gGGGTCGICGACGAggggG; (SEQ ID NO: 16)  
 gGGGICGICGACGAggggG; (SEQ ID NO: 17)  
 ggGGACGAGCICGTCggggggG; (SEQ ID NO: 18)  
 ggGGACGAGCICGTCggggggG; (SEQ ID NO: 19)  
 gGGGACGAGCICGTCggggggG; (SEQ ID NO: 20)  
 gGGGACGAGCICGTCggggggG; (SEQ ID NO: 21)  
 ggGACGAICGTCGggggggG; (SEQ ID NO: 22)  
 ggGGACGAICGTCGggggggG; (SEQ ID NO: 23)  
 gGGGACGAICGTCGggggggG; (SEQ ID NO: 24)  
 gGGGACGAICGTCGggggggG; (SEQ ID NO: 1)  
 ggGGACGAICGTCGggggggG; (SEQ ID NO: 25)  
 ggGACGAICGICGggggggG; (SEQ ID NO: 26)  
 gGGGACGAICGICGggggggG; (SEQ ID NO: 27)  
 gGGGACGAICGICGggggggG; (SEQ ID NO: 28)

-continued

gGGGACGAICGAACGTggggG;	(SEQ ID NO: 29)
ggGGACGAICGAACGTggggG;	(SEQ ID NO: 30)
gGGGACGAICGAACGTggggG;	(SEQ ID NO: 30)
gGGGACGAICGAACGTggggG;	(SEQ ID NO: 31)
gGGGACGAICGAACGTggggG;	(SEQ ID NO: 32)
ggGGACGAICGAACGTggggG;	(SEQ ID NO: 33)
gGGGACGAICGAACGTggggG;	(SEQ ID NO: 33)
gGGGACGAICGAACGTggggG;	(SEQ ID NO: 34)
gGGGACGAICGAACGTggggG;	(SEQ ID NO: 35)
ggGGICGACGTCGACGTCGAGggggG;	(SEQ ID NO: 10)
gGGGICGACGTCGACGTCGAGggggG;	(SEQ ID NO: 10)
gGGGICGACGTCGACGTCGAGggggG;	(SEQ ID NO: 36)
gGGGICGACGTCGACGTCGAGggggG;	(SEQ ID NO: 37)
ggGGICGACGTCGACGTCGAGggggG;	(SEQ ID NO: 11)
gGGGICGACGTCGACGTCGAGggggG;	(SEQ ID NO: 11)
gGGGICGACGTCGACGTCGAGggggG;	(SEQ ID NO: 38)
gGGGICGACGTCGACGTCGAGggggG;	(SEQ ID NO: 39)
gGGGICGACGTCGACGTCGAGggggG;	(SEQ ID NO: 12)
gGGGICGACGTCGACGTCGAGggggG;	(SEQ ID NO: 12)
gGGGICGACGTCGACGTCGAGggggG;	(SEQ ID NO: 40)
gGGGICGACGTCGACGTCGAGggggG;	(SEQ ID NO: 41)
gGGGICGACGTCGACGTCGAGggggG;	(SEQ ID NO: 13)
gGGGICGACGTCGACGTCGAGggggG;	(SEQ ID NO: 13)
gGGGICGACGTCGACGTCGAGggggG; and	(SEQ ID NO: 42)

where "I" represents 5-iodo-2'-deoxyuridine; each lower case letter represents a nucleotide linked to its 3'-adjacent nucleotide by a phosphorothioate (PS) linkage; and each upper case letter represents a nucleotide linked to its 3'-ad-

jacent nucleotide (if present) by a phosphodiester (PO) linkage, except that the 3'-terminal nucleotide is represented by an upper case letter since it has no 3'-adjacent nucleotide.

**[0324]** The preferred CpG ODN of the present disclosure are synthesized using standard methods well known in the art and described above. The activity of the ODN are evaluated using in vitro dose-response assays on human peripheral blood mononuclear cells (PBMC) for IFN- $\alpha$  and IL-10 secretion as described in the A-class and E-class patents (for example, U.S. Pat. No. 8,580,268, FIG. 27 for IFN- $\alpha$ , and U.S. Pat. No. 7,795,235, FIG. 27 for IL-10). Because humans show inter-individual variation in the magnitude of the IFN- $\alpha$  response to TLR9 stimulation, PBMC from a minimum of 3 different individuals are tested for all cytokine, chemokine, and IFN assays. Freshly collected PBMC are strongly preferred for maximal responsiveness-after 24 hr the magnitude of the in vitro responses to TLR9 ligation will be significantly lower. A-class CpG ODN are typically tested on human PBMC at concentrations from approximately 0.1  $\mu$ M to approximately 10  $\mu$ M. Supernatants are collected after approximately 24, 48, or 72 hr and tested by enzyme-linked immunosorbent assay (ELISA) or other standard assay for amount of IFN- $\alpha$  (usually the assay just measures one or more of the many isoforms of IFN- $\alpha$ ) and/or other IFN-induced chemokines and cytokines.

**[0325]** Preferred A-class and A/E-class CpG ODN of the present disclosure induce an average of greater than 1000  $\mu$ g/ml of IFN- $\alpha$  at the most effective concentration in the assay (potency is less important in this regard than peak efficacy), or more preferably greater than 3,000  $\mu$ g/ml of IFN- $\alpha$  and most preferably greater than 10,000  $\mu$ g/ml of IFN- $\alpha$ ; in any case preferred ODN induce the production of at least greater than 10 times the IFN- $\alpha$  induced by a positive control B-class CpG ODN. Supernatants from the same experiments are also tested for IL-10 secretion using similar ELISA assays. Preferred A or A/E-class ODN of the present disclosure induce less than 1000  $\mu$ g/ml, preferably less than 300  $\mu$ g/ml, and most preferably less than 100  $\mu$ g/ml of IL-10 secretion under these assay conditions.

**[0326]** The most preferred CpG ODN selected from these in vitro assays are evaluated in mouse tumor models, using standard systems well known in the art. The mouse assays are not used to select the most active ODN to be taken into human clinical trials, since the rank-order of the ODN will differ, as a result of structural differences between mouse and human TLR9 and species-specific differences in the cell types expressing TLR9. For these reasons the primary selection of a lead candidate CpG ODN to take into human clinical trials is based on the results from the in vitro assays using human cells.

**[0327]** Additional examples of preferred A-class CpG ODN described in detail in PCT/US2015/067269, are also contemplated by the present disclosure:

ggGGGACGAGCTCGTcgggggG	(SEQ ID NO: 517)
gGGGACGACGICGIGggggGG	(SEQ ID NO: 518)
tcaaacgttcgaacgttgcgaacgttcaat	(SEQ ID NO: 519)

-continued

mGmGmGmGACGACGTCGTGmGmGmGmG  
 (SEQ ID NO: 520)

GGGGACGACGTCGTGGGGGmG  
 (SEQ ID NO: 521)

GGGGACGACGTCGTGGGGGgtT  
 (SEQ ID NO: 522)

GGGGACGACGTCGTGGGGGmUmU  
 (SEQ ID NO: 523)

TCGTCGACGA  
 (SEQ ID NO: 524)

GACGATCGTC  
 (SEQ ID NO: 525)

ACGACGTCGT  
 (SEQ ID NO: 526)

G+190G+190GGGAGCATGCCTGGGG#G+#G  
 (SEQ ID NO: 527)

GGGGGGGGACGATCGTCGGGGGGGG  
 (SEQ ID NO: 528)

GGGGGGGGGGACGATCGTCGGGGGGGG  
 (SEQ ID NO: 529)

GGGGGGGGGGACGATCGTCGGGGGGGG  
 (SEQ ID NO: 530)

GGGGGGGGGGTCGTCGACGAGGGGGGGGG  
 (SEQ ID NO: 531)

GGGGGGGGGGACGAGCTCGTCGGGGGGGG  
 (SEQ ID NO: 532)

GGGGGGGGGGACGATCGTCGGGGGGGG  
 (SEQ ID NO: 533)

GGGGGGGGGGTCGACGTCGACGTCGAGGGGGGGGG  
 (SEQ ID NO: 534)

GGGGGGGGGGACGACGTCGTGGGGGGGGGG  
 (SEQ ID NO: 535)

GGGGGGGGGGAAACGACGTCGTGGGGGGGGGG  
 (SEQ ID NO: 536)

GGGGGGGGGGACGACGACGATCGTCGTGGGGGGGGGG  
 (SEQ ID NO: 537)

GGGGGGGGGGCACGACGTCGTGGGGGGGGGG  
 (SEQ ID NO: 538)

GGGGGGGGGGAACGTTCGAACGTTGGGGGGGGGG  
 (SEQ ID NO: 539)

GGGGGGGGGGAAACGTTCGAACGTTGGGGGGGGGG  
 (SEQ ID NO: 540)

GG  
 (SEQ ID NO: 541)

GGGGGGGGGGTCGAACGTTCGAACGGGGGGGGGG  
 (SEQ ID NO: 542)

GGGGGGGGGGACGTCGACGTCGGGGGGGGGG  
 (SEQ ID NO: 543)

GGGGGGGGGGTCGACGTCGACGGGGGGGGGG  
 (SEQ ID NO: 544)

-continued

(SEQ ID NO: 545)

GGGGGGGGGGTACGATATCGTAGGGGGGGGG  
 (SEQ ID NO: 546)

GGGGGGGGGGTACGTACGTAGGGGGGGGG  
 (SEQ ID NO: 547)

GGGGGGGGGGCAGCATGCTGGGGGGGGGG  
 (SEQ ID NO: 548)

ACGACGACGA  
 (SEQ ID NO: 549)

## Example 2—Injection Volume Effects

**[0328]** As used herein, CMP-001 refers to an A-class CpG-ODN, referred to as G10 and SEQ ID NO: 82, that is formulated in a VLP. CMP-001 has also been known as CYT003 and as QbG10, under which names it has previously been studied in mice and humans for non-oncology indications, for example in Klimek, L., et al. “Assessment of clinical efficacy of CYT003-QbG10 in patients with allergic rhinoconjunctivitis: a phase IIb study.” Clinical & Experimental Allergy 41.9 (2011): 1305-1312.; Casale, T. B., et al. “CYT003, a TLR9 agonist, in persistent allergic asthma—a randomized placebo-controlled Phase 2b study.” Allergy 70.9 (2015): 1160-1168.

**[0329]** There have been interesting observations in the clinic related to the effects of different CMP-001 intratumoral (IT) injection volumes on therapeutic response. Specifically, human clinical data show a trend toward higher anti-tumor effect when the CMP-001 is injected in a larger volume (e.g., 5 mg dose in 5 mL has ~40% objective response) vs. a larger dose, but smaller volume (e.g., 7.5 or 10 mg dose in 1.2 or 1.7 mL volume respectively, had a 16% response rate). In addition, the serum IP-10 responses also showed a trend to the greatest fold induction at the 5 mg (in a 5 mL volume) dose compared to the higher doses (7.5 and 10 mg) that were given in a more concentrated, smaller volume (1.2 or 1.7 mL respectively).

**[0330]** Based on these observations, preclinical studies were undertaken to explore and more precisely document the impact of small vs. large injection volumes on immune activation and anti-tumor efficacy.

**[0331]** In order to assess the effects of injection volumes on therapeutic response, two studies were performed using a syngeneic A20 lymphoma subcutaneous tumor model with groups of 5 Balb/C mice. In the first study, mice were challenged with a single tumor, and in the second study bilateral tumors were implanted, with only one tumor per animal receiving IT injections. Mice were treated IT with either saline (20 ul or 100 ul) or a fixed dose of 120 ug CMP-001 (30 ug CpG content) delivered in 20 uL or 100 uL (diluted with saline). All mice were treated with a standard anti-PD-1 regimen in addition to the IT treatments. Tumor volumes over time and survival were recorded, as well as serum IP-10 levels 24 hrs after the first IT injection. The 5x larger injection volume resulted in 100% and 50% higher 24 hr post treatment IP-10 levels in the first and second studies, respectively (FIGS. 1 and 3). In both studies the larger 100 ul IT injection volume resulted in a measurable improvement in tumor growth suppression relative to the 20 ul injection volume. The larger volume also led to a survival

increase from 20% to 40% in the single tumor study, and 40% to 80% in the dual tumor model (FIGS. 2 and 4).

#### Example 3—Priming Dose Volume Effects

**[0332]** In the CMP-001-001 melanoma clinical trial, all doses are administered IT and the initial dose level and volume are maintained for all subsequent doses. However, in mouse studies, a single subcutaneous smaller priming dose is generally given weeks in advance of the therapeutic regimen in order to initiate development of antibodies to the Qb proteins of the CMP-001 VLP. Anti-Qb antibodies are important for efficient and productive uptake of CMP-001 into the target plasmacytoid dendritic cells.

**[0333]** Specific, measurable volume and/or concentration dependent effects particular to the initial “priming” dose of CMP-001 are set out in FIG. 5. Results from this study will guide the selection of priming dose(s) in additional studies designed to explore in more detail the effects of the therapeutic dose volume and concentration (FIG. 6).

**[0334]** Because volume dependent effects on systemic/lymphatic distribution of CMP-001 may underlie the

observed effects on immune activation and anti-tumor efficacy, volume 5 dependent distribution studies with labeled CMP-001 are also designed (Figures. 5 and 7).

#### INCORPORATION BY REFERENCE

**[0335]** All patents and published patent applications mentioned in the description above are incorporated by reference herein in their entirety.

#### Equivalents

**[0336]** Having now fully described the present disclosure in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious to one of ordinary skill in the art that the same can be performed by modifying or changing the invention within a wide and equivalent range of conditions, formulations and other parameters without affecting the scope of the invention or any specific embodiment thereof, and that such modifications or changes are intended to be encompassed within the scope of the appended claims.

#### SEQUENCE LISTING

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Sequence total quantity: 681
SEQ ID NO: 1      moltype = DNA length = 18
FEATURE           Location/Qualifiers
misc_feature      1..18
                  note = Synthetic oligonucleotide
modified_base     9
                  mod_base = OTHER
source            1..18
                  mol_type = other DNA
                  organism = synthetic construct
modified_base     15..17
                  mod_base = OTHER
source            15..17
                  note = Phosphorothioate linkages
modified_base     2..14
                  mod_base = OTHER
source            2..14
                  note = Phosphodiester linkages

SEQUENCE: 1
ggggacganc gtcggggg                                         18

SEQ ID NO: 2      moltype = DNA length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
                  note = Synthetic oligonucleotide
modified_base     9
                  mod_base = OTHER
source            1..20
                  mol_type = other DNA
                  organism = synthetic construct
modified_base     16..19
                  mod_base = OTHER
source            16..19
                  note = Phosphorothioate linkages
modified_base     2..15
                  mod_base = OTHER
source            2..15
                  note = Phosphodiester linkages

SEQUENCE: 2
ggggacgana tcgtcgaaaa                                         20

SEQ ID NO: 3      moltype = DNA length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
                  note = Synthetic oligonucleotide
modified_base     11
                  mod_base = OTHER
source            1..20
                  note = 5-iodo-2-prime-deoxyuridine

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mol_type = other DNA
organism = synthetic construct
16..19
mod_base = OTHER
note = Phosphorothioate linkages
modified_base
2..15
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 3
ggggacgacg ngctcgaaaaa                                     20

SEQ ID NO: 4
FEATURE
misc_feature
1..19
note = Synthetic oligonucleotide
modified_base
5
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source
1..19
mol_type = other DNA
organism = synthetic construct
order(1..2,15..18)
mod_base = OTHER
note = Phosphorothioate linkages
modified_base
3..14
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 4
ggggncaccg gtgagggggg                                     19

SEQ ID NO: 5
FEATURE
misc_feature
1..23
note = Synthetic oligonucleotide
modified_base
5
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source
1..23
mol_type = other DNA
organism = synthetic construct
order(1..2,19..22)
mod_base = OTHER
note = Phosphorothioate linkages
modified_base
3..18
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 5
ggggncgacg tacgtcgagg ggg                                     23

SEQ ID NO: 6
FEATURE
misc_feature
1..23
note = Synthetic oligonucleotide
modified_base
5
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base
11
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source
1..23
mol_type = other DNA
organism = synthetic construct
order(1..2,19..22)
mod_base = OTHER
note = Phosphorothioate linkages
modified_base
3..18
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 6
ggggncgacg nacgtcgagg ggg                                     23

SEQ ID NO: 7
FEATURE
misc_feature
1..23
note = Synthetic oligonucleotide
modified_base
5

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-continued

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modified_base      mod_base = OTHER
                   note = 5-iodo-2-prime-deoxyuridine
15
modified_base      mod_base = OTHER
                   note = 5-iodo-2-prime-deoxyuridine
1..23
source            mol_type = other DNA
                   organism = synthetic construct
modified_base      order(1..2,19..22)
                   mod_base = OTHER
                   note = Phosphorothioate linkages
3..18
modified_base      mod_base = OTHER
                   note = Phosphodiester linkages
SEQUENCE: 7
ggggncgacg tacgnccagg ggg                                23

SEQ_ID NO: 8          moltype = DNA  length = 23
FEATURE             Location/Qualifiers
misc_feature        1..23
                     note = Synthetic oligonucleotide
modified_base       5
                     mod_base = OTHER
                     note = 5-iodo-2-prime-deoxyuridine
modified_base       11
                     mod_base = OTHER
                     note = 5-iodo-2-prime-deoxyuridine
15
modified_base       15
                     mod_base = OTHER
                     note = 5-iodo-2-prime-deoxyuridine
modified_base       1..23
                     mod_base = OTHER
                     note = 5-iodo-2-prime-deoxyuridine
source             mol_type = other DNA
                   organism = synthetic construct
modified_base       order(1..2,19..22)
                   mod_base = OTHER
                   note = Phosphorothioate linkages
3..18
modified_base       mod_base = OTHER
                   note = Phosphodiester linkages
SEQUENCE: 8
ggggncgacg nacgnccagg ggg                                23

SEQ_ID NO: 9          moltype = DNA  length = 18
FEATURE             Location/Qualifiers
misc_feature        1..18
                     note = Synthetic oligonucleotide
modified_base       8
                     mod_base = OTHER
                     note = 5-iodo-2-prime-deoxyuridine
source             1..18
                     mol_type = other DNA
                     organism = synthetic construct
modified_base       order(1..2,15..17)
                     mod_base = OTHER
                     note = Phosphorothioate linkages
3..14
modified_base       mod_base = OTHER
                     note = Phosphodiester linkages
SEQUENCE: 9
ggggacgncc acgtgggg                                         18

SEQ_ID NO: 10         moltype = DNA  length = 26
FEATURE             Location/Qualifiers
misc_feature        1..26
                     note = Synthetic oligonucleotide
modified_base       5
                     mod_base = OTHER
                     note = 5-iodo-2-prime-deoxyuridine
source             1..26
                     mol_type = other DNA
                     organism = synthetic construct
modified_base       order(1..2,22..25)
                     mod_base = OTHER
                     note = Phosphorothioate linkages
3..21
modified_base       mod_base = OTHER

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SEQUENCE: 10          note = Phosphodiester linkages
ggggncgacg tcgacgtcga gggggg                                26

SEQ ID NO: 11          moltype = DNA  length = 26
FEATURE
misc_feature           Location/Qualifiers
1..26
note = Synthetic oligonucleotide
modified_base           5
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base           11
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source                 1..26
mol_type = other DNA
organism = synthetic construct
order(1..2,22..25)
modified_base           mod_base = OTHER
note = Phosphorothioate linkages
modified_base           3..21
mod_base = OTHER
note = Phosphodiester linkages

SEQUENCE: 11          note = Phosphodiester linkages
ggggncgacg ncgacgtcga gggggg                                26

SEQ ID NO: 12          moltype = DNA  length = 26
FEATURE
misc_feature           Location/Qualifiers
1..26
note = Synthetic oligonucleotide
modified_base           5
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base           17
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source                 1..26
mol_type = other DNA
organism = synthetic construct
order(1..2,22..25)
modified_base           mod_base = OTHER
note = Phosphorothioate linkages
modified_base           3..21
mod_base = OTHER
note = Phosphodiester linkages

SEQUENCE: 12          note = Phosphodiester linkages
ggggncgacg tcgacgnnga gggggg                                26

SEQ ID NO: 13          moltype = DNA  length = 26
FEATURE
misc_feature           Location/Qualifiers
1..26
note = Synthetic oligonucleotide
modified_base           5
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base           11
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base           17
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source                 1..26
mol_type = other DNA
organism = synthetic construct
order(1..2,22..25)
modified_base           mod_base = OTHER
note = Phosphorothioate linkages
modified_base           3..21
mod_base = OTHER
note = Phosphodiester linkages

SEQUENCE: 13          note = Phosphodiester linkages
ggggncgacg ncgacgnnga gggggg                                26

SEQ ID NO: 14          moltype = DNA  length = 20
FEATURE
misc_feature           Location/Qualifiers
1..20

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-continued

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modified_base          note = Synthetic oligonucleotide
11
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
14
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
1..20
mol_type = other DNA
organism = synthetic construct
16..18
mod_base = OTHER
note = Phosphorothioate linkages
order(2..15,19..20)
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 14
ggggacgacg ncgnnggggg      20

SEQ ID NO: 15          moltype = DNA length = 19
FEATURE
misc_feature           Location/Qualifiers
1..19
note = Synthetic oligonucleotide
5
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
1..19
mol_type = other DNA
organism = synthetic construct
15..18
mod_base = OTHER
note = Phosphorothioate linkages
2..14
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 15
ggggncgtcg acgaggggg      19

SEQ ID NO: 16          moltype = DNA length = 19
FEATURE
misc_feature           Location/Qualifiers
1..19
note = Synthetic oligonucleotide
8
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
1..19
mol_type = other DNA
organism = synthetic construct
15..18
mod_base = OTHER
note = Phosphorothioate linkages
2..14
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 16
gggtcgncc acgaggggg      19

SEQ ID NO: 17          moltype = DNA length = 19
FEATURE
misc_feature           Location/Qualifiers
1..19
note = Synthetic oligonucleotide
5
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
8
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
1..19
mol_type = other DNA
organism = synthetic construct
15..18
mod_base = OTHER
note = Phosphorothioate linkages
2..14
mod_base = OTHER
note = Phosphodiester linkages

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-continued

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SEQUENCE: 17
ggggncgncg acgaggggg 19

SEQ ID NO: 18      moltype = DNA  length = 21
FEATURE          Location/Qualifiers
misc_feature    1..21
note = Synthetic oligonucleotide
modified_base   11
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source          1..21
mol_type = other DNA
organism = synthetic construct
order(1..2,16..20)
modified_base   mod_base = OTHER
note = Phosphorothioate linkages
modified_base   3..15
mod_base = OTHER
note = Phosphodiester linkages

SEQUENCE: 18
ggggacgagc ncgtcgaaaa g 21

SEQ ID NO: 19      moltype = DNA  length = 21
FEATURE          Location/Qualifiers
misc_feature    1..21
note = Synthetic oligonucleotide
modified_base   12
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source          1..21
mol_type = other DNA
organism = synthetic construct
order(1..2,17..20)
modified_base   mod_base = OTHER
note = Phosphorothioate linkages
modified_base   3..16
mod_base = OTHER
note = Phosphodiester linkages

SEQUENCE: 19
gggggacgag cncgtcgaaa g 21

SEQ ID NO: 20      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature    1..20
note = Synthetic oligonucleotide
modified_base   11
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source          1..20
mol_type = other DNA
organism = synthetic construct
modified_base   16..19
mod_base = OTHER
note = Phosphorothioate linkages
modified_base   2..15
mod_base = OTHER
note = Phosphodiester linkages

SEQUENCE: 20
ggggacgagc ncgtcgaaaa g 20

SEQ ID NO: 21      moltype = DNA  length = 19
FEATURE          Location/Qualifiers
misc_feature    1..19
note = Synthetic oligonucleotide
modified_base   11
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source          1..19
mol_type = other DNA
organism = synthetic construct
modified_base   16..18
mod_base = OTHER
note = Phosphorothioate linkages
modified_base   2..15
mod_base = OTHER
note = Phosphodiester linkages

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-continued

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SEQUENCE: 21
ggggacgagc ncgtcgaaaa                                     19

SEQ ID NO: 22      moltype = DNA  length = 20
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modified_base    9
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source          1..20
mol_type = other DNA
organism = synthetic construct
order(1..2,15..19)
modified_base    mod_base = OTHER
note = Phosphorothioate linkages
modified_base    3..14
mod_base = OTHER
note = Phosphodiester linkages

SEQUENCE: 22
ggggacganc gtcggggggg                                     20

SEQ ID NO: 23      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide
modified_base    10
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source          1..20
mol_type = other DNA
organism = synthetic construct
order(1..2,16..19)
modified_base    mod_base = OTHER
note = Phosphorothioate linkages
modified_base    3..15
mod_base = OTHER
note = Phosphodiester linkages

SEQUENCE: 23
gggggacgan cgtcgaaaaa                                     20

SEQ ID NO: 24      moltype = DNA  length = 19
FEATURE          Location/Qualifiers
misc_feature     1..19
note = Synthetic oligonucleotide
modified_base    9
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source          1..19
mol_type = other DNA
organism = synthetic construct
modified_base    15..18
mod_base = OTHER
note = Phosphorothioate linkages
modified_base    2..14
mod_base = OTHER
note = Phosphodiester linkages

SEQUENCE: 24
ggggacganc gtcggggggg                                     19

SEQ ID NO: 25      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide
modified_base    9
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base    12
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source          1..20
mol_type = other DNA
organism = synthetic construct
order(1..2,15..19)
modified_base    mod_base = OTHER
note = Phosphorothioate linkages

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modified_base	3..14	
	mod_base = OTHER	
	note = Phosphodiester linkages	
SEQUENCE: 25		
ggggacganc gncggggggg		20
SEQ ID NO: 26	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
modified_base	note = Synthetic oligonucleotide	
	10	
	mod_base = OTHER	
	note = 5-iodo-2-prime-deoxyuridine	
modified_base	13	
	mod_base = OTHER	
	note = 5-iodo-2-prime-deoxyuridine	
source	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
modified_base	order(1..2,15..19)	
	mod_base = OTHER	
	note = Phosphorothioate linkages	
modified_base	3..14	
	mod_base = OTHER	
	note = Phosphodiester linkages	
SEQUENCE: 26		
gggggacgan gncggggggg		20
SEQ ID NO: 27	moltype = DNA length = 19	
FEATURE	Location/Qualifiers	
misc_feature	1..19	
modified_base	note = Synthetic oligonucleotide	
	9	
	mod_base = OTHER	
	note = 5-iodo-2-prime-deoxyuridine	
modified_base	12	
	mod_base = OTHER	
	note = 5-iodo-2-prime-deoxyuridine	
source	1..19	
	mol_type = other DNA	
	organism = synthetic construct	
modified_base	15..18	
	mod_base = OTHER	
	note = Phosphorothioate linkages	
modified_base	2..14	
	mod_base = OTHER	
	note = Phosphodiester linkages	
SEQUENCE: 27		
ggggacganc gncgggggg		19
SEQ ID NO: 28	moltype = DNA length = 18	
FEATURE	Location/Qualifiers	
misc_feature	1..18	
modified_base	note = Synthetic oligonucleotide	
	9	
	mod_base = OTHER	
	note = 5-iodo-2-prime-deoxyuridine	
modified_base	12	
	mod_base = OTHER	
	note = 5-iodo-2-prime-deoxyuridine	
source	1..18	
	mol_type = other DNA	
	organism = synthetic construct	
modified_base	15..17	
	mod_base = OTHER	
	note = Phosphorothioate linkages	
modified_base	2..14	
	mod_base = OTHER	
	note = Phosphodiester linkages	
SEQUENCE: 28		
ggggacganc gncggggg		18
SEQ ID NO: 29	moltype = DNA length = 22	
FEATURE	Location/Qualifiers	
misc_feature	1..22	
	note = Synthetic oligonucleotide	

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modified_base      9
    mod_base = OTHER
    note = 5-iodo-2-prime-deoxyuridine
source          1..22
    mol_type = other DNA
    organism = synthetic construct
modified_base     17..21
    mod_base = OTHER
    note = Phosphorothioate linkages
modified_base     2..16
    mod_base = OTHER
    note = Phosphodiester linkages
SEQUENCE: 29
ggggacganc gaacgtgggg gg                                22

SEQ ID NO: 30      moltype = DNA length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide
modified_base      9
    mod_base = OTHER
    note = 5-iodo-2-prime-deoxyuridine
source          1..21
    mol_type = other DNA
    organism = synthetic construct
modified_base     17..20
    mod_base = OTHER
    note = Phosphorothioate linkages
modified_base     3..16
    mod_base = OTHER
    note = Phosphodiester linkages
SEQUENCE: 30
ggggacganc gaacgtgggg g                                21

SEQ ID NO: 31      moltype = DNA length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide
modified_base      9
    mod_base = OTHER
    note = 5-iodo-2-prime-deoxyuridine
source          1..20
    mol_type = other DNA
    organism = synthetic construct
modified_base     17..19
    mod_base = OTHER
    note = Phosphorothioate linkages
modified_base     2..16
    mod_base = OTHER
    note = Phosphodiester linkages
SEQUENCE: 31
ggggacganc gaacgtgggg                                20

SEQ ID NO: 32      moltype = DNA length = 22
FEATURE           Location/Qualifiers
misc_feature      1..22
note = Synthetic oligonucleotide
modified_base      9
    mod_base = OTHER
    note = 5-iodo-2-prime-deoxyuridine
modified_base     16
    mod_base = OTHER
    note = 5-iodo-2-prime-deoxyuridine
source          1..22
    mol_type = other DNA
    organism = synthetic construct
modified_base     17..21
    mod_base = OTHER
    note = Phosphorothioate linkages
modified_base     2..16
    mod_base = OTHER
    note = Phosphodiester linkages
SEQUENCE: 32
ggggacganc gaacgngggg gg                                22

SEQ ID NO: 33      moltype = DNA length = 21

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FEATURE Location/Qualifiers
misc_feature 1..21
modified_base note = Synthetic oligonucleotide
9
modified_base mod_base = OTHER
note = 5-ido-2-prime-deoxyuridine
16
modified_base mod_base = OTHER
note = 5-ido-2-prime-deoxyuridine
1..21
source mol_type = other DNA
organism = synthetic construct
order(1..2,17..20)
modified_base mod_base = OTHER
note = Phosphorothioate linkages
3..16
modified_base mod_base = OTHER
note = Phosphodiester linkages

SEQUENCE: 33
ggggacganc gaacgngggg g 21

SEQ ID NO: 34
FEATURE moltype = DNA length = 20
misc_feature Location/Qualifiers
1..20
modified_base note = Synthetic oligonucleotide
9
modified_base mod_base = OTHER
note = 5-ido-2-prime-deoxyuridine
16
modified_base mod_base = OTHER
note = 5-ido-2-prime-deoxyuridine
1..20
source mol_type = other DNA
organism = synthetic construct
17..19
modified_base mod_base = OTHER
note = Phosphorothioate linkages
2..16
modified_base mod_base = OTHER
note = Phosphodiester linkages

SEQUENCE: 34
ggggacganc gaacgngggg g 20

SEQ ID NO: 35
FEATURE moltype = DNA length = 27
misc_feature Location/Qualifiers
1..27
modified_base note = Synthetic oligonucleotide
5
modified_base mod_base = OTHER
note = 5-ido-2-prime-deoxyuridine
1..27
source mol_type = other DNA
organism = synthetic construct
22..26
modified_base mod_base = OTHER
note = Phosphorothioate linkages
2..21
modified_base mod_base = OTHER
note = Phosphodiester linkages

SEQUENCE: 35
ggggncgacg tcgacgtcga ggggggg 27

SEQ ID NO: 36
FEATURE moltype = DNA length = 25
misc_feature Location/Qualifiers
1..25
modified_base note = Synthetic oligonucleotide
5
modified_base mod_base = OTHER
note = 5-ido-2-prime-deoxyuridine
1..25
source mol_type = other DNA
organism = synthetic construct
22..24
modified_base mod_base = OTHER
note = Phosphorothioate linkages
2..21
modified_base mod_base = OTHER
note = Phosphodiester linkages

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SEQUENCE: 36          mod_base = OTHER
                      note = Phosphodiester linkages
ggggncgacg tcgacgtcga ggggg                         25

SEQ ID NO: 37          moltype = DNA  length = 27
FEATURE                  Location/Qualifiers
misc_feature             1..27
                        note = Synthetic oligonucleotide
modified_base            5
                        mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base            11
                        mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source                  1..27
                        mol_type = other DNA
organism = synthetic construct
modified_base            22..26
                        mod_base = OTHER
note = Phosphorothioate linkages
modified_base            2..21
                        mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 37          ggggnncgacg ncgacgtcga gggggggg                     27

SEQ ID NO: 38          moltype = DNA  length = 25
FEATURE                  Location/Qualifiers
misc_feature             1..25
                        note = Synthetic oligonucleotide
modified_base            5
                        mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base            11
                        mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source                  1..25
                        mol_type = other DNA
organism = synthetic construct
modified_base            22..24
                        mod_base = OTHER
note = Phosphorothioate linkages
modified_base            2..21
                        mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 38          ggggnncgacg ncgacgtcga gggggg                         25

SEQ ID NO: 39          moltype = DNA  length = 27
FEATURE                  Location/Qualifiers
misc_feature             1..27
                        note = Synthetic oligonucleotide
modified_base            5
                        mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base            17
                        mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source                  1..27
                        mol_type = other DNA
organism = synthetic construct
modified_base            22..26
                        mod_base = OTHER
note = Phosphorothioate linkages
modified_base            2..21
                        mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 39          ggggnncgacg tcgacgnncga gggggggg                     27

SEQ ID NO: 40          moltype = DNA  length = 25
FEATURE                  Location/Qualifiers
misc_feature             1..25
                        note = Synthetic oligonucleotide
modified_base            5

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modified_base      mod_base = OTHER
                   note = 5-iodo-2-prime-deoxyuridine
17
modified_base      mod_base = OTHER
                   note = 5-iodo-2-prime-deoxyuridine
source           1..25
                   mol_type = other DNA
                   organism = synthetic construct
modified_base      22..24
                   mod_base = OTHER
                   note = Phosphorothioate linkages
modified_base      2..21
                   mod_base = OTHER
                   note = Phosphodiester linkages
SEQUENCE: 40
ggggncgacg tcgacgncga gggggg                                         25

SEQ_ID NO: 41      moltype = DNA length = 27
FEATURE          Location/Qualifiers
misc_feature     1..27
                   note = Synthetic oligonucleotide
modified_base      5
                   mod_base = OTHER
                   note = 5-iodo-2-prime-deoxyuridine
modified_base      11
                   mod_base = OTHER
                   note = 5-iodo-2-prime-deoxyuridine
modified_base      17
                   mod_base = OTHER
                   note = 5-iodo-2-prime-deoxyuridine
modified_base      1..27
                   mol_type = other DNA
                   organism = synthetic construct
source           22..26
                   mod_base = OTHER
                   note = Phosphorothioate linkages
modified_base      2..21
                   mod_base = OTHER
                   note = Phosphodiester linkages
SEQUENCE: 41
ggggncgacg ncgacgncga gggggggg                                         27

SEQ_ID NO: 42      moltype = DNA length = 25
FEATURE          Location/Qualifiers
misc_feature     1..25
                   note = Synthetic oligonucleotide
modified_base      5
                   mod_base = OTHER
                   note = 5-iodo-2-prime-deoxyuridine
modified_base      11
                   mod_base = OTHER
                   note = 5-iodo-2-prime-deoxyuridine
modified_base      17
                   mod_base = OTHER
                   note = 5-iodo-2-prime-deoxyuridine
modified_base      1..25
                   mol_type = other DNA
                   organism = synthetic construct
source           22..24
                   mod_base = OTHER
                   note = Phosphorothioate linkages
modified_base      2..21
                   mod_base = OTHER
                   note = Phosphodiester linkages
SEQUENCE: 42
ggggncgacg ncgacgncga gggggg                                         25

SEQ_ID NO: 43      moltype = DNA length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
                   note = Synthetic oligonucleotide
source           1..20
                   mol_type = other DNA
                   organism = synthetic construct
modified_base      order(1..2,15..19)
                   mod_base = OTHER

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note = Phosphorothioate linkages  
 modified\_base  
 SEQUENCE: 43  
 ggggtcaacg ttgagggggg  
 SEQ ID NO: 44 moltype = DNA length = 24  
 FEATURE Location/Qualifiers  
 misc\_feature 1..24  
 source note = Synthetic oligonucleotide  
 1..24  
 mol\_type = other DNA  
 organism = synthetic construct  
 modified\_base 1..24  
 mod\_base = OTHER  
 note = Phosphorothioate linkages  
 SEQUENCE: 44  
 tcgtcgttt gtcgttttgt cgtt  
 SEQ ID NO: 45 moltype = DNA length = 20  
 FEATURE Location/Qualifiers  
 misc\_feature 1..20  
 source note = Synthetic oligonucleotide  
 1..20  
 mol\_type = other DNA  
 organism = synthetic construct  
 modified\_base 1..20  
 mod\_base = OTHER  
 note = Phosphorothioate linkages  
 SEQUENCE: 45  
 ggggtcgctg ttttgggggg  
 SEQ ID NO: 46 moltype = DNA length = 24  
 FEATURE Location/Qualifiers  
 misc\_feature 1..24  
 source note = Synthetic oligonucleotide  
 1..24  
 mol\_type = other DNA  
 organism = synthetic construct  
 modified\_base 1..24  
 mod\_base = OTHER  
 note = Phosphorothioate linkages  
 SEQUENCE: 46  
 tcgtcgttt gtcgttttgt gggg  
 SEQ ID NO: 47 moltype = DNA length = 20  
 FEATURE Location/Qualifiers  
 misc\_feature 1..20  
 source note = Synthetic oligonucleotide  
 1..20  
 mol\_type = other DNA  
 organism = synthetic construct  
 modified\_base 1..20  
 mod\_base = OTHER  
 note = Phosphorothioate linkages  
 SEQUENCE: 47  
 ggggtcgacg tcgagggggg  
 SEQ ID NO: 48 moltype = DNA length = 20  
 FEATURE Location/Qualifiers  
 misc\_feature 1..20  
 source note = Synthetic oligonucleotide  
 1..20  
 mol\_type = other DNA  
 organism = synthetic construct  
 modified\_base 1..20  
 mod\_base = OTHER  
 note = Phosphorothioate linkages  
 SEQUENCE: 48  
 ggggtcatcg atgagggggg  
 SEQ ID NO: 49 moltype = DNA length = 20  
 FEATURE Location/Qualifiers  
 misc\_feature 1..20  
 note = Synthetic oligonucleotide

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source          1..20
               mol_type = other DNA
               organism = synthetic construct
modified_base   order(1..2,15..19)
               mod_base = OTHER
               note = Phosphorothioate linkages
modified_base   3..14
               mod_base = OTHER
               note = Phosphodiester linkages
SEQUENCE: 49
gggggacat cgtcgaaaaa                                         20

SEQ ID NO: 50      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide
source          1..20
               mol_type = other DNA
               organism = synthetic construct
modified_base   1..20
               mod_base = OTHER
               note = Phosphorothioate linkages
SEQUENCE: 50
gggggtcgta cgacgggggg                                         20

SEQ ID NO: 51      moltype = DNA  length = 22
FEATURE          Location/Qualifiers
misc_feature     1..22
note = Synthetic oligonucleotide
source          1..22
               mol_type = other DNA
               organism = synthetic construct
modified_base   order(1..2,17..21)
               mod_base = OTHER
               note = Phosphorothioate linkages
modified_base   3..16
               mod_base = OTHER
               note = Phosphodiester linkages
SEQUENCE: 51
gggggacat atcgctgggg gg                                         22

SEQ ID NO: 52      moltype = DNA  length = 22
FEATURE          Location/Qualifiers
misc_feature     1..22
note = Synthetic oligonucleotide
source          1..22
               mol_type = other DNA
               organism = synthetic construct
modified_base   order(1..2,17..21)
               mod_base = OTHER
               note = Phosphorothioate linkages
modified_base   3..16
               mod_base = OTHER
               note = Phosphodiester linkages
SEQUENCE: 52
gggggacgac gtcgtcgaaa gg                                         22

SEQ ID NO: 53      moltype = DNA  length = 22
FEATURE          Location/Qualifiers
misc_feature     1..22
note = Synthetic oligonucleotide
source          1..22
               mol_type = other DNA
               organism = synthetic construct
modified_base   order(1..2,17..21)
               mod_base = OTHER
               note = Phosphorothioate linkages
modified_base   3..16
               mod_base = OTHER
               note = Phosphodiester linkages
SEQUENCE: 53
gggggacgag ctgctcgaaa gg                                         22

SEQ ID NO: 54      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20

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source          note = Synthetic oligonucleotide
1..20
mol_type = other DNA
organism = synthetic construct
modified_base   order(1..2,15..19)
mod_base = OTHER
note = Phosphorothioate linkages
3..14
modified_base   mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 54
gggggacgtc cgtcggggggg                                     20

SEQ ID NO: 55      moltype = DNA length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide
source            1..21
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..2,16..20)
mod_base = OTHER
note = Phosphorothioate linkages
3..15
modified_base     mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 55
gggggacgtat cgttgggggg g                                         21

SEQ ID NO: 56      moltype = DNA length = 19
FEATURE           Location/Qualifiers
misc_feature      1..19
note = Synthetic oligonucleotide
source            1..19
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..2,15..18)
mod_base = OTHER
note = Phosphorothioate linkages
3..14
modified_base     mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 56
gggggaacgtat cgtcgggggg                                     19

SEQ ID NO: 57      moltype = DNA length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide
source            1..21
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..2,16..20)
mod_base = OTHER
note = Phosphorothioate linkages
3..15
modified_base     mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 57
ggggggacgtat tcgtcggggg g                                         21

SEQ ID NO: 58      moltype = DNA length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide
source            1..21
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..2,16..20)
mod_base = OTHER
note = Phosphorothioate linkages
3..15
modified_base     mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 58
gggggacgtat cgtcgggggg g                                         21

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SEQ_ID NO: 59          moltype = DNA  length = 21
FEATURE
misc_feature           Location/Qualifiers
1..21
note = Synthetic oligonucleotide
source
1..21
mol_type = other DNA
organism = synthetic construct
modified_base           order(1..2,16..20)
mod_base = OTHER
note = Phosphorothioate linkages
modified_base           3..15
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 59
gggggtcatc gatgaggggg g                                21

SEQ_ID NO: 60          moltype = DNA  length = 20
FEATURE
misc_feature           Location/Qualifiers
1..20
note = Synthetic oligonucleotide
source
1..20
mol_type = other DNA
organism = synthetic construct
modified_base           order(1..2,15..19)
mod_base = OTHER
note = Phosphorothioate linkages
modified_base           3..14
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 60
gggtcgctcg acgagggggg                                20

SEQ_ID NO: 61          moltype = DNA  length = 22
FEATURE
misc_feature           Location/Qualifiers
1..22
note = Synthetic oligonucleotide
source
1..22
mol_type = other DNA
organism = synthetic construct
modified_base           order(1..2,17..21)
mod_base = OTHER
note = Phosphorothioate linkages
modified_base           3..16
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 61
gggtcgttc gaacgagggg gg                                22

SEQ_ID NO: 62          moltype = DNA  length = 22
FEATURE
misc_feature           Location/Qualifiers
1..22
note = Synthetic oligonucleotide
source
1..22
mol_type = other DNA
organism = synthetic construct
modified_base           order(1..2,17..21)
mod_base = OTHER
note = Phosphorothioate linkages
modified_base           3..16
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 62
ggggacgttc gaacgtgggg gg                                22

SEQ_ID NO: 63          moltype = DNA  length = 22
FEATURE
misc_feature           Location/Qualifiers
1..22
note = Synthetic oligonucleotide
source
1..22
mol_type = other DNA
organism = synthetic construct
modified_base           order(1..2,17..21)
mod_base = OTHER
note = Phosphorothioate linkages
modified_base           3..16

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mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 63
ggggAACGAC gtcgttgggg gg                                22

SEQ ID NO: 64      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
                  note = Synthetic oligonucleotide
source           1..20
                  mol_type = other DNA
organism          synthetic construct
modified_base    order(1..2,15..19)
mod_base          OTHER
note = Phosphorothioate linkages
modified_base    3..14
mod_base          OTHER
note = Phosphodiester linkages
SEQUENCE: 64
ggggAACGTA cgtcgggggg                                20

SEQ ID NO: 65      moltype = DNA  length = 24
FEATURE          Location/Qualifiers
misc_feature     1..24
                  note = Synthetic oligonucleotide
source           1..24
                  mol_type = other DNA
organism          synthetic construct
modified_base    order(1..2,19..23)
mod_base          OTHER
note = Phosphorothioate linkages
modified_base    3..18
mod_base          OTHER
note = Phosphodiester linkages
SEQUENCE: 65
ggggAACGTA cgtacgttgg gggg                                24

SEQ ID NO: 66      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
                  note = Synthetic oligonucleotide
source           1..20
                  mol_type = other DNA
organism          synthetic construct
modified_base    order(1..2,15..19)
mod_base          OTHER
note = Phosphorothioate linkages
modified_base    3..14
mod_base          OTHER
note = Phosphodiester linkages
SEQUENCE: 66
ggggTCACCG gtgagggggg                                20

SEQ ID NO: 67      moltype = DNA  length = 24
FEATURE          Location/Qualifiers
misc_feature     1..24
                  note = Synthetic oligonucleotide
source           1..24
                  mol_type = other DNA
organism          synthetic construct
modified_base    order(1..2,19..23)
mod_base          OTHER
note = Phosphorothioate linkages
modified_base    3..18
mod_base          OTHER
note = Phosphodiester linkages
SEQUENCE: 67
ggggTcgcacg tacgtcgagg gggg                                24

SEQ ID NO: 68      moltype = DNA  length = 22
FEATURE          Location/Qualifiers
misc_feature     1..22
                  note = Synthetic oligonucleotide
source           1..22
                  mol_type = other DNA
organism          synthetic construct

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modified_base	order(1..2,17..21) mod_base = OTHER note = Phosphorothioate linkages	
modified_base	3..16 mod_base = OTHER note = Phosphodiester linkages	
SEQUENCE: 68	ggggaccggt accgggtgggg gg	22
SEQ ID NO: 69	moltype = DNA length = 19 Location/Qualifiers	
FEATURE	1..19	
misc_feature	note = Synthetic oligonucleotide	
source	1..19 mol_type = other DNA organism = synthetic construct	
modified_base	order(1..2,14..18) mod_base = OTHER note = Phosphorothioate linkages	
modified_base	3..13 mod_base = OTHER note = Phosphodiester linkages	
SEQUENCE: 69	gggtcgacgt cgagggggg	19
SEQ ID NO: 70	moltype = DNA length = 18 Location/Qualifiers	
FEATURE	1..18	
misc_feature	note = Synthetic oligonucleotide	
source	1..18 mol_type = other DNA organism = synthetic construct	
modified_base	order(1..2,14..18) mod_base = OTHER note = Phosphorothioate linkages	
modified_base	3..13 mod_base = OTHER note = Phosphodiester linkages	
SEQUENCE: 70	gggtcgacgt tcgagggg	18
SEQ ID NO: 71	moltype = DNA length = 22 Location/Qualifiers	
FEATURE	1..22	
misc_feature	note = Synthetic oligonucleotide	
source	1..22 mol_type = other DNA organism = synthetic construct	
modified_base	order(1..2,17..21) mod_base = OTHER note = Phosphorothioate linkages	
modified_base	3..16 mod_base = OTHER note = Phosphodiester linkages	
SEQUENCE: 71	gggaaacgtt aacgttgggg gg	22
SEQ ID NO: 72	moltype = DNA length = 19 Location/Qualifiers	
FEATURE	1..19	
misc_feature	note = Synthetic oligonucleotide	
source	1..19 mol_type = other DNA organism = synthetic construct	
modified_base	order(1..2,15..18) mod_base = OTHER note = Phosphorothioate linkages	
modified_base	3..14 mod_base = OTHER note = Phosphodiester linkages	
SEQUENCE: 72	ggggacgtcg acgtggggg	19
SEQ ID NO: 73	moltype = DNA length = 20 Location/Qualifiers	
FEATURE	1..20	
misc_feature		

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source          note = Synthetic oligonucleotide
1..20
mol_type = other DNA
organism = synthetic construct
modified_base   order(1..2,15..19)
mod_base = OTHER
note = Phosphorothioate linkages
3..14
modified_base   mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 73
gggggtcggtt cgttggggggg                                         20

SEQ ID NO: 74          moltype = DNA length = 19
FEATURE          Location/Qualifiers
misc_feature    1..19
note = Synthetic oligonucleotide
source          1..19
mol_type = other DNA
organism = synthetic construct
modified_base   order(1..2,14..18)
mod_base = OTHER
note = Phosphorothioate linkages
3..13
modified_base   mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 74
gggacgatcg tcggggggg                                         19

SEQ ID NO: 75          moltype = DNA length = 20
FEATURE          Location/Qualifiers
misc_feature    1..20
note = Synthetic oligonucleotide
source          1..20
mol_type = other DNA
organism = synthetic construct
modified_base   order(1..2,14..19)
mod_base = OTHER
note = Phosphorothioate linkages
3..13
modified_base   mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 75
gggtcgctga cgagggggggg                                         20

SEQ ID NO: 76          moltype = DNA length = 19
FEATURE          Location/Qualifiers
misc_feature    1..19
note = Synthetic oligonucleotide
source          1..19
mol_type = other DNA
organism = synthetic construct
modified_base   order(1..2,14..18)
mod_base = OTHER
note = Phosphorothioate linkages
3..13
modified_base   mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 76
ggtcgtcgac gagggggggg                                         19

SEQ ID NO: 77          moltype = DNA length = 20
FEATURE          Location/Qualifiers
misc_feature    1..20
note = Synthetic oligonucleotide
source          1..20
mol_type = other DNA
organism = synthetic construct
modified_base   order(1..2,15..19)
mod_base = OTHER
note = Phosphorothioate linkages
3..14
modified_base   mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 77
ggggacgatc gtcggggggg                                         20

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SEQ_ID NO: 78      moltype = DNA  length = 27
FEATURE
misc_feature
1..27
note = Synthetic oligonucleotide
source
1..27
mol_type = other DNA
organism = synthetic construct
modified_base
order(1..2,22..26)
mod_base = OTHER
note = Phosphorothioate linkages
modified_base
3..21
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 78
gggttcgacg tcgacgtcga gggggggg                                27

SEQ_ID NO: 79      moltype = DNA  length = 21
FEATURE
misc_feature
1..21
note = Synthetic oligonucleotide
source
1..21
mol_type = other DNA
organism = synthetic construct
modified_base
order(1..2,16..20)
mod_base = OTHER
note = Phosphorothioate linkages
modified_base
3..15
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 79
ggggacgacg tcgtgggggg g                                21

SEQ_ID NO: 80      moltype = DNA  length = 22
FEATURE
misc_feature
1..22
note = Synthetic oligonucleotide
source
1..22
mol_type = other DNA
organism = synthetic construct
modified_base
order(1..2,17..21)
mod_base = OTHER
note = Phosphorothioate linkages
modified_base
3..16
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 80
gggggacgag ctgcgtgggg gg                                22

SEQ_ID NO: 81      moltype = DNA  length = 22
FEATURE
misc_feature
1..22
note = Synthetic oligonucleotide
source
1..22
mol_type = other DNA
organism = synthetic construct
modified_base
order(1..2,17..21)
mod_base = OTHER
note = Phosphorothioate linkages
modified_base
3..16
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 81
ggggacgatc gaacgtgggg gg                                22

SEQ_ID NO: 82      moltype = DNA  length = 30
FEATURE
misc_feature
1..30
note = Synthetic oligonucleotide
source
1..30
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 82
gggggggggg gacgatcgta gggggggggg                                30

SEQ_ID NO: 83      moltype = DNA  length = 22

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FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Synthetic oligonucleotide
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 83	
tcgtcgttt cggcgcgcgc cg	22
SEQ ID NO: 84	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Synthetic oligonucleotide
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 84	
tcgtcgttt cggcggccgc cg	22
SEQ ID NO: 85	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Synthetic oligonucleotide
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 85	
tcgtcgttt cggcgcgcgc cg	22
SEQ ID NO: 86	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Synthetic oligonucleotide
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 86	
tcgtcgttt cggcgcgcgc cg	22
SEQ ID NO: 87	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Synthetic oligonucleotide
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 87	
tcgtcgttt cggccgcgc gc gg	22
SEQ ID NO: 88	moltype = DNA length = 27
FEATURE	Location/Qualifiers
misc_feature	1..27
	note = Synthetic oligonucleotide
source	1..27
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 88	
tcgtcgttt cggcgcgcgc cgtttt	27
SEQ ID NO: 89	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Synthetic oligonucleotide
source	1..22
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 89	
tcctgacgtt cggcgcgcgc cg	22
SEQ ID NO: 90	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Synthetic oligonucleotide
modified_base	2
	mod_base = m5c
modified_base	5

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modified_base    mod_base = m5c
modified_base    11
modified_base    mod_base = m5c
modified_base    14
modified_base    mod_base = m5c
modified_base    16
modified_base    mod_base = m5c
modified_base    18
modified_base    mod_base = m5c
modified_base    20..21
modified_base    mod_base = m5c
source          1..22
source          mol_type = other DNA
source          organism = synthetic construct
SEQUENCE: 90
tntgtngttt rggngngnngn ng                                22

SEQ ID NO: 91      moltype = DNA  length = 22
FEATURE           Location/Qualifiers
misc_feature      1..22
note = Synthetic oligonucleotide
source           1..22
source           mol_type = other DNA
source           organism = synthetic construct
SEQUENCE: 91
tcctgacgtt cggcgccgc cc                                22

SEQ ID NO: 92      moltype = DNA  length = 22
FEATURE           Location/Qualifiers
misc_feature      1..22
note = Synthetic oligonucleotide
source           1..22
source           mol_type = other DNA
source           organism = synthetic construct
SEQUENCE: 92
tcggcgcgcg ccgtcgctgt tt                                22

SEQ ID NO: 93      moltype = DNA  length = 22
FEATURE           Location/Qualifiers
misc_feature      1..22
note = Synthetic oligonucleotide
source           1..22
source           mol_type = other DNA
source           organism = synthetic construct
SEQUENCE: 93
tcgtcggtt cggcgccga cg                                22

SEQ ID NO: 94      moltype = DNA  length = 22
FEATURE           Location/Qualifiers
misc_feature      1..22
note = Synthetic oligonucleotide
source           1..22
source           mol_type = other DNA
source           organism = synthetic construct
SEQUENCE: 94
tcgtcggtt cgtcgccgc cg                                22

SEQ ID NO: 95      moltype = DNA  length = 22
FEATURE           Location/Qualifiers
misc_feature      1..22
note = Synthetic oligonucleotide
source           1..22
source           mol_type = other DNA
source           organism = synthetic construct
SEQUENCE: 95
tcgtcggtt cgacggccgc cg                                22

SEQ ID NO: 96      moltype = DNA  length = 22
FEATURE           Location/Qualifiers
misc_feature      1..22
note = Synthetic oligonucleotide
source           1..22
source           mol_type = other DNA
source           organism = synthetic construct
SEQUENCE: 96
tcgtcggtt cggcgccgt cg                                22

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SEQ ID NO: 97      moltype = DNA  length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
source            note = Synthetic oligonucleotide
                  1..21
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 97      tcgtcgttc gacggccgtc g          21
                  

SEQ ID NO: 98      moltype = DNA  length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
source            note = Synthetic oligonucleotide
                  1..21
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 98      tcgtcgttc gacgatcgtc g          21
                  

SEQ ID NO: 99      moltype = DNA  length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
source            note = Synthetic oligonucleotide
                  1..21
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 99      tcgtcgttc gacgtacgtc g          21
                  

SEQ ID NO: 100     moltype = DNA  length = 18
FEATURE           Location/Qualifiers
misc_feature      1..18
source            note = Synthetic oligonucleotide
                  1..18
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 100     tcgtcgcgac ggccgtcg          18
                  

SEQ ID NO: 101     moltype = DNA  length = 18
FEATURE           Location/Qualifiers
misc_feature      1..18
source            note = Synthetic oligonucleotide
                  1..18
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 101     tcgtcgcgac gatcgctg          18
                  

SEQ ID NO: 102     moltype = DNA  length = 18
FEATURE           Location/Qualifiers
misc_feature      1..18
source            note = Synthetic oligonucleotide
                  1..18
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 102     tcgtcgcgac gtacgtcg          18
                  

SEQ ID NO: 103     moltype = DNA  length = 22
FEATURE           Location/Qualifiers
misc_feature      1..22
source            note = Synthetic oligonucleotide
                  1..22
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 103     tcgtttttt cgacggccgt cg          22
                  

SEQ ID NO: 104     moltype = DNA  length = 22
FEATURE           Location/Qualifiers
misc_feature      1..22
source            note = Synthetic oligonucleotide
                  1..22

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mol_type = other DNA
organism = synthetic construct
SEQUENCE: 104
tcgtttttt cgacgatcggt cg                                22

SEQ_ID NO: 105      moltype = DNA  length = 22
FEATURE           Location/Qualifiers
misc_feature      1..22
                  note = Synthetic oligonucleotide
source            1..22
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 105
tcgtttttt cgacgtacgt cg                                22

SEQ_ID NO: 106      moltype = DNA  length = 18
FEATURE           Location/Qualifiers
misc_feature      1..18
                  note = Synthetic oligonucleotide
source            1..18
                  mol_type = other DNA
                  organism = synthetic construct
modified_base     order(1..4,5..7,8..12,13..15,16..18)
mod_base          OTHER
modified_base     note = Stabilized internucleotide linkages
                  order(4..5,7..8,12..13,15..16)
mod_base          OTHER
note              = Phosphodiester or phosphodiester-like
                  internucleotide linkages
SEQUENCE: 106
tttcgtcggt tcgtcgtt                                         18

SEQ_ID NO: 107      moltype = DNA  length = 18
FEATURE           Location/Qualifiers
misc_feature      1..18
                  note = Synthetic oligonucleotide
source            1..18
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 107
tcgtcgttcg ggcggccg                                         18

SEQ_ID NO: 108      moltype = DNA  length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
                  note = Synthetic oligonucleotide
source            1..23
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 108
tcgtcgttgt tcggcgccg ccg                                23

SEQ_ID NO: 109      moltype = DNA  length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
                  note = Synthetic oligonucleotide
source            1..23
                  mol_type = other DNA
                  organism = synthetic construct
modified_base     order(1..2,3..5,6..8,9..12,13..17,18..23)
mod_base          OTHER
modified_base     note = Phosphorothioate internucleotide linkages
                  order(2..3,5..6,8..9,12..13,17..18)
mod_base          OTHER
note              = Phosphodiester internucleotide linkages
SEQUENCE: 109
tcgtcgacga tcggcgccg ccg                                23

SEQ_ID NO: 110      moltype = DNA  length = 17
FEATURE           Location/Qualifiers
misc_feature      1..17
                  note = Synthetic oligonucleotide
source            1..17
                  mol_type = other DNA
                  organism = synthetic construct
SEQUENCE: 110

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ttcgtcgtt tgcgtt	17
SEQ ID NO: 111	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
source	note = Synthetic oligonucleotide
	1..22
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..5,6..8,9..12,13..17,18..22)
	mod_base = OTHER
modified_base	note = Stabilized internucleotide linkages
	order(2..3,5..6,8..9,12..13,17..18)
	mod_base = OTHER
	note = Phosphodiester or phosphodiester-like
	internucleotide linkages
SEQUENCE: 111	
tcgtcgct tcggcgcc	22
SEQ ID NO: 112	moltype = DNA length = 17
FEATURE	Location/Qualifiers
misc_feature	1..17
source	note = Synthetic oligonucleotide
	1..17
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..5,6..8,9..12,13..17)
	mod_base = OTHER
modified_base	note = Stabilized internucleotide linkages
	order(2..3,5..6,8..9,12..13)
	mod_base = OTHER
	note = Phosphodiester or phosphodiester-like
	internucleotide linkages
SEQUENCE: 112	
tcgtcgct tcggcgcc	17
SEQ ID NO: 113	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
source	note = Synthetic oligonucleotide
	1..21
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..5,6..8,9..12,13..17,18..21)
	mod_base = OTHER
modified_base	note = Stabilized internucleotide linkages
	order(2..3,5..6,8..9,12..13,17..18)
	mod_base = OTHER
	note = Phosphodiester or phosphodiester-like
	internucleotide linkages
SEQUENCE: 113	
tcgtcgct tcggcgcc	21
SEQ ID NO: 114	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
source	note = Synthetic oligonucleotide
	1..22
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(2..4,5..7,8..11,12..16,17..22)
	mod_base = OTHER
modified_base	note = Stabilized internucleotide linkages
	order(1..2,4..5,7..8,11..12,16..17)
	mod_base = OTHER
	note = Phosphodiester or phosphodiester-like
	internucleotide linkages
SEQUENCE: 114	
cgtcgctt cggcgccg	22
SEQ ID NO: 115	moltype = DNA length = 21
FEATURE	Location/Qualifiers
misc_feature	1..21
source	note = Synthetic oligonucleotide
	1..21
	mol_type = other DNA

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modified_base      organism = synthetic construct
                  order(1..3,4..6,7..10,11..15,16..21)
                  mod_base = OTHER
modified_base      note = Stabilized internucleotide linkages
                  order(3..4,6..7,10..11,15..16)
                  mod_base = OTHER
                  note = Phosphodiester or phosphodiester-like
                         internucleotide linkages
SEQUENCE: 115
gtcgtcgttc ggcgcgcgccc g                                21

SEQ ID NO: 116      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide
source           1..20
mol_type = other DNA
organism = synthetic construct
order(1..2,3..5,6..9,10..14,15..20)
mod_base = OTHER
modified_base     note = Stabilized internucleotide linkages
                  order(2..3,5..6,9..10,14..15)
                  mod_base = OTHER
                  note = Phosphodiester or phosphodiester-like
                         internucleotide linkages
SEQUENCE: 116
tcgtcgttcg ggcgcgcgccc                                20

SEQ ID NO: 117      moltype = DNA  length = 19
FEATURE          Location/Qualifiers
misc_feature     1..19
note = Synthetic oligonucleotide
source           1..19
mol_type = other DNA
organism = synthetic construct
order(2..4,5..8,9..13,14..19)
mod_base = OTHER
modified_base     note = Stabilized internucleotide linkages
                  order(1..2,4..5,8..9,13..14)
                  mod_base = OTHER
                  note = Phosphodiester or phosphodiester-like
                         internucleotide linkages
SEQUENCE: 117
cgtcggttcgg cgccgcgcgccc                                19

SEQ ID NO: 118      moltype = DNA  length = 18
FEATURE          Location/Qualifiers
misc_feature     1..18
note = Synthetic oligonucleotide
source           1..18
mol_type = other DNA
organism = synthetic construct
order(1..3,4..7,8..12,13..18)
mod_base = OTHER
modified_base     note = Stabilized internucleotide linkages
                  order(3..4,7..8,12..13)
                  mod_base = OTHER
                  note = Phosphodiester or phosphodiester-like
                         internucleotide linkages
SEQUENCE: 118
gtcggttcggc ggcgcgcgccc                                18

SEQ ID NO: 119      moltype = DNA  length = 17
FEATURE          Location/Qualifiers
misc_feature     1..17
note = Synthetic oligonucleotide
source           1..17
mol_type = other DNA
organism = synthetic construct
order(1..2,3..6,7..11,12..17)
mod_base = OTHER
modified_base     note = Stabilized internucleotide linkages
                  order(2..3,6..7,11..12)
                  mod_base = OTHER
                  note = Phosphodiester or phosphodiester-like
                         internucleotide linkages

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SEQUENCE: 119          moltype = DNA  length = 28
tcgttccggcg  cgcgcgg                                17

SEQ ID NO: 120          moltype = DNA  length = 28
FEATURE          Location/Qualifiers
misc_feature      1..28
note = Synthetic oligonucleotide
source           1..28
mol_type = other DNA
organism = synthetic construct
modified_base     order(11..14,25..28)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     order(1..11,14..25)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 120          moltype = DNA  length = 28
tcgtcgaacgta ttttacgacg tcgtttt                                28

SEQ ID NO: 121          moltype = DNA  length = 27
FEATURE          Location/Qualifiers
misc_feature      1..27
note = Synthetic oligonucleotide
source           1..27
mol_type = other DNA
organism = synthetic construct
modified_base     1..27
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 121          moltype = DNA  length = 27
tcgtcgaacgta ttttacgacg tcgtttt                                27

SEQ ID NO: 122          moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide
source           1..20
mol_type = other DNA
organism = synthetic construct
modified_base     1..20
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 122          moltype = DNA  length = 20
tcgtcgaacgta acgacgtcgt                                20

SEQ ID NO: 123          moltype = DNA  length = 27
FEATURE          Location/Qualifiers
misc_feature      1..27
note = Synthetic oligonucleotide
source           1..27
mol_type = other DNA
organism = synthetic construct
modified_base     order(11..14,25..27)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     order(1..11,14..25)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 123          moltype = DNA  length = 27
tcgtcgaacgta tttttcgtcg acgattt                                27

SEQ ID NO: 124          moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide
source           1..20
mol_type = other DNA
organism = synthetic construct
modified_base     1..20
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 124          moltype = DNA  length = 20
tcgtcgaacgta tcgtcgaacgta                                20

SEQ ID NO: 125          moltype = DNA  length = 20
FEATURE          Location/Qualifiers

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misc_feature          1..20
source               note = Synthetic oligonucleotide
                     1..20
                     mol_type = other DNA
                     organism = synthetic construct
modified_base         1..20
                     mod_base = OTHER
                     note = Phosphorothioate internucleotide linkages
SEQUENCE: 125        cgcgcgcg cgcgcgcg
                     20

SEQ ID NO: 126       moltype = DNA length = 20
FEATURE              Location/Qualifiers
misc_feature          1..20
                     note = Synthetic oligonucleotide
modified_base         20
                     mod_base = OTHER
                     note = Biotin appended
source               1..20
                     mol_type = other DNA
                     organism = synthetic construct
modified_base         1..20
                     mod_base = OTHER
                     note = Phosphorothioate internucleotide linkages
SEQUENCE: 126        gagaacgctc gaccttcgat
                     20

SEQ ID NO: 127       moltype = DNA length = 19
FEATURE              Location/Qualifiers
misc_feature          1..19
                     note = Synthetic oligonucleotide
source               1..19
                     mol_type = other DNA
                     organism = synthetic construct
modified_base         1..19
                     mod_base = OTHER
                     note = Phosphorothioate internucleotide linkages
SEQUENCE: 127        agtccatgg tgctcaactg
                     19

SEQ ID NO: 128       moltype = DNA length = 18
FEATURE              Location/Qualifiers
misc_feature          1..18
                     note = Synthetic oligonucleotide
source               1..18
                     mol_type = other DNA
                     organism = synthetic construct
modified_base         1..18
                     mod_base = OTHER
                     note = Phosphorothioate internucleotide linkages
SEQUENCE: 128        tctcccagcg tgcgccat
                     18

SEQ ID NO: 129       moltype = DNA length = 20
FEATURE              Location/Qualifiers
misc_feature          1..20
                     note = Synthetic oligonucleotide
source               1..20
                     mol_type = other DNA
                     organism = synthetic construct
modified_base         1..20
                     mod_base = OTHER
                     note = Phosphorothioate internucleotide linkages
SEQUENCE: 129        tccatgacgt tcctgaggtt
                     20

SEQ ID NO: 130       moltype = DNA length = 20
FEATURE              Location/Qualifiers
misc_feature          1..20
                     note = Synthetic oligonucleotide
source               1..20
                     mol_type = other DNA
                     organism = synthetic construct
modified_base         1..20
                     mod_base = OTHER
                     note = Phosphorothioate internucleotide linkages

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SEQUENCE: 130
tccaggactt ctctcaggtt                                20

SEQ ID NO: 131      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide
source          1..20
mol_type = other DNA
organism = synthetic construct
modified_base    1..20
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 131
tccacgacgt ttgcacgtt                                20

SEQ ID NO: 132      moltype = DNA  length = 24
FEATURE          Location/Qualifiers
misc_feature     1..24
note = Synthetic oligonucleotide
source          1..24
mol_type = other DNA
organism = synthetic construct
modified_base    1..24
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 132
tcgtcggtt gacgttttga cgtt                                24

SEQ ID NO: 133      moltype = DNA  length = 27
FEATURE          Location/Qualifiers
misc_feature     1..27
note = Synthetic oligonucleotide
source          1..27
mol_type = other DNA
organism = synthetic construct
modified_base    1..27
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 133
tcgcgtcggt tttgtcggtt tgacgtt                                27

SEQ ID NO: 134      moltype = DNA  length = 22
FEATURE          Location/Qualifiers
misc_feature     1..22
note = Synthetic oligonucleotide
source          1..22
mol_type = other DNA
organism = synthetic construct
modified_base    1..22
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 134
tcgcgacgtt cggcgccgcg cgcg                                22

SEQ ID NO: 135      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide
modified_base    1
mod_base = OTHER
note = Digoxigenin appended
source          1..20
mol_type = other DNA
organism = synthetic construct
modified_base    1..20
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 135
ccggccggcc ggccggccgg                                20

SEQ ID NO: 136      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide
modified_base    1

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source          mod_base = OTHER
                note = Digoxigenin appended
1..20
mol_type = other DNA
organism = synthetic construct
modified_base   1..20
                mod_base = OTHER
                note = Phosphorothioate internucleotide linkages
SEQUENCE: 136
cgcgcgcg cgcgcgcg 20

SEQ ID NO: 137      moltype = DNA length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
source            1..24
mol_type = other DNA
organism = synthetic construct
modified_base     1..24
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 137
tcaggactt ctctcagggtt tttt 24

SEQ ID NO: 138      moltype = DNA length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide
source            1..21
mol_type = other DNA
organism = synthetic construct
modified_base     1..21
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 138
gtgctcgagg atgcgcttcg c 21

SEQ ID NO: 139      moltype = DNA length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide
source            1..21
mol_type = other DNA
organism = synthetic construct
modified_base     1..21
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 139
gccgaggtcc atgtcgtaacg c 21

SEQ ID NO: 140      moltype = DNA length = 30
FEATURE           Location/Qualifiers
misc_feature      1..30
note = Synthetic oligonucleotide
source            1..30
mol_type = other DNA
organism = synthetic construct
modified_base     1..30
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 140
accgataacg gtgccgggtga cggcaccacg 30

SEQ ID NO: 141      moltype = DNA length = 30
FEATURE           Location/Qualifiers
misc_feature      1..30
note = Synthetic oligonucleotide
source            1..30
mol_type = other DNA
organism = synthetic construct
modified_base     1..30
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 141
accgataacg ttgccgggtga cggcaccacg 30

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SEQ ID NO: 142      moltype = DNA length = 30
FEATURE           Location/Qualifiers
misc_feature      1..30
note = Synthetic oligonucleotide
source            1..30
mol_type = other DNA
organism = synthetic construct
modified_base     1..30
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 142
accgatgacg tcgcgggtga cggcaccacg                                30

SEQ ID NO: 143      moltype = DNA length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
source            1..24
mol_type = other DNA
organism = synthetic construct
modified_base     1..24
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 143
cggcgccgcgc cgcggcgccgc gccc                                24

SEQ ID NO: 144      moltype = DNA length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
note = Synthetic oligonucleotide
source            1..23
mol_type = other DNA
organism = synthetic construct
modified_base     1..23
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 144
tcgatcgtt ttctgtcggtt ttt                                23

SEQ ID NO: 145      moltype = DNA length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
note = Synthetic oligonucleotide
source            1..23
mol_type = other DNA
organism = synthetic construct
modified_base     1..23
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 145
tcgtccagga ctctctcag gtt                                23

SEQ ID NO: 146      moltype = DNA length = 26
FEATURE           Location/Qualifiers
misc_feature      1..26
note = Synthetic oligonucleotide
source            1..26
mol_type = other DNA
organism = synthetic construct
modified_base     1..26
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 146
tcgtcgcca ggacttctct cagggt                                26

SEQ ID NO: 147      moltype = DNA length = 22
FEATURE           Location/Qualifiers
misc_feature      1..22
note = Synthetic oligonucleotide
source            1..22
mol_type = other DNA
organism = synthetic construct
modified_base     1..22
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 147

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tcgtgacggg cggcgccgc cc	22
SEQ ID NO: 148	moltype = DNA length = 23
FEATURE	Location/Qualifiers
misc_feature	1..23
	note = Synthetic oligonucleotide
source	1..23
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..11,12..23)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
SEQUENCE: 148	
acgacgtcgt tcggcgcccg ccg	23
SEQ ID NO: 149	moltype = DNA length = 27
FEATURE	Location/Qualifiers
misc_feature	1..27
	note = Synthetic oligonucleotide
source	1..27
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..3,16..27)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
modified_base	3..16
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 149	
ggggacgacg tcgtgcggcg gcccggc	27
SEQ ID NO: 150	moltype = DNA length = 29
FEATURE	Location/Qualifiers
misc_feature	1..29
	note = Synthetic oligonucleotide
source	1..29
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..4,5..7,8..10,11..13,17..19,20..22,23..25,26..27,28..29)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
modified_base	order(2..3,4..5,7..8,10..11,13..17,19..20,22..23,25..26,27..28)
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 150	
ccacgacgtc gtcgaagacg acgtcgtgg	29
SEQ ID NO: 151	moltype = DNA length = 24
FEATURE	Location/Qualifiers
misc_feature	1..24
	note = Synthetic oligonucleotide
source	1..24
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..6,7..8,10..12,13..14,16..18,19..20,21..24)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
modified_base	order(2..3,6..7,8..10,12..13,14..16,18..19,20..21)
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 151	
ctgcagctgc agctgcagct gcag	24
SEQ ID NO: 152	moltype = DNA length = 24
FEATURE	Location/Qualifiers
misc_feature	1..24
	note = Synthetic oligonucleotide
source	1..24
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..3,4..5,6..8,9..11,13..14,15..17,18..20,21..24)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
modified_base	order(3..4,5..6,8..9,11..13,14..15,17..18,20..21)
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages

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SEQUENCE: 152
cggccgcgtgc agcgccgcgt gcag                                24

SEQ ID NO: 153      moltype = DNA  length = 18
FEATURE          Location/Qualifiers
misc_feature     1..18
source           note = Synthetic oligonucleotide
modified_base    1..18
                  mol_type = other DNA
                  organism = synthetic construct
                  1..18
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages

SEQUENCE: 153
catgacgttt ttgatgtt                                         18

SEQ ID NO: 154      moltype = DNA  length = 17
FEATURE          Location/Qualifiers
misc_feature     1..17
source           note = Synthetic oligonucleotide
modified_base    1..17
                  mol_type = other DNA
                  organism = synthetic construct
                  1..17
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages

SEQUENCE: 154
atgacgtttt tgatgtt                                         17

SEQ ID NO: 155      moltype = DNA  length = 16
FEATURE          Location/Qualifiers
misc_feature     1..16
source           note = Synthetic oligonucleotide
modified_base    1..16
                  mol_type = other DNA
                  organism = synthetic construct
                  1..16
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages

SEQUENCE: 155
tgacgtttt gatgtt                                         16

SEQ ID NO: 156      moltype = DNA  length = 19
FEATURE          Location/Qualifiers
misc_feature     1..19
source           note = Synthetic oligonucleotide
modified_base    1..19
                  mol_type = other DNA
                  organism = synthetic construct
                  1..19
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages

SEQUENCE: 156
atgacgtttt tgatgttgt                                         19

SEQ ID NO: 157      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
source           note = Synthetic oligonucleotide
modified_base    1..20
                  mol_type = other DNA
                  organism = synthetic construct
                  order(1..8,10..20)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base    8..10
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages

SEQUENCE: 157
tccatgacgt ttttgatgtt                                         20

SEQ ID NO: 158      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
source           note = Synthetic oligonucleotide
modified_base    1..20

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modified_base      mol_type = other DNA
                   organism = synthetic construct
1..20             mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
SEQUENCE: 158     tccatgcgtt tttgaatgtt                                20

SEQ ID NO: 159     moltype = DNA length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
                   note = Synthetic oligonucleotide
source           1..20
                   mol_type = other DNA
                   organism = synthetic construct
modified_base     1..20
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
SEQUENCE: 159     tccatgacgt ctttgatgtc                                20

SEQ ID NO: 160     moltype = DNA length = 22
FEATURE          Location/Qualifiers
misc_feature     1..22
                   note = Synthetic oligonucleotide
modified_base    22
                   mod_base = OTHER
                   note = Cholesterol appended
source           1..22
                   mol_type = other DNA
                   organism = synthetic construct
modified_base    1..22
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 160     acgacgtcgt tcacgacgtc gt                                22

SEQ ID NO: 161     moltype = DNA length = 27
FEATURE          Location/Qualifiers
misc_feature     1..27
                   note = Synthetic oligonucleotide
modified_base    25..27
                   mod_base = OTHER
                   note = 1-Prime-2-prime-dideoxyribose (D spacer)
source           1..27
                   mol_type = other DNA
                   organism = synthetic construct
modified_base    1..27
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 161     acgacgtcgt ggccacgacg tcgtnnn                                27

SEQ ID NO: 162     moltype = DNA length = 27
FEATURE          Location/Qualifiers
misc_feature     1..27
                   note = Synthetic oligonucleotide
modified_base    11..14
                   mod_base = OTHER
                   note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base    25..27
                   mod_base = OTHER
                   note = 1-Prime-2-prime-dideoxyribose (D spacer)
source           1..27
                   mol_type = other DNA
                   organism = synthetic construct
modified_base    1..27
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 162     acgacgtcgt nnnnacgacg tcgtnnn                                27

SEQ ID NO: 163     moltype = DNA length = 30
FEATURE          Location/Qualifiers
misc_feature     1..30
                   note = Synthetic oligonucleotide

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modified_base      1..3
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)

modified_base      14..17
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)

modified_base      28..30
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)

source            1..30
mol_type = other DNA
organism = synthetic construct

modified_base      1..30
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 163
nnnacgacgt cgttnnnnacg acgtcgtnnn                                30

SEQ ID NO: 164          moltype = DNA length = 27
FEATURE             Location/Qualifiers
misc_feature        1..27
note = Synthetic oligonucleotide

modified_base      1..3
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)

modified_base      14..17
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)

modified_base      27
mod_base = OTHER
note = Cholesterol appended
source            1..27
mol_type = other DNA
organism = synthetic construct

modified_base      1..27
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 164
nnnacgacgt cgttnnnnacg acgtcggt                                27

SEQ ID NO: 165          moltype = DNA length = 30
FEATURE             Location/Qualifiers
misc_feature        1..30
note = Synthetic oligonucleotide

source            1..30
mol_type = other DNA
organism = synthetic construct
order(1..3,14..17,28..30)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

modified_base      order(3..14,17..28)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 165
gggacgacgt cgtggccacg acgtcggtccc                                30

SEQ ID NO: 166          moltype = DNA length = 16
FEATURE             Location/Qualifiers
misc_feature        1..16
note = Synthetic oligonucleotide

source            1..16
mol_type = other DNA
organism = synthetic construct
order(1..3,14..16)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

modified_base      3..14
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 166
cccacgacgt cgtggg                                16

SEQ ID NO: 167          moltype = DNA length = 18
FEATURE             Location/Qualifiers
misc_feature        1..18
note = Synthetic oligonucleotide

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source          1..18
               mol_type = other DNA
               organism = synthetic construct
modified_base   order(1..4,15..18)
               mod_base = OTHER
               note = Phosphorothioate internucleotide linkages
modified_base   4..15
               mod_base = OTHER
               note = Phosphodiester internucleotide linkages
SEQUENCE: 167
cccvacgacg tcgtgggg                                         18

SEQ ID NO: 168      moltype = DNA length = 17
FEATURE           Location/Qualifiers
misc_feature      1..17
note = Synthetic oligonucleotide
source            1..17
mol_type = other DNA
organism = synthetic construct
order(1..2,3..5,6..11,12..14,15..17)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     order(2..3,5..6,11..12,14..15)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 168
atgacgttt tgacggt                                         17

SEQ ID NO: 169      moltype = DNA length = 17
FEATURE           Location/Qualifiers
misc_feature      1..17
note = Synthetic oligonucleotide
source            1..17
mol_type = other DNA
organism = synthetic construct
order(1..2,3..5,6..11,12..14,15..17)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     order(2..3,5..6,11..12,14..15)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 169
acgacgttt tgatgtt                                         17

SEQ ID NO: 170      moltype = DNA length = 17
FEATURE           Location/Qualifiers
misc_feature      1..17
note = Synthetic oligonucleotide
source            1..17
mol_type = other DNA
organism = synthetic construct
order(1..2,3..5,6..11,12..14,15..17)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     order(2..3,5..6,11..12,14..15)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 170
atgatgttt tgatgtt                                         17

SEQ ID NO: 171      moltype = DNA length = 16
FEATURE           Location/Qualifiers
misc_feature      1..16
note = Synthetic oligonucleotide
source            1..16
mol_type = other DNA
organism = synthetic construct
order(1..2,3..5,6..11,12..14,15..16)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     order(2..3,5..6,11..12,14..15)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 171
atgacgttt gatgtt                                          16

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SEQ ID NO: 172      moltype = DNA length = 17
FEATURE
misc_feature
source
modified_base
modified_base
SEQUENCE: 172
atgacgttt tgatgtt                                17

SEQ ID NO: 173      moltype = DNA length = 17
FEATURE
misc_feature
source
modified_base
modified_base
SEQUENCE: 173
ttgacgttt tgatgtt                                17

SEQ ID NO: 174      moltype = DNA length = 17
FEATURE
misc_feature
source
modified_base
modified_base
SEQUENCE: 174
atgagcttt gtatgtt                                17

SEQ ID NO: 175      moltype = DNA length = 22
FEATURE
misc_feature
source
modified_base
SEQUENCE: 175
tcgacgttt cggcgccgc cg                                22

SEQ ID NO: 176      moltype = DNA length = 24
FEATURE
misc_feature
source
modified_base
SEQUENCE: 176
tcctgacgtt ttccggcgcc gccc                                24

SEQ ID NO: 177      moltype = DNA length = 22
FEATURE

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misc_feature          1..22
                      note = Synthetic oligonucleotide
source               1..22
                      mol_type = other DNA
                      organism = synthetic construct
modified_base         1..22
                      mod_base = OTHER
                      note = Phosphorothioate internucleotide linkages
SEQUENCE: 177
tcctgacgtt cggcgccgc cg                                22

SEQ ID NO: 178      moltype = DNA  length = 23
FEATURE             Location/Qualifiers
misc_feature         1..23
                      note = Synthetic oligonucleotide
source              1..23
                      mol_type = other DNA
                      organism = synthetic construct
modified_base        1..23
                      mod_base = OTHER
                      note = Phosphorothioate internucleotide linkages
SEQUENCE: 178
tccatgacgt tcggcgccgc ccc                               23

SEQ ID NO: 179      moltype = DNA  length = 21
FEATURE             Location/Qualifiers
misc_feature         1..21
                      note = Synthetic oligonucleotide
source              1..21
                      mol_type = other DNA
                      organism = synthetic construct
modified_base        1..21
                      mod_base = OTHER
                      note = Phosphorothioate internucleotide linkages
SEQUENCE: 179
tcctgacgtt cggcgccgc c                                21

SEQ ID NO: 180      moltype = DNA  length = 22
FEATURE             Location/Qualifiers
misc_feature         1..22
                      note = Synthetic oligonucleotide
source              1..22
                      mol_type = other DNA
                      organism = synthetic construct
modified_base        1..22
                      mod_base = OTHER
                      note = Phosphorothioate internucleotide linkages
modified_base        9..14
                      mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
SEQUENCE: 180
tcgacgttt cggcgccgc cg                                22

SEQ ID NO: 181      moltype = DNA  length = 24
FEATURE             Location/Qualifiers
misc_feature         1..24
                      note = Synthetic oligonucleotide
source              1..24
                      mol_type = other DNA
                      organism = synthetic construct
modified_base        1..24
                      mod_base = OTHER
                      note = Phosphorothioate internucleotide linkages
modified_base        9..21
                      mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
SEQUENCE: 181
tcgacgtcga cgtagggtt aggg                               24

SEQ ID NO: 182      moltype = DNA  length = 21
FEATURE             Location/Qualifiers
misc_feature         1..21
                      note = Synthetic oligonucleotide
source              1..21
                      mol_type = other DNA
                      organism = synthetic construct

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modified_base      order(1..9,18..21)
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base      9..18
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 182
acgacgtcgt tagggtagg g                                21

SEQ ID NO: 183      moltype = DNA length = 12
FEATURE          Location/Qualifiers
misc_feature      1..12
                   note = Synthetic oligonucleotide
source           1..12
                   mol_type = other DNA
                   organism = synthetic construct
modified_base     order(1..3,4..6,7..9,10..12)
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base     order(3..4,6..7,9..10)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 183
gtcggcgttg ac                                12

SEQ ID NO: 184      moltype = DNA length = 25
FEATURE          Location/Qualifiers
misc_feature      1..25
                   note = Synthetic oligonucleotide
modified_base    13..16
                   mod_base = OTHER
                   note = 1-Prime-2-prime-dideoxyribose (D spacer)
source           1..25
                   mol_type = other DNA
                   organism = synthetic construct
modified_base     1..25
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 184
acgacgtcgt cgnnnncggc cgccc                                25

SEQ ID NO: 185      moltype = DNA length = 18
FEATURE          Location/Qualifiers
misc_feature      1..18
                   note = Synthetic oligonucleotide
source           1..18
                   mol_type = other DNA
                   organism = synthetic construct
modified_base     7..18
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base     1..7
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 185
tcgtcgaacga cgtcgatc                                18

SEQ ID NO: 186      moltype = DNA length = 22
FEATURE          Location/Qualifiers
misc_feature      1..22
                   note = Synthetic oligonucleotide
modified_base    19..22
                   mod_base = OTHER
                   note = 1-Prime-2-prime-dideoxyribose (D spacer)
source           1..22
                   mol_type = other DNA
                   organism = synthetic construct
modified_base     1..22
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 186
tcgtcgaacga cgtcgatcnn nn                                22

SEQ ID NO: 187      moltype = DNA length = 25
FEATURE          Location/Qualifiers
misc_feature      1..25

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modified_base      note = Synthetic oligonucleotide
25
mod_base = OTHER
note = Triethylene glycol
source           1..25
mol_type = other DNA
organism = synthetic construct
modified_base     11..14
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
order(1..11,14..25)
modified_base     mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 187
acgacgtcgt ttttacgacg tcgttn          25

SEQ ID NO: 188      moltype = DNA length = 27
FEATURE           Location/Qualifiers
misc_feature      1..27
note = Synthetic oligonucleotide
modified_base     25..27
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source            1..27
mol_type = other DNA
organism = synthetic construct
modified_base     11..14
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
order(1..11,14..27)
modified_base     mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 188
acgacgtcgt ttttacgacg tcgttnn          27

SEQ ID NO: 189      moltype = DNA length = 27
FEATURE           Location/Qualifiers
misc_feature      1..27
note = Synthetic oligonucleotide
source            1..27
mol_type = other DNA
organism = synthetic construct
modified_base     order(11..14,25..27)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
order(1..11,14..25)
modified_base     mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 189
acgacgtcgt ttttacgacg tcgttt          27

SEQ ID NO: 190      moltype = DNA length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
source            1..24
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..2,11..14,23..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
order(2..11,14..23)
modified_base     mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 190
acgacgtcgt ttttacgacg tcgt             24

SEQ ID NO: 191      moltype = DNA length = 25
FEATURE           Location/Qualifiers
misc_feature      1..25
note = Synthetic oligonucleotide
modified_base     11..14
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base     25
mod_base = OTHER

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source          note = Hexaethylene glycol
                1..25
                mol_type = other DNA
                organism = synthetic construct
modified_base   1..25
                mod_base = OTHER
                note = Phosphodiester internucleotide linkages
SEQUENCE: 191 acgacgtcgt nnnnacgacg tcgtt                               25

SEQ ID NO: 192      moltype = DNA length = 22
FEATURE
misc_feature        Location/Qualifiers
                    1..22
                    note = Synthetic oligonucleotide
modified_base       11
                    mod_base = OTHER
                    note = Hexaethylene glycol
modified_base       22
                    mod_base = OTHER
                    note = Hexaethylene glycol
source            1..22
                    mol_type = other DNA
                    organism = synthetic construct
modified_base       1..22
                    mod_base = OTHER
                    note = Phosphodiester internucleotide linkages
SEQUENCE: 192 acgacgtcgt nacgacgtcg tn                                         22

SEQ ID NO: 193      moltype = DNA length = 23
FEATURE
misc_feature        Location/Qualifiers
                    1..23
                    note = Synthetic oligonucleotide
modified_base       11..12
                    mod_base = OTHER
                    note = Triethylene glycol
modified_base       23
                    mod_base = OTHER
                    note = Triethylene glycol
source            1..23
                    mol_type = other DNA
                    organism = synthetic construct
modified_base       1..22
                    mod_base = OTHER
                    note = Phosphodiester internucleotide linkages
SEQUENCE: 193 acgacgtcgt nnacgacgtc gtn                                         23

SEQ ID NO: 194      moltype = DNA length = 25
FEATURE
misc_feature        Location/Qualifiers
                    1..25
                    note = Synthetic oligonucleotide
modified_base       10..13
                    mod_base = OTHER
                    note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base       23..25
                    mod_base = OTHER
                    note = 1-Prime-2-prime-dideoxyribose (D spacer)
source            1..25
                    mol_type = other DNA
                    organism = synthetic construct
modified_base       1..25
                    mod_base = OTHER
                    note = Phosphodiester internucleotide linkages
SEQUENCE: 194 cgacgtcgt nnnacgacgt cgnnn                                     25

SEQ ID NO: 195      moltype = DNA length = 25
FEATURE
misc_feature        Location/Qualifiers
                    1..25
                    note = Synthetic oligonucleotide
modified_base       10..13
                    mod_base = OTHER
                    note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base       23..25
                    mod_base = OTHER

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source          note = 1-Prime-2-prime-dideoxyribose (D spacer)
1..25
mol_type = other DNA
organism = synthetic construct
modified_base   1..25
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 195 acgacgtcgn nnncgacgtc gtnnn 25

SEQ ID NO: 196 moltype = DNA length = 23
FEATURE Location/Qualifiers
misc_feature 1..23
note = Synthetic oligonucleotide
modified_base 9..12
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base 21..23
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source        1..23
mol_type = other DNA
organism = synthetic construct
modified_base 1..23
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 196 cgacgtcggn nnncgacgtcg nnn 23

SEQ ID NO: 197 moltype = DNA length = 27
FEATURE Location/Qualifiers
misc_feature 1..27
note = Synthetic oligonucleotide
modified_base 11..14
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base 25..27
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source        1..27
mol_type = other DNA
organism = synthetic construct
modified_base 1..27
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 197 tcgacgtcgt nnnnacgacg tcgannn 27

SEQ ID NO: 198 moltype = DNA length = 27
FEATURE Location/Qualifiers
misc_feature 1..27
note = Synthetic oligonucleotide
modified_base 11..14
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base 25..27
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source        1..27
mol_type = other DNA
organism = synthetic construct
modified_base 1..27
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 198 acgtcgtcgt nnnnacgacg acgttnnn 27

SEQ ID NO: 199 moltype = DNA length = 27
FEATURE Location/Qualifiers
misc_feature 1..27
note = Synthetic oligonucleotide
modified_base 11..14
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base 25..27
mod_base = OTHER

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source          note = 1-Prime-2-prime-dideoxyribose (D spacer)
1..27
mol_type = other DNA
organism = synthetic construct
modified_base   1..27
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 199
tcgtcgacgt nnnnacgtcg acgannn                                         27

SEQ ID NO: 200      moltype = DNA length = 27
FEATURE           Location/Qualifiers
misc_feature      1..27
note = Synthetic oligonucleotide
modified_base     11..14
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base     25..27
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source          1..27
mol_type = other DNA
organism = synthetic construct
modified_base     1..27
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 200
tcgacgtcgt nnnnacgacg tcgttnn                                         27

SEQ ID NO: 201      moltype = DNA length = 27
FEATURE           Location/Qualifiers
misc_feature      1..27
note = Synthetic oligonucleotide
modified_base     11..14
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base     25..27
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source          1..27
mol_type = other DNA
organism = synthetic construct
modified_base     1..27
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 201
acgacgtcgt nnnnacgtcg tcgttnn                                         27

SEQ ID NO: 202      moltype = DNA length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
note = Synthetic oligonucleotide
modified_base     9..12
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base     21..23
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source          1..23
mol_type = other DNA
organism = synthetic construct
modified_base     1..23
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 202
acgacgttnn mnaacgtcgt nnn                                         23

SEQ ID NO: 203      moltype = DNA length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide
modified_base     8..11
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base     19..21
mod_base = OTHER

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source          note = 1-Prime-2-prime-dideoxyribose (D spacer)
1..21
mol_type = other DNA
organism = synthetic construct
modified_base   1..21
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 203 acgtcgtnnn nacgacgtgnn n                               21

SEQ ID NO: 204      moltype = DNA length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
note = Synthetic oligonucleotide
modified_base     9..12
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base     21..23
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source           1..23
mol_type = other DNA
organism = synthetic construct
modified_base     1..23
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 204 ggcggccgnn nnccggccgccc nnn                           23

SEQ ID NO: 205      moltype = DNA length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
note = Synthetic oligonucleotide
modified_base     9..12
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base     21..23
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source           1..23
mol_type = other DNA
organism = synthetic construct
modified_base     1..23
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 205 gcgccggnn nnccggccgc nnn                           23

SEQ ID NO: 206      moltype = DNA length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
modified_base     8..11
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base     22..24
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source           1..24
mol_type = other DNA
organism = synthetic construct
modified_base     1..24
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 206 acgtcgtnnn nacgacgtcg tnnn                           24

SEQ ID NO: 207      moltype = DNA length = 26
FEATURE           Location/Qualifiers
misc_feature      1..26
note = Synthetic oligonucleotide
modified_base     1
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base     12..15
mod_base = OTHER

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modified_base          note = 1-Prime-2-prime-dideoxyribose (D spacer)
                      26
                      mod_base = OTHER
                      note = 1-Prime-2-prime-dideoxyribose (D spacer)
source                1..26
                      mol_type = other DNA
                      organism = synthetic construct
modified_base          1..26
                      mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
SEQUENCE: 207          nacgacgtcg tnnnnacgac gtcgtt                               26
                      SEQ ID NO: 208          moltype = DNA length = 28
FEATURE               Location/Qualifiers
misc_feature           1..28
                      note = Synthetic oligonucleotide
modified_base          26..27
                      mod_base = OTHER
                      note = 1-Prime-2-prime-dideoxyribose (D spacer)
source                1..28
                      mol_type = other DNA
                      organism = synthetic construct
modified_base          1..2
                      mod_base = OTHER
                      note = Phosphorothioate internucleotide linkages
modified_base          2..28
                      mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
SEQUENCE: 208          acgacgtcgt cgaagacgac gtcgttnt                               28
                      SEQ ID NO: 209          moltype = DNA length = 28
FEATURE               Location/Qualifiers
misc_feature           1..28
                      note = Synthetic oligonucleotide
modified_base          26..27
                      mod_base = OTHER
                      note = 1-Prime-2-prime-dideoxyribose (D spacer)
source                1..28
                      mol_type = other DNA
                      organism = synthetic construct
modified_base          1..2
                      mod_base = OTHER
                      note = Phosphorothioate internucleotide linkages
modified_base          2..28
                      mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
SEQUENCE: 209          tcgacgtcgt cgaagacgtc gtcgttnt                               28
                      SEQ ID NO: 210          moltype = DNA length = 20
FEATURE               Location/Qualifiers
misc_feature           1..20
                      note = Synthetic oligonucleotide
modified_base          5
                      mod_base = OTHER
                      note = 1-Prime-2-prime-dideoxyribose (D spacer)
source                1..20
                      mol_type = other DNA
                      organism = synthetic construct
modified_base          1..20
                      mod_base = OTHER
                      note = Phosphorothioate internucleotide linkages
SEQUENCE: 210          tccangacgt ttttgatgtt                               20
                      SEQ ID NO: 211          moltype = DNA length = 20
FEATURE               Location/Qualifiers
misc_feature           1..20
                      note = Synthetic oligonucleotide
modified_base          12
                      mod_base = OTHER
                      note = 1-Prime-2-prime-dideoxyribose (D spacer)
source                1..20
                      mol_type = other DNA

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modified_base      organism = synthetic construct
                   1..20
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
SEQUENCE: 211      tccatgacgt tnttgatgtt                               20

SEQ ID NO: 212      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature      1..20
                   note = Synthetic oligonucleotide
modified_base      5
                   mod_base = OTHER
                   note = 1,3-propane-diol
source            1..20
                   mol_type = other DNA
                   organism = synthetic construct
modified_base      1..20
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
SEQUENCE: 212      tccangacgt ttttgatgtt                               20

SEQ ID NO: 213      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature      1..20
                   note = Synthetic oligonucleotide
modified_base      12
                   mod_base = OTHER
                   note = 1,3-propane-diol
source            1..20
                   mol_type = other DNA
                   organism = synthetic construct
modified_base      1..20
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
SEQUENCE: 213      tccatgacgt tnttgatgtt                               20

SEQ ID NO: 214      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature      1..20
                   note = Synthetic oligonucleotide
modified_base      20
                   mod_base = OTHER
                   note =
                     Bis-hydroxypropyl-3,3',3-Prime,3-Prime-tetramethyl-4,5-benzin
                     docarbocyanine chloride appended
source            1..20
                   mol_type = other DNA
                   organism = synthetic construct
modified_base      1..20
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
SEQUENCE: 214      tccatgacgt ttttgatgtt                               20

SEQ ID NO: 215      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature      1..20
                   note = Synthetic oligonucleotide
modified_base      1..5
                   mod_base = OTHER
                   note = 1,3-propane-diol
source            1..20
                   mol_type = other DNA
                   organism = synthetic construct
modified_base      1..20
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
SEQUENCE: 215      nnnnngacgt ttttgatgtt                               20

SEQ ID NO: 216      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature      1..20

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modified_base      note = Synthetic oligonucleotide
5
mod_base = OTHER
note = 1,3-propane-diol
12
mod_base = OTHER
note = 1,3-propane-diol
1..20
mol_type = other DNA
organism = synthetic construct
1..20
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 216
tccangacgt tnttgatgtt                                20

SEQ ID NO: 217
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide
modified_base
5
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
12
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
1..20
mol_type = other DNA
organism = synthetic construct
1..20
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 217
tccangacgt tnttgatgtt                                20

SEQ ID NO: 218
FEATURE
misc_feature
1..28
note = Synthetic oligonucleotide
modified_base
11..14
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
25..27
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
28
mod_base = OTHER
note = Ribouracil
source
1..28
mol_type = other DNA
organism = synthetic construct
1..28
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 218
acgacgtcgtnnnnacgacg tcgtnnnn                                28

SEQ ID NO: 219
FEATURE
misc_feature
1..28
note = Synthetic oligonucleotide
modified_base
11..14
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
25..27
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
28
mod_base = OTHER
note = Riboguanidine
source
1..28
mol_type = other DNA
organism = synthetic construct
1..28
mod_base = OTHER
note = Phosphodiester internucleotide linkages
modified_base

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SEQUENCE: 219
acgacgtcgt nnnnacgacg tcgttnng                                28

SEQ ID NO: 220      moltype = DNA  length = 28
FEATURE          Location/Qualifiers
misc_feature     1..28
note = Synthetic oligonucleotide
modified_base    11..14
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base    25..27
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base    28
mod_base = OTHER
note = Riboadenine
source           1..28
mol_type = other DNA
organism = synthetic construct
modified_base    1..28
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 220
acgacgtcgt nnnnacgacg tcgttnna                                28

SEQ ID NO: 221      moltype = DNA  length = 31
FEATURE          Location/Qualifiers
misc_feature     1..31
note = Synthetic oligonucleotide
modified_base    1..3
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base    14..17
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base    28..30
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base    31
mod_base = OTHER
note = Ribouracil
source           1..31
mol_type = other DNA
organism = synthetic construct
modified_base    1..31
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 221
nnnacgacgt cgttnnnnacg acgtcgtnnn n                                31

SEQ ID NO: 222      moltype = DNA  length = 31
FEATURE          Location/Qualifiers
misc_feature     1..31
note = Synthetic oligonucleotide
modified_base    11..14
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base    25..27
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base    28..31
mod_base = OTHER
note = Riboadenines
source           1..31
mol_type = other DNA
organism = synthetic construct
modified_base    1..31
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 222
acgacgtcgt nnnnacgacg tcgttnnnaa a                                31

SEQ ID NO: 223      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide

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source          1..20
               mol_type = other DNA
               organism = synthetic construct
modified_base   1..20
               mod_base = OTHER
               note = Phosphorothioate internucleotide linkages
SEQUENCE: 223
tcgatgacgt tcctgacggtt                                         20

SEQ ID NO: 224          moltype = DNA length = 31
FEATURE           Location/Qualifiers
misc_feature      1..31
note = Synthetic oligonucleotide
modified_base     14..17
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base     28..30
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base     31
mod_base = OTHER
note = Ribouracil
source           1..31
mol_type = other DNA
organism = synthetic construct
modified_base     1..31
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 224
tttacgacgt cgtnnnnnacg acgtcgtnnn n                                         31

SEQ ID NO: 225          moltype = DNA length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide
source           1..20
mol_type = other DNA
organism = synthetic construct
order(1..7,8..15,16..20)
modified_base     mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     order(7..8,15..16)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 225
tcgcgacgtt cgccgcgcgcg                                         20

SEQ ID NO: 226          moltype = DNA length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide
modified_base     1
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source           1..20
mol_type = other DNA
organism = synthetic construct
modified_base     1..20
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 226
nccatgacgt ttttgatgtt                                         20

SEQ ID NO: 227          moltype = DNA length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide
modified_base     2
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source           1..20
mol_type = other DNA
organism = synthetic construct
modified_base     1..20
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

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SEQUENCE: 227
tncatgacgt ttttgatgtt                                20

SEQ ID NO: 228      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide
modified_base    3
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source          1..20
mol_type = other DNA
organism = synthetic construct
modified_base    1..20
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 228
tcnatgacgt ttttgatgtt                                20

SEQ ID NO: 229      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide
modified_base    4
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source          1..20
mol_type = other DNA
organism = synthetic construct
modified_base    1..20
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 229
tccntgacgt ttttgatgtt                                20

SEQ ID NO: 230      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide
modified_base    14
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source          1..20
mol_type = other DNA
organism = synthetic construct
modified_base    1..20
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 230
tccatgacgt ttngatgtt                                20

SEQ ID NO: 231      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide
modified_base    13
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source          1..20
mol_type = other DNA
organism = synthetic construct
modified_base    1..20
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 231
tccatgacgt ttngatgtt                                20

SEQ ID NO: 232      moltype = DNA  length = 21
FEATURE          Location/Qualifiers
misc_feature     1..21
note = Synthetic oligonucleotide
source          1..21
mol_type = other DNA
organism = synthetic construct
modified_base    order(1..6,7..21)
mod_base = OTHER

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modified_base      note = Phosphorothioate internucleotide linkages
6..7
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 232
tcgaacgttc ggcgcgcgcc g                                21

SEQ ID NO: 233      moltype = DNA  length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
source            1..24
mol_type = other DNA
organism = synthetic construct
order(1..9,10..24)
mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
9..10
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 233
tcgtcgaacg ttccggcgccg gccg                                24

SEQ ID NO: 234      moltype = DNA  length = 25
FEATURE           Location/Qualifiers
misc_feature      1..25
note = Synthetic oligonucleotide
source            1..25
mol_type = other DNA
organism = synthetic construct
order(1..9,10..25)
mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
9..10
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 234
tcgtcgaacg ttccggcgctg cgccg                                25

SEQ ID NO: 235      moltype = DNA  length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
source            1..24
mol_type = other DNA
organism = synthetic construct
order(1..7,8..24)
mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
7..8
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 235
tcgcgacgtt cgttgcgcgc gccc                                24

SEQ ID NO: 236      moltype = DNA  length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide
source            1..21
mol_type = other DNA
organism = synthetic construct
order(1..6,7..21)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
6..7
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 236
tacgtcgttc ggccgcgcgccc g                                21

SEQ ID NO: 237      moltype = DNA  length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
note = Synthetic oligonucleotide
source            1..23

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mol_type = other DNA
organism = synthetic construct
order(1..8,9..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base
8..9
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 237
ttgcgcacgt tcggcgcgcg ccg 23

SEQ ID NO: 238      moltype = DNA length = 22
FEATURE           Location/Qualifiers
misc_feature      1..22
note = Synthetic oligonucleotide
source            1..22
mol_type = other DNA
organism = synthetic construct
order(1..12,13..22)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     12..13
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 238
tcggcgcgcg ccgtcgcgt gt 22

SEQ ID NO: 239      moltype = DNA length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
source            1..24
mol_type = other DNA
organism = synthetic construct
order(1..4,5..8,9..16,17..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     order(4..5,8..9,16..17)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 239
tagcgtgcgt tttgacgttt tttt 24

SEQ ID NO: 240      moltype = DNA length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
source            1..24
mol_type = other DNA
organism = synthetic construct
order(1..4,5..8,9..16,17..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     order(4..5,8..9,16..17)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 240
tagcgagcgt tttgacgttt tttt 24

SEQ ID NO: 241      moltype = DNA length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
source            1..24
mol_type = other DNA
organism = synthetic construct
order(1..4,5..8,9..16,17..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     order(4..5,8..9,16..17)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 241
ttgcgagcgt tttgacgttt tttt 24

SEQ ID NO: 242      moltype = DNA length = 24

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FEATURE                                Location/Qualifiers
misc_feature                          1..24
                                         note = Synthetic oligonucleotide
source                                 1..24
                                         mol_type = other DNA
                                         organism = synthetic construct
                                         order(1..4,5..8,9..16,17..24)
                                         mod_base = OTHER
modified_base                         note = Phosphorothioate internucleotide linkages
                                         order(4..5,8..9,16..17)
                                         mod_base = OTHER
                                         note = Phosphodiester internucleotide linkages
SEQUENCE: 242
atgcgtgcgt tttgacgttt tttt                               24

SEQ ID NO: 243          moltype = DNA length = 24
FEATURE                                Location/Qualifiers
misc_feature                          1..24
                                         note = Synthetic oligonucleotide
source                                 1..24
                                         mol_type = other DNA
                                         organism = synthetic construct
                                         order(1..4,5..8,9..16,17..24)
                                         mod_base = OTHER
modified_base                         note = Phosphorothioate internucleotide linkages
                                         order(4..5,8..9,16..17)
                                         mod_base = OTHER
                                         note = Phosphodiester internucleotide linkages
SEQUENCE: 243
ttacgtgcgt tttgacgttt tttt                               24

SEQ ID NO: 244          moltype = DNA length = 24
FEATURE                                Location/Qualifiers
misc_feature                          1..24
                                         note = Synthetic oligonucleotide
source                                 1..24
                                         mol_type = other DNA
                                         organism = synthetic construct
                                         order(1..4,5..8,9..16,17..24)
                                         mod_base = OTHER
modified_base                         note = Phosphorothioate internucleotide linkages
                                         order(4..5,8..9,16..17)
                                         mod_base = OTHER
                                         note = Phosphodiester internucleotide linkages
SEQUENCE: 244
ttgcatgcgt tttgacgttt tttt                               24

SEQ ID NO: 245          moltype = DNA length = 24
FEATURE                                Location/Qualifiers
misc_feature                          1..24
                                         note = Synthetic oligonucleotide
source                                 1..24
                                         mol_type = other DNA
                                         organism = synthetic construct
                                         order(1..4,5..8,9..16,17..24)
                                         mod_base = OTHER
modified_base                         note = Phosphorothioate internucleotide linkages
                                         order(4..5,8..9,16..17)
                                         mod_base = OTHER
                                         note = Phosphodiester internucleotide linkages
SEQUENCE: 245
ttgcgtacgt tttgacgttt tttt                               24

SEQ ID NO: 246          moltype = DNA length = 24
FEATURE                                Location/Qualifiers
misc_feature                          1..24
                                         note = Synthetic oligonucleotide
source                                 1..24
                                         mol_type = other DNA
                                         organism = synthetic construct
                                         order(1..4,5..8,9..16,17..24)
                                         mod_base = OTHER
modified_base                         note = Phosphorothioate internucleotide linkages
                                         order(4..5,8..9,16..17)
                                         mod_base = OTHER
                                         note = Phosphodiester internucleotide linkages

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SEQUENCE: 246 ttgcgtgcat tttgacgttt tttt 24
SEQ ID NO: 247 moltype = DNA length = 24
FEATURE Location/Qualifiers
misc_feature 1..24
source note = Synthetic oligonucleotide
1..24
modified_base mol_type = other DNA
organism = synthetic construct
order(1..4,5..8,9..16,17..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base order(4..5,8..9,16..17)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 247 ttgcgtgca tttgacgttt tttt 24
SEQ ID NO: 248 moltype = DNA length = 24
FEATURE Location/Qualifiers
misc_feature 1..24
source note = Synthetic oligonucleotide
1..24
modified_base mol_type = other DNA
organism = synthetic construct
order(1..4,5..8,9..16,17..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base order(4..5,8..9,16..17)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 248 ttgcgcgcgt tttgacgttt tttt 24
SEQ ID NO: 249 moltype = DNA length = 24
FEATURE Location/Qualifiers
misc_feature 1..24
source note = Synthetic oligonucleotide
1..24
modified_base mol_type = other DNA
organism = synthetic construct
order(1..4,5..8,9..16,17..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base order(4..5,8..9,16..17)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 249 ttgcgtgcgc tttgacgttt tttt 24
SEQ ID NO: 250 moltype = DNA length = 24
FEATURE Location/Qualifiers
misc_feature 1..24
source note = Synthetic oligonucleotide
1..24
modified_base mol_type = other DNA
organism = synthetic construct
order(1..4,5..8,9..16,17..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base order(4..5,8..9,16..17)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 250 ttgcgtgcgt ttgcacgttt tttt 24
SEQ ID NO: 251 moltype = DNA length = 25
FEATURE Location/Qualifiers
misc_feature 1..25
source note = Synthetic oligonucleotide
1..25
modified_base mol_type = other DNA
organism = synthetic construct
order(1..5,6..13,14..25)
mod_base = OTHER

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modified_base          note = Phosphorothioate internucleotide linkages
                      order(5..6,13..14)
                      mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
SEQUENCE: 251          tcgtcgacg ttcggcgctg cgccg                               25

SEQ ID NO: 252          moltype = DNA  length = 24
FEATURE                 Location/Qualifiers
misc_feature            1..24
note = Synthetic oligonucleotide
source                  1..24
mol_type = other DNA
organism = synthetic construct
order(1..2,3..11,12..18,19..24)
mod_base = OTHER
modified_base           note = Phosphorothioate internucleotide linkages
                      order(2..3,11..12,18..19)
                      mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
SEQUENCE: 252          tggcgacgtt cgttgcgcgc gccc                               24

SEQ ID NO: 253          moltype = DNA  length = 20
FEATURE                 Location/Qualifiers
misc_feature            1..20
note = Synthetic oligonucleotide
source                  1..20
mol_type = other DNA
organism = synthetic construct
order(1..7,8..16,17..20)
mod_base = OTHER
modified_base           note = Phosphorothioate internucleotide linkages
                      order(7..8,16..17)
                      mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
SEQUENCE: 253          tcgcgacgtt ttgcgcgcg                                           20

SEQ ID NO: 254          moltype = DNA  length = 23
FEATURE                 Location/Qualifiers
misc_feature            1..23
note = Synthetic oligonucleotide
source                  1..23
mol_type = other DNA
organism = synthetic construct
order(1..7,8..15,16..23)
mod_base = OTHER
modified_base           note = Phosphorothioate internucleotide linkages
                      order(7..8,15..16)
                      mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
SEQUENCE: 254          tcgcgacgtc gttgcgcgcg ccg                                23

SEQ ID NO: 255          moltype = DNA  length = 24
FEATURE                 Location/Qualifiers
misc_feature            1..24
note = Synthetic oligonucleotide
source                  1..24
mol_type = other DNA
organism = synthetic construct
order(1..7,8..16,17..24)
mod_base = OTHER
modified_base           note = Phosphorothioate internucleotide linkages
                      order(7..8,16..17)
                      mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
SEQUENCE: 255          tcgcgacgtt cgaaggcgccg gccc                               24

SEQ ID NO: 256          moltype = DNA  length = 24
FEATURE                 Location/Qualifiers
misc_feature            1..24
note = Synthetic oligonucleotide
source                  1..24

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mol_type = other DNA
organism = synthetic construct
order(1..7,8..16,17..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base
note = Phosphodiester internucleotide linkages
SEQUENCE: 256
tcgcgaccaa cgttgcgcgc gccg                                24

SEQ ID NO: 257      moltype = DNA length = 27
FEATURE           Location/Qualifiers
misc_feature      1..27
note = Synthetic oligonucleotide
modified_base      11..14
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base      25..27
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source            1..27
mol_type = other DNA
organism = synthetic construct
modified_base      1..27
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 257
tcgacgtcgt nnnntcgacg tcgttnnn                            27

SEQ ID NO: 258      moltype = DNA length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
source            1..24
mol_type = other DNA
organism = synthetic construct
modified_base      1..24
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 258
tcgtcgtag ctcgttagct cgtt                                24

SEQ ID NO: 259      moltype = DNA length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
source            1..24
mol_type = other DNA
organism = synthetic construct
modified_base      1..24
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 259
tcgtcgtagt gtaattacgt cgtt                                24

SEQ ID NO: 260      moltype = DNA length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
source            1..24
mol_type = other DNA
organism = synthetic construct
modified_base      1..24
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 260
tcgtcgtagc gtcgttagt aatt                                24

SEQ ID NO: 261      moltype = DNA length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
source            1..24
mol_type = other DNA
organism = synthetic construct

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modified_base      1..24
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
SEQUENCE: 261
tcgtcgttac gtaattacgt aatt                                24

SEQ ID NO: 262      moltype = DNA  length = 19
FEATURE
misc_feature        Location/Qualifiers
1..19
note = Synthetic oligonucleotide
1..19
source
mol_type = other DNA
organism = synthetic construct
order(1..9,11..19)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base       9..11
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 262
tcgacgtcga cgtgacggg                                     19

SEQ ID NO: 263      moltype = DNA  length = 23
FEATURE
misc_feature        Location/Qualifiers
1..23
note = Synthetic oligonucleotide
1..23
source
mol_type = other DNA
organism = synthetic construct
order(1..4,5..11,12..16,17..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base       order(4..5,11..12,16..17)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 263
tcgcgacgtt cggcgcgctg ccg                                23

SEQ ID NO: 264      moltype = DNA  length = 23
FEATURE
misc_feature        Location/Qualifiers
1..23
note = Synthetic oligonucleotide
1..23
source
mol_type = other DNA
organism = synthetic construct
order(1..4,5..11,12..16,17..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base       order(4..5,11..12,16..17)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 264
tcgcgacgtt cggcgcgctg ccg                                23

SEQ ID NO: 265      moltype = DNA  length = 23
FEATURE
misc_feature        Location/Qualifiers
1..23
note = Synthetic oligonucleotide
1..23
source
mol_type = other DNA
organism = synthetic construct
order(1..4,5..11,12..17,18..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base       order(4..5,11..12,17..18)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 265
tcgcgacgtt cggcgcgctg ccg                                23

SEQ ID NO: 266      moltype = DNA  length = 10
FEATURE
misc_feature        Location/Qualifiers
1..10
note = Synthetic oligonucleotide
10
modified_base       mod_base = OTHER

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source          note = Vitamin E appended
               1..10
               mol_type = other DNA
               organism = synthetic construct
modified_base   1..10
               mod_base = OTHER
               note = Phosphodiester internucleotide linkages
SEQUENCE: 266
tcgacgtcgt                10

SEQ ID NO: 267      moltype = DNA length = 19
FEATURE
misc_feature        Location/Qualifiers
1..19
note = Synthetic oligonucleotide
1..19
source
1..19
mol_type = other DNA
organism = synthetic construct
modified_base       1..19
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 267
tcgacgtcga cgtgacgtc                19

SEQ ID NO: 268      moltype = DNA length = 17
FEATURE
misc_feature        Location/Qualifiers
1..17
note = Synthetic oligonucleotide
1..17
source
1..17
mol_type = other DNA
organism = synthetic construct
modified_base       1..17
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 268
tcgacgtcga cgtgacg                17

SEQ ID NO: 269      moltype = DNA length = 10
FEATURE
misc_feature        Location/Qualifiers
1..10
note = Synthetic oligonucleotide
1..10
source
1..10
mol_type = other DNA
organism = synthetic construct
modified_base       1..10
mod_base = OTHER
note = Vitamin E appended
note = Phosphodiester internucleotide linkages
SEQUENCE: 269
tcgacgtcga                10

SEQ ID NO: 270      moltype = DNA length = 24
FEATURE
misc_feature        Location/Qualifiers
1..24
note = Synthetic oligonucleotide
1..24
source
1..24
mol_type = other DNA
organism = synthetic construct
modified_base       1..24
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 270
tcgtcgttac gtaactacgt cgtt                24

SEQ ID NO: 271      moltype = DNA length = 24
FEATURE
misc_feature        Location/Qualifiers
1..24
note = Synthetic oligonucleotide
1..24
source
1..24
mol_type = other DNA
organism = synthetic construct
modified_base       1..24
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 271

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tcgtcgttac gtaacgacgt cgtt	24
SEQ ID NO: 272	moltype = DNA length = 24
FEATURE	Location/Qualifiers
misc_feature	1..24
source	note = Synthetic oligonucleotide
	1..24
	mol_type = other DNA
	organism = synthetic construct
modified_base	1..24
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
SEQUENCE: 272	
tcgtcgtag ctaattagct cgtt	24
SEQ ID NO: 273	moltype = DNA length = 24
FEATURE	Location/Qualifiers
misc_feature	1..24
source	note = Synthetic oligonucleotide
	1..24
	mol_type = other DNA
	organism = synthetic construct
modified_base	1..24
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
SEQUENCE: 273	
tcgtcgttac gtaattagct cgtt	24
SEQ ID NO: 274	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
source	note = Synthetic oligonucleotide
	1..20
	mol_type = other DNA
	organism = synthetic construct
modified_base	1..20
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
SEQUENCE: 274	
cccatgacgt tcctgacgtt	20
SEQ ID NO: 275	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
source	note = Synthetic oligonucleotide
	1..20
	mol_type = other DNA
	organism = synthetic construct
modified_base	1..20
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
SEQUENCE: 275	
cccatgacgt tcctgacgtt	20
SEQ ID NO: 276	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
source	note = Synthetic oligonucleotide
	1..20
	mol_type = other DNA
	organism = synthetic construct
modified_base	1..20
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
SEQUENCE: 276	
accatgacgt tcctgacgtt	20
SEQ ID NO: 277	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
source	note = Synthetic oligonucleotide
	1..20
	mol_type = other DNA
	organism = synthetic construct
modified_base	1..20
	mod_base = OTHER

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SEQUENCE: 277          note = Phosphorothioate internucleotide linkages
tggatgacgt tcctgacgtt                                20

SEQ ID NO: 278      moltype = DNA length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide
source
1..20
mol_type = other DNA
organism = synthetic construct
1..20
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 278          note = Phosphorothioate internucleotide linkages
tttatgacgt tcctgacggt                                20

SEQ ID NO: 279      moltype = DNA length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide
source
1..20
mol_type = other DNA
organism = synthetic construct
1..20
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 279          note = Phosphorothioate internucleotide linkages
taaatgacgt tcctgacggt                                20

SEQ ID NO: 280      moltype = DNA length = 19
FEATURE
misc_feature
1..19
note = Synthetic oligonucleotide
source
1..19
mol_type = other DNA
organism = synthetic construct
1..19
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 280          note = Phosphorothioate internucleotide linkages
ccatgacggt cctgacggt                                19

SEQ ID NO: 281      moltype = DNA length = 18
FEATURE
misc_feature
1..18
note = Synthetic oligonucleotide
source
1..18
mol_type = other DNA
organism = synthetic construct
1..18
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 281          note = Phosphorothioate internucleotide linkages
catgacgttc ctgacggt                                18

SEQ ID NO: 282      moltype = DNA length = 17
FEATURE
misc_feature
1..17
note = Synthetic oligonucleotide
source
1..17
mol_type = other DNA
organism = synthetic construct
1..17
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 282          note = Phosphorothioate internucleotide linkages
atgacggtcc tgacggt                                17

SEQ ID NO: 283      moltype = DNA length = 16
FEATURE
misc_feature
1..16
note = Synthetic oligonucleotide
source
1..16
mol_type = other DNA
organism = synthetic construct

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modified_base      1..16
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 283
tgacgttccct gacgtt                                16

SEQ ID NO: 284          moltype = DNA  length = 24
FEATURE
misc_feature           Location/Qualifiers
1..24
note = Synthetic oligonucleotide
modified_base          11..14
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base          24
mod_base = OTHER
note = Cholesterol appended
source                 1..24
mol_type = other DNA
organism = synthetic construct
modified_base          1..24
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 284
tcgacgtcga nnnnntcgacg tcga                                24

SEQ ID NO: 285          moltype = DNA  length = 22
FEATURE
misc_feature           Location/Qualifiers
1..22
note = Synthetic oligonucleotide
modified_base          1
mod_base = OTHER
note = Triethylene glycol
modified_base          12..15
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base          22
mod_base = OTHER
note = Cholesterol appended
source                 1..22
mol_type = other DNA
organism = synthetic construct
modified_base          1..22
mod_base = OTHER
note = Phosphodiester internucleotide linkages
modified_base          2..11
mod_base = OTHER
note = Inverse nucleotide (inverse orientation: 3-prime and
5-primeswitched)
SEQUENCE: 285
nagctgcagc tnnnnntcgac ga                                22

SEQ ID NO: 286          moltype = DNA  length = 21
FEATURE
misc_feature           Location/Qualifiers
1..21
note = Synthetic oligonucleotide
source                 1..21
mol_type = other DNA
organism = synthetic construct
modified_base          order(1..2,3..4,5..7,8..11,12..15,16..17,18..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base          order(2..3,4..5,7..8,11..12,15..16,17..18,20..21)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 286
tcgcgcacgtt cgggcgcgcc g                                21

SEQ ID NO: 287          moltype = DNA  length = 23
FEATURE
misc_feature           Location/Qualifiers
1..23
note = Synthetic oligonucleotide
source                 1..23
mol_type = other DNA
organism = synthetic construct
modified_base          order(1..2,3..5,6..8,9..12,13..17,18..23)
mod_base = OTHER

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modified_base          note = Phosphorothioate internucleotide linkages
                      order(2..3,5..6,8..9,12..13,17..18)
                      mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
SEQUENCE: 287          tcgtcgacgt tcggcgcgcg ccg                               23
SEQ ID NO: 288          moltype = DNA  length = 21
FEATURE                Location/Qualifiers
misc_feature           1..21
note = Synthetic oligonucleotide
source                 1..21
mol_type = other DNA
organism = synthetic construct
order(1..2,3..6,7..10,11..15,16..21)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base          order(2..3,6..7,10..11,15..16)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 288          tcggacgttc ggcgcgcgccc g                                21
SEQ ID NO: 289          moltype = DNA  length = 19
FEATURE                Location/Qualifiers
misc_feature           1..19
note = Synthetic oligonucleotide
source                 1..19
mol_type = other DNA
organism = synthetic construct
order(1..2,3..6,7..10,11..19)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base          order(2..3,6..7,10..11)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 289          tcggacgttc ggcgcgcgccc                               19
SEQ ID NO: 290          moltype = DNA  length = 20
FEATURE                Location/Qualifiers
misc_feature           1..20
note = Synthetic oligonucleotide
source                 1..20
mol_type = other DNA
organism = synthetic construct
order(1..2,3..4,5..7,8..11,12..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base          order(2..3,4..5,7..8,11..12)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 290          tcgcgacgtt cggcgccgccc                               20
SEQ ID NO: 291          moltype = DNA  length = 20
FEATURE                Location/Qualifiers
misc_feature           1..20
note = Synthetic oligonucleotide
source                 1..20
mol_type = other DNA
organism = synthetic construct
order(1..2,3..5,6..9,10..14,15..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base          order(2..3,5..6,9..10,14..15)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 291          tcgacgttcg gcgcgccgccc                               20
SEQ ID NO: 292          moltype = DNA  length = 18
FEATURE                Location/Qualifiers
misc_feature           1..18
note = Synthetic oligonucleotide
source                 1..18

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modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..2,3..5,6..9,10..18)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(2..3,5..6,9..10)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 292      tcgacgttcg ggcggccg                               18

SEQ ID NO: 293      moltype = DNA length = 18
FEATURE           Location/Qualifiers
misc_feature       1..18
source             note = Synthetic oligonucleotide
1..18
modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..2,3..4,5..7,8..11,12..18)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(2..3,4..5,7..8,11..12)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 293      tcgcgacgtt cggcgccg                               18

SEQ ID NO: 294      moltype = DNA length = 16
FEATURE           Location/Qualifiers
misc_feature       1..16
source             note = Synthetic oligonucleotide
1..16
modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..2,3..4,5..7,8..11,12..16)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(2..3,4..5,7..8,11..12)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 294      tcgcgacgtt cggcgccg                               16

SEQ ID NO: 295      moltype = DNA length = 16
FEATURE           Location/Qualifiers
misc_feature       1..16
source             note = Synthetic oligonucleotide
1..16
modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..2,3..5,6..9,10..16)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(2..3,5..6,9..10)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 295      tcgacgttcg ggcggccg                               16

SEQ ID NO: 296      moltype = DNA length = 21
FEATURE           Location/Qualifiers
misc_feature       1..21
source             note = Synthetic oligonucleotide
1..21
modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..2,3..5,6..8,9..12,13..16,17..21)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(2..3,5..6,8..9,12..13,16..17)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 296      tcgtcgacgt tcggcgccg g                               21

SEQ ID NO: 297      moltype = DNA length = 20

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FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Synthetic oligonucleotide
source	1..20
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..5,6..8,9..12,13..16,17..20)
	mod_base = OTHER
modified_base	note = Phosphorothioate internucleotide linkages
	order(2..3,5..6,8..9,12..13,16..17)
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 297	
tcgtcgacgt tcgggcgcg	20
SEQ ID NO: 298	moltype = DNA length = 23
FEATURE	Location/Qualifiers
misc_feature	1..23
	note = Synthetic oligonucleotide
source	1..23
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..5,6..8,9..12,13..17,18..23)
	mod_base = OTHER
modified_base	note = Phosphorothioate internucleotide linkages
	order(2..3,5..6,8..9,12..13,17..18)
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 298	
tcgacgacgt tcggcgcgcg ccg	23
SEQ ID NO: 299	moltype = DNA length = 23
FEATURE	Location/Qualifiers
misc_feature	1..23
	note = Synthetic oligonucleotide
source	1..23
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..5,6..8,9..12,13..17,18..23)
	mod_base = OTHER
modified_base	note = Phosphorothioate internucleotide linkages
	order(2..3,5..6,8..9,12..13,17..18)
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 299	
tcgacgtcgt tcggcgcgcg ccg	23
SEQ ID NO: 300	moltype = DNA length = 23
FEATURE	Location/Qualifiers
misc_feature	1..23
	note = Synthetic oligonucleotide
source	1..23
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..5,6..8,9..12,13..17,18..23)
	mod_base = OTHER
modified_base	note = Phosphorothioate internucleotide linkages
	order(2..3,5..6,8..9,12..13,17..18)
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 300	
tcgtcgacgt tcggcgcgcg gcg	23
SEQ ID NO: 301	moltype = DNA length = 24
FEATURE	Location/Qualifiers
misc_feature	1..24
	note = Synthetic oligonucleotide
source	1..24
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..5,6..8,9..12,13..18,19..24)
	mod_base = OTHER
modified_base	note = Phosphorothioate internucleotide linkages
	order(2..3,5..6,8..9,12..13,18..19)
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages

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SEQUENCE: 301
tcgtcgacgt tcggcgccgt gccg                                24

SEQ ID NO: 302      moltype = DNA  length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
note = Synthetic oligonucleotide
source            1..23
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..2,3..5,6..8,9..12,13..17,18..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     order(2..3,5..6,8..9,12..13,17..18)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 302
tcgtcgacgt tcgactcgag tcg                                23

SEQ ID NO: 303      moltype = DNA  length = 19
FEATURE           Location/Qualifiers
misc_feature      1..19
note = Synthetic oligonucleotide
source            1..19
mol_type = other DNA
organism = synthetic construct
modified_base     1..19
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 303
tcgacgtcga cgtgacgtt                                     19

SEQ ID NO: 304      moltype = DNA  length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide
source            1..21
mol_type = other DNA
organism = synthetic construct
modified_base     1..21
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 304
tcgtcgacgt tcggcgccg g                                21

SEQ ID NO: 305      moltype = DNA  length = 28
FEATURE           Location/Qualifiers
misc_feature      1..28
note = Synthetic oligonucleotide
modified_base     11..14
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base     25..27
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base     28
mod_base = OTHER
note = Inverse orientation ribouracil
source            1..28
mol_type = other DNA
organism = synthetic construct
modified_base     1..28
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 305
acgacgtcgt nnnnacgacg tcgttnnnn                          28

SEQ ID NO: 306      moltype = DNA  length = 25
FEATURE           Location/Qualifiers
misc_feature      1..25
note = Synthetic oligonucleotide
source            1..25
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..2,3..5,6..8,9..12,13..19,20..25)
mod_base = OTHER

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modified_base          note = Phosphorothioate internucleotide linkages
                      order(2..3,5..6,8..9,12..13,19..20)
                      mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
SEQUENCE: 306          tcgtcgacga tcgggcgccc tgccg                               25

SEQ ID NO: 307          moltype = DNA  length = 24
FEATURE                 Location/Qualifiers
misc_feature            1..24
note = Synthetic oligonucleotide
source                  1..24
mol_type = other DNA
organism = synthetic construct
order(1..2,3..5,6..8,9..12,13..18,19..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base           order(2..3,5..6,8..9,12..13,18..19)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 307          tcgtcgacga tcgggcgcgt gccg                               24

SEQ ID NO: 308          moltype = DNA  length = 23
FEATURE                 Location/Qualifiers
misc_feature            1..23
note = Synthetic oligonucleotide
source                  1..23
mol_type = other DNA
organism = synthetic construct
order(1..2,3..5,6..8,9..11,12..17,18..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base           order(2..3,5..6,8..9,11..12,17..18)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 308          tcgtcgacga cggcgccgtg ccg                               23

SEQ ID NO: 309          moltype = DNA  length = 19
FEATURE                 Location/Qualifiers
misc_feature            1..19
note = Synthetic oligonucleotide
source                  1..19
mol_type = other DNA
organism = synthetic construct
order(1..6,7..12,13..19)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base           order(6..7,12..13)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 309          tcgtcgacga cgtgtcgt                               19

SEQ ID NO: 310          moltype = DNA  length = 24
FEATURE                 Location/Qualifiers
misc_feature            1..24
note = Synthetic oligonucleotide
source                  1..24
mol_type = other DNA
organism = synthetic construct
order(1..7,8..16,17..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base           order(7..8,16..17)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 310          tcgtcgacga cggcgccgtg ccgt                               24

SEQ ID NO: 311          moltype = DNA  length = 25
FEATURE                 Location/Qualifiers
misc_feature            1..25
note = Synthetic oligonucleotide
source                  1..25

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modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..5,6..8,9..12,13..18,19..25)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(5..6,8..9,12..13,18..19)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 311      tcgtcgacga tcggcgccgt gccgt          25
SEQ ID NO: 312      moltype = DNA length = 25
FEATURE           Location/Qualifiers
misc_feature       1..25
source             note = Synthetic oligonucleotide
                   1..25
modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..2,3..5,6..8,9..12,13..18,19..25)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(2..3,5..6,8..9,12..13,18..19)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 312      tcgtcgacgt tcggcgccgt gccgt          25
SEQ ID NO: 313      moltype = DNA length = 24
FEATURE           Location/Qualifiers
misc_feature       1..24
source             note = Synthetic oligonucleotide
                   1..24
modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..2,3..5,6..8,9..11,12..24)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(2..3,5..6,8..9,11..12,17..18)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 313      tcgtcgacgt cggcgccgtc ccgt          24
SEQ ID NO: 314      moltype = DNA length = 23
FEATURE           Location/Qualifiers
misc_feature       1..23
source             note = Synthetic oligonucleotide
                   1..23
modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..2,3..5,6..8,9..10,11..16,17..23)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(2..3,5..6,8..9,10..11,16..17)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 314      tcgtcgacgc ggcgcccgtc cgt           23
SEQ ID NO: 315      moltype = DNA length = 20
FEATURE           Location/Qualifiers
misc_feature       1..20
source             note = Synthetic oligonucleotide
                   1..20
modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..5,6..10,11..14,15..20)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(5..6,10..11,14..15)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 315      tcgtcgacga agtcgacgtat          20
SEQ ID NO: 316      moltype = DNA length = 24

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FEATURE Location/Qualifiers  
 misc\_feature 1..24  
 source note = Synthetic oligonucleotide  
 modified\_base 1..24  
 mol\_type = other DNA  
 organism = synthetic construct  
 order(1..5,6..12,13..18,19..24)  
 mod\_base = OTHER  
 note = Phosphorothioate internucleotide linkages  
 modified\_base order(5..6,12..13,18..19)  
 mod\_base = OTHER  
 note = Phosphodiester internucleotide linkages

SEQUENCE: 316  
 tcgtcgacga gaatcgtcga cgtat 24

SEQ ID NO: 317  
 FEATURE Location/Qualifiers  
 misc\_feature 1..22  
 source note = Synthetic oligonucleotide  
 modified\_base 1..22  
 mol\_type = other DNA  
 organism = synthetic construct  
 order(1..5,6..9,10..15,16..22)  
 mod\_base = OTHER  
 note = Phosphorothioate internucleotide linkages  
 modified\_base order(5..6,9..10,15..16)  
 mod\_base = OTHER  
 note = Phosphodiester internucleotide linkages

SEQUENCE: 317  
 tcgtcgtagc ggcgcgtgcc gt 22

SEQ ID NO: 318  
 FEATURE Location/Qualifiers  
 misc\_feature 1..25  
 source note = Synthetic oligonucleotide  
 modified\_base 1..25  
 mol\_type = other DNA  
 organism = synthetic construct  
 order(1..5,6..8,9..12,13..18,19..25)  
 mod\_base = OTHER  
 note = Phosphorothioate internucleotide linkages  
 modified\_base order(5..6,8..9,12..13,18..19)  
 mod\_base = OTHER  
 note = Phosphodiester internucleotide linkages

SEQUENCE: 318  
 tcgtcgacga tggcgccgt gccgt 25

SEQ ID NO: 319  
 FEATURE Location/Qualifiers  
 misc\_feature 1..19  
 source note = Synthetic oligonucleotide  
 modified\_base 1..19  
 mol\_type = other DNA  
 organism = synthetic construct  
 order(1..5,6..11,13..19)  
 mod\_base = OTHER  
 note = Phosphorothioate internucleotide linkages  
 modified\_base 5..6  
 mod\_base = OTHER  
 note = Phosphodiester internucleotide linkages

SEQUENCE: 319  
 tcgtcgacga cgtgtcgtat 19

SEQ ID NO: 320  
 FEATURE Location/Qualifiers  
 misc\_feature 1..20  
 source note = Synthetic oligonucleotide  
 modified\_base 1..20  
 mol\_type = other DNA  
 organism = synthetic construct  
 order(1..5,6..10,11..14,15..20)  
 mod\_base = OTHER  
 note = Phosphorothioate internucleotide linkages  
 modified\_base order(5..6,10..11,14..15)  
 mod\_base = OTHER  
 note = Phosphodiester internucleotide linkages

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SEQUENCE: 320          moltype = DNA  length = 24
tcgacgtcga agacgtcgat                                20

SEQ ID NO: 321          moltype = DNA  length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
source            1..24
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..5,6..12,13..18,19..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     order(5..6,12..13,18..19)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 321          moltype = DNA  length = 24
tcgacgtcga gaatcgacgt cgat                                24

SEQ ID NO: 322          moltype = DNA  length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide
source            1..21
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..5,6..8,9..15,16..21)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     order(5..6,8..9,15..16)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 322          moltype = DNA  length = 21
tcgtcga gggcgaagcc g                                21

SEQ ID NO: 323          moltype = DNA  length = 22
FEATURE           Location/Qualifiers
misc_feature      1..22
note = Synthetic oligonucleotide
source            1..22
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..5,6..8,9..15,16..22)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     order(5..6,8..9,15..16)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 323          moltype = DNA  length = 22
tcgtcga gggcgaagcc gt                                22

SEQ ID NO: 324          moltype = DNA  length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide
source            1..21
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..5,6..11,12..17,18..21)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     order(5..6,11..12,17..18)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 324          moltype = DNA  length = 21
tcgacgtcga cgtgacgttg t                                21

SEQ ID NO: 325          moltype = DNA  length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
note = Synthetic oligonucleotide
modified_base    23
mod_base = OTHER
note = Butyrate appended
source            1..23
mol_type = other DNA

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modified_base      organism = synthetic construct
                   order(1..2,3..5,6..8,9..12,13..17,18..23)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(5..6,8..9,12..13,17..18)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 325      tcgtcgacga tcggcgcgcg ccg                         23
SEQ ID NO: 326      moltype = DNA length = 17
FEATURE           Location/Qualifiers
misc_feature       1..17
source             note = Synthetic oligonucleotide
                   1..17
                   mol_type = other DNA
modified_base      organism = synthetic construct
                   order(1..2,3..5,6..11,12..14,15..17)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(2..3,5..6,11..12,14..15)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 326      acgacgtttt cgacgtt                                         17
SEQ ID NO: 327      moltype = DNA length = 25
FEATURE           Location/Qualifiers
misc_feature       1..25
source             note = Synthetic oligonucleotide
                   1..25
                   mol_type = other DNA
modified_base      organism = synthetic construct
                   order(1..2,3..5,6..12,13..17,18..24)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(2..3,5..6,12..13,17..18)
                   mod_base = OTHER
modified_base      note = Phosphodiester internucleotide linkages
                   25
                   mod_base = OTHER
modified_base      note = Inverse nucleotide ( 3-prime and 5-prime switched)
SEQUENCE: 327      tcgtcgacga tcggcgcgcg cccgt                         25
SEQ ID NO: 328      moltype = DNA length = 26
FEATURE           Location/Qualifiers
misc_feature       1..26
source             note = Synthetic oligonucleotide
                   1..26
                   mol_type = other DNA
modified_base      organism = synthetic construct
                   order(2..3,4..6,7..13,14..18,19..25)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(1..2,3..4,6..7,13..14,18..19,25..26)
                   mod_base = OTHER
modified_base      note = Phosphodiester internucleotide linkages
                   1
                   mod_base = OTHER
modified_base      note = Inverse nucleotide ( 3-prime and 5-prime switched)
                   26
                   mod_base = OTHER
modified_base      note = Inverse nucleotide ( 3-prime and 5-prime switched)
SEQUENCE: 328      ttctcgacg atcggcgcg gcgggt                         26
SEQ ID NO: 329      moltype = DNA length = 23
FEATURE           Location/Qualifiers
misc_feature       1..23
source             note = Synthetic oligonucleotide
                   1..23
                   mol_type = other DNA
modified_base      organism = synthetic construct
                   order(1..2,3..5,6..8,9..12,13..17,18..23)
                   mod_base = OTHER

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modified_base          note = Phosphorothioate internucleotide linkages
                      order(2..3,5..6,8..9,12..13,17..18)
                      mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
SEQUENCE: 329          tcgtcgacga tcgacgcgcg tcg                                23
SEQ ID NO: 330          moltype = DNA  length = 23
FEATURE                Location/Qualifiers
misc_feature           1..23
note = Synthetic oligonucleotide
source                 1..23
mol_type = other DNA
organism = synthetic construct
order(1..2,3..5,6..8,9..12,13..17,18..23)
mod_base = OTHER
modified_base          note = Phosphorothioate internucleotide linkages
                      order(2..3,5..6,8..9,12..13,17..18)
                      mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
SEQUENCE: 330          tcgtcgacga tcaacgcgcg ttg                                23
SEQ ID NO: 331          moltype = DNA  length = 23
FEATURE                Location/Qualifiers
misc_feature           1..23
note = Synthetic oligonucleotide
source                 1..23
mol_type = other DNA
organism = synthetic construct
order(1..2,3..5,6..8,9..12,13..17,18..23)
mod_base = OTHER
modified_base          note = Phosphorothioate internucleotide linkages
                      order(2..3,5..6,8..9,12..13,17..18)
                      mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
SEQUENCE: 331          tcgtcgacga tcggcacgtg ccg                                23
SEQ ID NO: 332          moltype = DNA  length = 23
FEATURE                Location/Qualifiers
misc_feature           1..23
note = Synthetic oligonucleotide
source                 1..23
mol_type = other DNA
organism = synthetic construct
order(1..2,3..5,6..8,9..12,13..17,18..23)
mod_base = OTHER
modified_base          note = Phosphorothioate internucleotide linkages
                      order(2..3,5..6,8..9,12..13,17..18)
                      mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
SEQUENCE: 332          tcgtcgacga tcggcatatg ccg                                23
SEQ ID NO: 333          moltype = DNA  length = 23
FEATURE                Location/Qualifiers
misc_feature           1..23
note = Synthetic oligonucleotide
source                 1..23
mol_type = other DNA
organism = synthetic construct
order(1..2,3..5,6..8,9..12,13..17,18..23)
mod_base = OTHER
modified_base          note = Phosphorothioate internucleotide linkages
                      order(2..3,5..6,8..9,12..13,17..18)
                      mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
SEQUENCE: 333          tcgtcgacga tgccgcgcgc ggc                                23
SEQ ID NO: 334          moltype = DNA  length = 24
FEATURE                Location/Qualifiers
misc_feature           1..24
note = Synthetic oligonucleotide
source                 1..24

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modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..2,3..24)
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base      2..3
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 334     tcgtcgacga tgccgcgctg cgcc                               24
SEQ ID NO: 335     moltype = DNA length = 24
FEATURE          Location/Qualifiers
misc_feature      1..24
                   note = Synthetic oligonucleotide
source            1..24
                   mol_type = other DNA
                   organism = synthetic construct
                   order(1..2,3..24)
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base      2..3
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 335     tcgtcgtacg atgccgcgcg cgcc                               24
SEQ ID NO: 336     moltype = DNA length = 25
FEATURE          Location/Qualifiers
misc_feature      1..25
                   note = Synthetic oligonucleotide
source            1..25
                   mol_type = other DNA
                   organism = synthetic construct
                   order(1..2,3..25)
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base      2..3
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 336     tcgtcgtacg atgccgcgcg gccg                               25
SEQ ID NO: 337     moltype = DNA length = 24
FEATURE          Location/Qualifiers
misc_feature      1..24
                   note = Synthetic oligonucleotide
source            1..24
                   mol_type = other DNA
                   organism = synthetic construct
                   order(1..5,6..23)
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base      order(5..6,23..24)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
modified_base      24
                   mod_base = OTHER
                   note = Inverse nucleotide ( 3-prime and 5-prime switched)
SEQUENCE: 337     tcgtcgacga tcggcgccgc ccgt                               24
SEQ ID NO: 338     moltype = DNA length = 23
FEATURE          Location/Qualifiers
misc_feature      1..23
                   note = Synthetic oligonucleotide
source            1..23
                   mol_type = other DNA
                   organism = synthetic construct
                   order(1..2,3..5,6..8,9..12,13..17,18..23)
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base      order(2..3,5..6,8..9,12..13,17..18)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 338

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tcgtgcacga tcggcgcgccg ccg	23
SEQ ID NO: 339	moltype = DNA length = 23
FEATURE	Location/Qualifiers
misc_feature	1..23
	note = Synthetic oligonucleotide
modified_base	2
	mod_base = m5c
source	1..23
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..5,6..8,9..12,13..17,18..23)
	mod_base = OTHER
modified_base	note = Phosphorothioate internucleotide linkages
	order(2..3,5..6,8..9,12..13,17..18)
modified_base	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 339	
tngtcgacga tcggcgcgccg ccg	23
SEQ ID NO: 340	moltype = DNA length = 23
FEATURE	Location/Qualifiers
misc_feature	1..23
	note = Synthetic oligonucleotide
modified_base	5
	mod_base = m5c
source	1..23
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..5,6..8,9..12,13..17,18..23)
	mod_base = OTHER
modified_base	note = Phosphorothioate internucleotide linkages
	order(2..3,5..6,8..9,12..13,17..18)
modified_base	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 340	
tcgtngacga tcggcgcgccg ccg	23
SEQ ID NO: 341	moltype = DNA length = 23
FEATURE	Location/Qualifiers
misc_feature	1..23
	note = Synthetic oligonucleotide
modified_base	8
	mod_base = m5c
source	1..23
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..5,6..8,9..12,13..17,18..23)
	mod_base = OTHER
modified_base	note = Phosphorothioate internucleotide linkages
	order(2..3,5..6,8..9,12..13,17..18)
modified_base	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 341	
tcgtcganga tcggcgcgccg ccg	23
SEQ ID NO: 342	moltype = DNA length = 23
FEATURE	Location/Qualifiers
misc_feature	1..23
	note = Synthetic oligonucleotide
modified_base	12
	mod_base = m5c
source	1..23
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..5,6..8,9..12,13..17,18..23)
	mod_base = OTHER
modified_base	note = Phosphorothioate internucleotide linkages
	order(2..3,5..6,8..9,12..13,17..18)
modified_base	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 342	
tcgtcgacga tngcgcgccg ccg	23
SEQ ID NO: 343	moltype = DNA length = 18
FEATURE	Location/Qualifiers

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misc_feature          1..18
source               note = Synthetic oligonucleotide
                     1..18
                     mol_type = other DNA
                     organism = synthetic construct
modified_base         order(1..2,3..8,9..14,15..18)
                     mod_base = OTHER
                     note = Phosphorothioate internucleotide linkages
modified_base         order(2..3,8..9,14..15)
                     mod_base = OTHER
                     note = Phosphodiester internucleotide linkages
SEQUENCE: 343        note = Phosphodiester internucleotide linkages
tcgacgtcga cgtcgacg                         18

SEQ ID NO: 344      moltype = DNA length = 25
FEATURE              Location/Qualifiers
misc_feature         1..25
source               note = Synthetic oligonucleotide
                     1..25
                     mol_type = other DNA
                     organism = synthetic construct
modified_base         order(1..2,3..24)
                     mod_base = OTHER
                     note = Phosphorothioate internucleotide linkages
modified_base         order(2..3,24..25)
                     mod_base = OTHER
                     note = Phosphodiester internucleotide linkages
                     25
modified_base         mod_base = OTHER
                     note = Inverse nucleotide ( 3-prime and 5-prime switched)
SEQUENCE: 344        note = Inverse nucleotide ( 3-prime and 5-prime switched)
tcgtcgacgt tcggcgccgt gccgt                         25

SEQ ID NO: 345      moltype = DNA length = 23
FEATURE              Location/Qualifiers
misc_feature         1..23
source               note = Synthetic oligonucleotide
                     1..23
                     mol_type = other DNA
                     organism = synthetic construct
modified_base         order(1..6,7..11,12..15,16..18,19..21,22..23)
                     mod_base = OTHER
                     note = Phosphorothioate internucleotide linkages
modified_base         order(6..7,11..12,15..16,18..19,21..22)
                     mod_base = OTHER
                     note = Phosphodiester internucleotide linkages
modified_base         13..23
                     mod_base = OTHER
                     note = Inverse nucleotide (inverse orientation: 3-prime and
                           5-prime switched)
SEQUENCE: 345        note = Inverse nucleotide (inverse orientation: 3-prime and
gccgcgcgcg gctagcagct gct                         23
                           5-prime switched)

SEQ ID NO: 346      moltype = DNA length = 23
FEATURE              Location/Qualifiers
misc_feature         1..23
source               note = Synthetic oligonucleotide
                     1..23
                     mol_type = other DNA
                     organism = synthetic construct
modified_base         order(1..6,7..11,12..15,16..18,19..21,22..23)
                     mod_base = OTHER
                     note = Phosphorothioate internucleotide linkages
modified_base         order(6..7,11..12,15..16,18..19,21..22)
                     mod_base = OTHER
                     note = Phosphodiester internucleotide linkages
modified_base         13..23
                     mod_base = OTHER
                     note = Inverse nucleotide (inverse orientation: 3-prime and
                           5-prime switched)
SEQUENCE: 346        note = Inverse nucleotide (inverse orientation: 3-prime and
cggcgccgcg cgttagcagct gct                         23
                           5-prime switched)

SEQ ID NO: 347      moltype = DNA length = 24
FEATURE              Location/Qualifiers
misc_feature         1..24

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source          note = Synthetic oligonucleotide
1..24
mol_type = other DNA
organism = synthetic construct
modified_base   order(1..7,8..19,20..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base   order(7..8,19..20)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
modified_base   14..24
mod_base = OTHER
note = Inverse nucleotide (inverse orientation: 3-prime and
      5-prime switched)

SEQUENCE: 347
cgcgcgcgtg ccgttgccgc tgct                                24

SEQ ID NO: 348      moltype = DNA  length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
source            1..24
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..6,7..12,13..19,20..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     order(6..7,12..13,19..20)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
modified_base     14..24
mod_base = OTHER
note = Inverse nucleotide (inverse orientation: 3-prime and
      5-prime switched)

SEQUENCE: 348
ggcgtgcgcg ggcttgccgc tgct                                24

SEQ ID NO: 349      moltype = DNA  length = 25
FEATURE           Location/Qualifiers
misc_feature      1..25
note = Synthetic oligonucleotide
source            1..25
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..7,8..12,13..17,18..20,21..23,24..25)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     order(7..8,12..13,17..18,20..21,23..24)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
modified_base     15..25
mod_base = OTHER
note = Inverse nucleotide (inverse orientation: 3-prime and
      5-prime switched)

SEQUENCE: 349
tcggcgcgccg ccgatagcag ctgct                                25

SEQ ID NO: 350      moltype = DNA  length = 25
FEATURE           Location/Qualifiers
misc_feature      1..25
note = Synthetic oligonucleotide
source            1..25
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..20,21..25)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     20..21
mod_base = OTHER
note = Phosphodiester internucleotide linkages
modified_base     15..25
mod_base = OTHER
note = Inverse nucleotide (inverse orientation: 3-prime and
      5-prime switched)

SEQUENCE: 350
tcggcgccgt ggcgttgccag ctgct                               25

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SEQ ID NO: 351      moltype = DNA  length = 13
FEATURE
misc_feature
1..13
note = Synthetic oligonucleotide
source
1..13
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 351
cggcgcnngcg  ccg                                13

SEQ ID NO: 352      moltype = DNA  length = 22
FEATURE
misc_feature
1..22
note = Synthetic oligonucleotide
source
1..22
mol_type = other DNA
organism = synthetic construct
modified_base
1..22
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 352
tcgtcgaacga  cggcgcgccgc  cg                                22

SEQ ID NO: 353      moltype = DNA  length = 23
FEATURE
misc_feature
1..23
note = Synthetic oligonucleotide
modified_base
11
mod_base = OTHER
note = 1,3-propane-diol
source
1..23
mol_type = other DNA
organism = synthetic construct
modified_base
1..23
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 353
tcgtcgaacga  ncggcgcgcg  ccg                                23

SEQ ID NO: 354      moltype = DNA  length = 23
FEATURE
misc_feature
1..23
note = Synthetic oligonucleotide
modified_base
11
mod_base = OTHER
note = Hexaethylene glycol
source
1..23
mol_type = other DNA
organism = synthetic construct
modified_base
1..23
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 354
tcgtcgaacga  ncggcgcgcg  ccg                                23

SEQ ID NO: 355      moltype = DNA  length = 23
FEATURE
misc_feature
1..23
note = Synthetic oligonucleotide
modified_base
11
mod_base = OTHER
note = 1-Prime-2-prime-dideoxyribose (D spacer)
source
1..23
mol_type = other DNA
organism = synthetic construct
modified_base
1..23
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 355
tcgtcgaacga  ncggcgcgcg  ccg                                23

SEQ ID NO: 356      moltype = DNA  length = 15
FEATURE
misc_feature
1..15
note = Synthetic oligonucleotide

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source          1..15
               mol_type = other DNA
               organism = synthetic construct
modified_base   order(1..2,12..15)
               mod_base = OTHER
               note = Phosphorothioate internucleotide linkages
modified_base   2..12
               mod_base = OTHER
               note = Phosphodiester internucleotide linkages
SEQUENCE: 356
tcgacgtgt ggggg                                         15

SEQ ID NO: 357
FEATURE
misc_feature
source          1..16
               note = Synthetic oligonucleotide
modified_base   1..16
               mol_type = other DNA
               organism = synthetic construct
               note = Phosphorothioate internucleotide linkages
SEQUENCE: 357
tccaggactt ctctca                                         16

SEQ ID NO: 358
FEATURE
misc_feature
source          1..23
               note = Synthetic oligonucleotide
modified_base   1..23
               mol_type = other DNA
               organism = synthetic construct
               note = Phosphorothioate internucleotide linkages
modified_base   5..6
               mod_base = OTHER
               note = Phosphodiester internucleotide linkages
modified_base   order(1..2,4..5,8..9,11,13,15,18)
               mod_base = OTHER
               note = 2-Prime-O-methyl nucleosides
SEQUENCE: 358
tcgtcgacga tcggcgcgcc ccc                                23

SEQ ID NO: 359
FEATURE
misc_feature
source          1..23
               note = Synthetic oligonucleotide
modified_base   1..23
               mol_type = other DNA
               organism = synthetic construct
               note = Phosphorothioate internucleotide linkages
modified_base   order(3..6..7,9..10,13..14,16,18,20,23)
               mod_base = OTHER
               note = 2-Prime-O-methyl nucleosides
SEQUENCE: 359
tcgtcgacga tcggcgcgcc ccg                                23

SEQ ID NO: 360
FEATURE
misc_feature
modified_base   1..20
               note = Synthetic oligonucleotide
               3
               mod_base = OTHER
               note = 2,4-difluorotoluene
source          1..20
               mol_type = other DNA
               organism = synthetic construct
modified_base   order(1..4,5..20)
               mod_base = OTHER
               note = Phosphorothioate internucleotide linkages
modified_base   4..5
               mod_base = OTHER
               note = Phosphodiester internucleotide linkages

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SEQUENCE: 360
tgncgtttt tttttttttt                                         20

SEQ ID NO: 361      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide
modified_base    6
mod_base = OTHER
note = 2,4-difluorotoluene
source           1..20
mol_type = other DNA
organism = synthetic construct
order(1..4,5..20)
modified_base    mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base    4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 361
tgtcgnnttt tttttttttt                                         20

SEQ ID NO: 362      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide
modified_base    3
mod_base = OTHER
note = 2,4-difluorotoluene
modified_base    6
mod_base = OTHER
note = 2,4-difluorotoluene
source           1..20
mol_type = other DNA
organism = synthetic construct
order(1..4,5..20)
modified_base    mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base    4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 362
tgncgnnttt tttttttttt                                         20

SEQ ID NO: 363      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide
modified_base    4
mod_base = OTHER
note = 2,4-difluorotoluene
source           1..20
mol_type = other DNA
organism = synthetic construct
order(1..4,5..20)
modified_base    mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base    4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 363
tgtnngtttt tttttttttt                                         20

SEQ ID NO: 364      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide
modified_base    5
mod_base = OTHER
note = 2,4-difluorotoluene
source           1..20
mol_type = other DNA
organism = synthetic construct
order(1..4,5..20)
modified_base    mod_base = OTHER
note = Phosphorothioate internucleotide linkages

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modified_base      4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 364
tgtcnntttt tttttttttt                                20

SEQ ID NO: 365          moltype = DNA  length = 20
FEATURE
misc_feature           Location/Qualifiers
1..20
note = Synthetic oligonucleotide
modified_base          2
mod_base = OTHER
note = 2,4-difluorotoluene
source                 1..20
mol_type = other DNA
organism = synthetic construct
modified_base          order(1..3,4..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base          3..4
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 365
thcgtttttt tttttttttt                                20

SEQ ID NO: 366          moltype = DNA  length = 20
FEATURE
misc_feature           Location/Qualifiers
1..20
note = Synthetic oligonucleotide
modified_base          7
mod_base = OTHER
note = 2,4-difluorotoluene
source                 1..20
mol_type = other DNA
organism = synthetic construct
modified_base          order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base          4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 366
tgtcgtnntt tttttttttt                                20

SEQ ID NO: 367          moltype = DNA  length = 20
FEATURE
misc_feature           Location/Qualifiers
1..20
note = Synthetic oligonucleotide
modified_base          3
mod_base = OTHER
note = 5-bromo-2-prime-deoxyuridine
source                 1..20
mol_type = other DNA
organism = synthetic construct
modified_base          order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base          4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 367
tgnncgtttt tttttttttt                                20

SEQ ID NO: 368          moltype = DNA  length = 20
FEATURE
misc_feature           Location/Qualifiers
1..20
note = Synthetic oligonucleotide
modified_base          6
mod_base = OTHER
note = 5-bromo-2-prime-deoxyuridine
source                 1..20
mol_type = other DNA
organism = synthetic construct
modified_base          order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

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modified_base      4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 368
tgtcgnnttt tttttttttt                                20

SEQ ID NO: 369          moltype = DNA  length = 20
FEATURE
misc_feature           Location/Qualifiers
1..20
note = Synthetic oligonucleotide
modified_base          3
mod_base = OTHER
note = 5-bromo-2-prime-deoxyuridine
modified_base          6
mod_base = OTHER
note = 5-bromo-2-prime-deoxyuridine
source                1..20
mol_type = other DNA
organism = synthetic construct
order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base          4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 369
tgncgntttt tttttttttt                                20

SEQ ID NO: 370          moltype = DNA  length = 19
FEATURE
misc_feature           Location/Qualifiers
1..19
note = Synthetic oligonucleotide
modified_base          3
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source                1..19
mol_type = other DNA
organism = synthetic construct
order(1..4,5..19)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base          4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 370
tgncgtttt tttttttttt                                19

SEQ ID NO: 371          moltype = DNA  length = 20
FEATURE
misc_feature           Location/Qualifiers
1..20
note = Synthetic oligonucleotide
modified_base          6
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source                1..20
mol_type = other DNA
organism = synthetic construct
order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base          4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 371
tgtcgnnttt tttttttttt                                20

SEQ ID NO: 372          moltype = DNA  length = 20
FEATURE
misc_feature           Location/Qualifiers
1..20
note = Synthetic oligonucleotide
modified_base          3
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base          6
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine

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source          1..20
               mol_type = other DNA
               organism = synthetic construct
modified_base   order(1..4,5..20)
               mod_base = OTHER
               note = Phosphorothioate internucleotide linkages
modified_base   4..5
               mod_base = OTHER
               note = Phosphodiester internucleotide linkages
SEQUENCE: 372
tgcgcgtttt tttttttttt                                         20

SEQ ID NO: 373      moltype = DNA  length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide
modified_base     3
mod_base = OTHER
note = Uridine
source            1..20
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 373
tgtcggtttt tttttttttt                                         20

SEQ ID NO: 374      moltype = DNA  length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide
modified_base     6
mod_base = OTHER
note = Uridine
source            1..20
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 374
tgtcggtttt tttttttttt                                         20

SEQ ID NO: 375      moltype = DNA  length = 19
FEATURE           Location/Qualifiers
misc_feature      1..19
note = Synthetic oligonucleotide
modified_base     3
mod_base = OTHER
note = Uridine
modified_base     6
mod_base = OTHER
note = Uridine
source            1..19
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..4,5..19)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 375
tgncgcgtttt tttttttttt                                         19

SEQ ID NO: 376      moltype = DNA  length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide

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modified_base      1
source          mod_base = OTHER
                note = 5-iodo-2-prime-deoxyuridine
                1..21
                mol_type = other DNA
                organism = synthetic construct
modified_base      1..21
                mod_base = OTHER
                note = Phosphorothioate internucleotide linkages
SEQUENCE: 376
ncgtcgttt tcggtcgttt t                                21

SEQ ID NO: 377      moltype = DNA length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide
modified_base      4
source          mod_base = OTHER
                note = 5-iodo-2-prime-deoxyuridine
                1..21
                mol_type = other DNA
                organism = synthetic construct
modified_base      1..21
                mod_base = OTHER
                note = Phosphorothioate internucleotide linkages
SEQUENCE: 377
tcgnccgttt tcggtcgttt t                                21

SEQ ID NO: 378      moltype = DNA length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide
modified_base      15
source          mod_base = OTHER
                note = 5-iodo-2-prime-deoxyuridine
                1..21
                mol_type = other DNA
                organism = synthetic construct
modified_base      1..21
                mod_base = OTHER
                note = Phosphorothioate internucleotide linkages
SEQUENCE: 378
tcgtcggtt tcggncgttt t                                21

SEQ ID NO: 379      moltype = DNA length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide
modified_base      1
modified_base      mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base      4
modified_base      mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source          1..21
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base      mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 379
ncgnccgttt tcggtcgttt t                                21

SEQ ID NO: 380      moltype = DNA length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide
modified_base      4
modified_base      mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base      7
modified_base      mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source          1..21
mod_type = other DNA
organism = synthetic construct

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modified_base      1..21
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
SEQUENCE: 380
tcgnncgttt tcggtcgttt t                               21

SEQ ID NO: 381      moltype = DNA  length = 21
FEATURE          Location/Qualifiers
misc_feature     1..21
                  note = Synthetic oligonucleotide
modified_base    15
                  mod_base = OTHER
                  note = 5-ido-2-prime-deoxyuridine
modified_base    18
                  mod_base = OTHER
                  note = 5-ido-2-prime-deoxyuridine
source           1..21
                  mol_type = other DNA
                  organism = synthetic construct
modified_base    1..21
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
SEQUENCE: 381
tcgtcgttt tcggncgtt t                               21

SEQ ID NO: 382      moltype = DNA  length = 24
FEATURE          Location/Qualifiers
misc_feature     1..24
                  note = Synthetic oligonucleotide
modified_base    1
                  mod_base = OTHER
                  note = 5-ido-2-prime-deoxyuridine
source           1..24
                  mol_type = other DNA
                  organism = synthetic construct
modified_base    order(1..2,3..24)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base    2..3
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
SEQUENCE: 382
ncgtcggtt acggcgccgt gccg                           24

SEQ ID NO: 383      moltype = DNA  length = 24
FEATURE          Location/Qualifiers
misc_feature     1..24
                  note = Synthetic oligonucleotide
modified_base    4
                  mod_base = OTHER
                  note = 5-ido-2-prime-deoxyuridine
source           1..24
                  mol_type = other DNA
                  organism = synthetic construct
modified_base    order(1..5,6..24)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base    5..6
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
SEQUENCE: 383
tcgnccgttt acggcgccgt gccg                           24

SEQ ID NO: 384      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
                  note = Synthetic oligonucleotide
modified_base    6
                  mod_base = OTHER
                  note = 5-ethyl-2-prime-deoxyuridine
source           1..20
                  mol_type = other DNA
                  organism = synthetic construct
modified_base    order(1..4,5..20)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages

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modified_base      4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 384
tgtcgnnttt tttttttttt                                20

SEQ ID NO: 385          moltype = DNA  length = 20
FEATURE
misc_feature           Location/Qualifiers
1..20
note = Synthetic oligonucleotide
modified_base          3
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
modified_base          6
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source                1..20
mol_type = other DNA
organism = synthetic construct
order(1..4,5..20)
modified_base          mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base          4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 385
tgncgnnttt tttttttttt                                20

SEQ ID NO: 386          moltype = DNA  length = 23
FEATURE
misc_feature           Location/Qualifiers
1..23
note = Synthetic oligonucleotide
modified_base          1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source                1..23
mol_type = other DNA
organism = synthetic construct
order(1..2,3..23)
modified_base          mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base          2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 386
ncgtcgacga tcggcgcgcg ccg                           23

SEQ ID NO: 387          moltype = DNA  length = 23
FEATURE
misc_feature           Location/Qualifiers
1..23
note = Synthetic oligonucleotide
modified_base          4
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source                1..23
mol_type = other DNA
organism = synthetic construct
order(1..5,6..23)
modified_base          mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base          5..6
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 387
tcgnccgacga tcggcgcgcg ccg                           23

SEQ ID NO: 388          moltype = DNA  length = 23
FEATURE
misc_feature           Location/Qualifiers
1..23
note = Synthetic oligonucleotide
modified_base          1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base          4
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine

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source          1..23
               mol_type = other DNA
               organism = synthetic construct
modified_base   order(1..2,3..23)
               mod_base = OTHER
               note = Phosphorothioate internucleotide linkages
modified_base   2..3
               mod_base = OTHER
               note = Phosphodiester internucleotide linkages
SEQUENCE: 388
ncgnccgacga tcggcgcgcc ccg                                23

SEQ ID NO: 389      moltype = DNA  length = 15
FEATURE           Location/Qualifiers
misc_feature      1..15
note = Synthetic oligonucleotide
modified_base     1
               mod_base = OTHER
               note = 5-iodo-2-prime-deoxyuridine
source          1..15
               mol_type = other DNA
               organism = synthetic construct
modified_base   order(1..2,12..15)
               mod_base = OTHER
               note = Phosphorothioate internucleotide linkages
modified_base   2..12
               mod_base = OTHER
               note = Phosphodiester internucleotide linkages
SEQUENCE: 389
ncgacgtcgt ggggg                                15

SEQ ID NO: 390      moltype = DNA  length = 15
FEATURE           Location/Qualifiers
misc_feature      1..15
note = Synthetic oligonucleotide
7
modified_base     7
               mod_base = OTHER
               note = 5-iodo-2-prime-deoxyuridine
source          1..15
               mol_type = other DNA
               organism = synthetic construct
modified_base   order(1..2,12..15)
               mod_base = OTHER
               note = Phosphorothioate internucleotide linkages
modified_base   2..12
               mod_base = OTHER
               note = Phosphodiester internucleotide linkages
SEQUENCE: 390
tcgacgncgt ggggg                                15

SEQ ID NO: 391      moltype = DNA  length = 15
FEATURE           Location/Qualifiers
misc_feature      1..15
note = Synthetic oligonucleotide
7
modified_base     7
               mod_base = OTHER
               note = 5-iodo-2-prime-deoxyuridine
10
modified_base    10
               mod_base = OTHER
               note = 5-iodo-2-prime-deoxyuridine
source          1..15
               mol_type = other DNA
               organism = synthetic construct
modified_base   order(1..2,12..15)
               mod_base = OTHER
               note = Phosphorothioate internucleotide linkages
modified_base   2..12
               mod_base = OTHER
               note = Phosphodiester internucleotide linkages
SEQUENCE: 391
tcgacgncgn ggggg                                15

SEQ ID NO: 392      moltype = DNA  length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide

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modified_base      3
source          mod_base = OTHER
                note = 5-chloro-2-prime-deoxyuridine
1..20
mol_type = other DNA
organism = synthetic construct
order(1..3,4..5,6..20)
modified_base      mod_base = OTHER
note = Phosphorothioate internucleotide linkages
5..6
modified_base      mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 392
tgncgtttt tttttttt                                         20

SEQ_ID NO: 393      moltype = DNA length = 20
FEATURE          Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide
modified_base      3
source          mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
1..20
mol_type = other DNA
organism = synthetic construct
order(1..4,5..20)
modified_base      mod_base = OTHER
note = Phosphorothioate internucleotide linkages
4..5
modified_base      mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 393
tgncgtttt tttttttt                                         20

SEQ_ID NO: 394      moltype = DNA length = 24
FEATURE          Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
modified_base      1
source          mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base      4
source          mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
1..24
mol_type = other DNA
organism = synthetic construct
order(1..2,3..24)
modified_base      mod_base = OTHER
note = Phosphorothioate internucleotide linkages
2..3
modified_base      mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 394
nccnccgtt acggcgccgt gccg                                         24

SEQ_ID NO: 395      moltype = DNA length = 24
FEATURE          Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
modified_base      4
source          mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base      7
source          mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
1..24
mol_type = other DNA
organism = synthetic construct
order(1..2,3..24)
modified_base      mod_base = OTHER
note = Phosphorothioate internucleotide linkages
2..3
modified_base      mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 395

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tcgnccgntt acggcgccgt gccg	24
SEQ ID NO: 396	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Synthetic oligonucleotide
modified_base	10
	mod_base = OTHER
	note = 5-iodo-2-prime-deoxyuridine
source	1..22
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..11,12..22)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
modified_base	11..12
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 396	
tctttttgn cgttttttt tt	22
SEQ ID NO: 397	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Synthetic oligonucleotide
modified_base	10
	mod_base = OTHER
	note = 5-iodo-2-prime-deoxyuridine
modified_base	13
	mod_base = OTHER
	note = 5-iodo-2-prime-deoxyuridine
source	1..22
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..11,12..22)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
modified_base	11..12
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 397	
tctttttgn cgnttttttt tt	22
SEQ ID NO: 398	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Synthetic oligonucleotide
modified_base	1
	mod_base = OTHER
	note = 5-iodo-2-prime-deoxyuridine
source	1..22
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..11,12..22)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
modified_base	11..12
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 398	
ncttttttgt cgtttttttt tt	22
SEQ ID NO: 399	moltype = DNA length = 22
FEATURE	Location/Qualifiers
misc_feature	1..22
	note = Synthetic oligonucleotide
modified_base	10
	mod_base = OTHER
	note = Uridine
source	1..22
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..11,12..22)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
modified_base	11..12

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mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 399
tctttttgn cgttttttt tt                                22

SEQ ID NO: 400      moltype = DNA length = 23
FEATURE          Location/Qualifiers
misc_feature     1..23
note = Synthetic oligonucleotide
modified_base    1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source          1..23
mol_type = other DNA
organism = synthetic construct
order(1..2,3..23)
modified_base    mod_base = OTHER
note = Phosphorothioate internucleotide linkages
2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 400
ncgacgtcga tcggcgcg cg                                23

SEQ ID NO: 401      moltype = DNA length = 24
FEATURE          Location/Qualifiers
misc_feature     1..24
note = Synthetic oligonucleotide
modified_base    1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source          1..24
mol_type = other DNA
organism = synthetic construct
order(1..2,3..24)
modified_base    mod_base = OTHER
note = Phosphorothioate internucleotide linkages
2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 401
ncgacgtcga tcggcgcg cg                                24

SEQ ID NO: 402      moltype = DNA length = 23
FEATURE          Location/Qualifiers
misc_feature     1..23
note = Synthetic oligonucleotide
modified_base    1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source          1..23
mol_type = other DNA
organism = synthetic construct
order(1..2,3..23)
modified_base    mod_base = OTHER
note = Phosphorothioate internucleotide linkages
2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 402
ncgacgtcga tcggcgcg cg                                23

SEQ ID NO: 403      moltype = DNA length = 24
FEATURE          Location/Qualifiers
misc_feature     1..24
note = Synthetic oligonucleotide
modified_base    1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source          1..24
mol_type = other DNA
organism = synthetic construct
order(1..2,3..24)
modified_base    mod_base = OTHER
note = Phosphorothioate internucleotide linkages
2..3

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SEQUENCE: 403          mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
ncgtcgacga tcggcgccg ccgt                                24

SEQ ID NO: 404          moltype = DNA length = 23
FEATURE                 Location/Qualifiers
misc_feature            1..23
note = Synthetic oligonucleotide
modified_base           1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source                  1..23
mol_type = other DNA
organism = synthetic construct
order(1..2,3..23)
modified_base           mod_base = OTHER
note = Phosphorothioate internucleotide linkages
2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 404          mod_base = OTHER
ncgtcgacga tcggcgccg ccgt                                23

SEQ ID NO: 405          moltype = DNA length = 23
FEATURE                 Location/Qualifiers
misc_feature            1..23
note = Synthetic oligonucleotide
modified_base           1
mod_base = OTHER
note = 5-ido-2-prime-deoxyuridine
source                  1..23
mol_type = other DNA
organism = synthetic construct
order(1..2,3..23)
modified_base           mod_base = OTHER
note = Phosphorothioate internucleotide linkages
2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 405          mod_base = OTHER
ncgtcgacga tcggcgccg ccgt                                23

SEQ ID NO: 406          moltype = DNA length = 20
FEATURE                 Location/Qualifiers
misc_feature            1..20
note = Synthetic oligonucleotide
modified_base           6
mod_base = OTHER
note = 5-fluorodeoxyuridine
source                  1..20
mol_type = other DNA
organism = synthetic construct
order(1..4,5..6,7..20)
modified_base           mod_base = OTHER
note = Phosphorothioate internucleotide linkages
4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 406          mod_base = OTHER
tgtcgnnttt tttttttttt                                20

SEQ ID NO: 407          moltype = DNA length = 20
FEATURE                 Location/Qualifiers
misc_feature            1..20
note = Synthetic oligonucleotide
modified_base           3
mod_base = OTHER
note = 5-fluorodeoxyuridine
modified_base           6
mod_base = OTHER
note = 5-fluorodeoxyuridine
source                  1..20
mol_type = other DNA
organism = synthetic construct
order(1..3,4..5,6..7,8..20)
modified_base

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modified_base      mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
5..6
modified_base      mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 407
tgnccgnttt tttttttt                                         20

SEQ ID NO: 408      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
                   note = Synthetic oligonucleotide
modified_base    3
                   mod_base = OTHER
                   note = Uridine
modified_base    6
                   mod_base = OTHER
                   note = Uridine
source           1..20
                   mol_type = other DNA
                   organism = synthetic construct
modified_base    order(1..4,5..6,7..20)
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base    4..5
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 408
tgnccgnttt tttttttt                                         20

SEQ ID NO: 409      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
                   note = Synthetic oligonucleotide
modified_base    5
                   mod_base = OTHER
                   note = 6-nitro-benzimidizol
source           1..20
                   mol_type = other DNA
                   organism = synthetic construct
modified_base    order(1..4,5..20)
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base    4..5
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 409
tgtcnnttt tttttttt                                         20

SEQ ID NO: 410      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
                   note = Synthetic oligonucleotide
modified_base    4
                   mod_base = OTHER
                   note = 6-nitro-benzimidazol
source           1..20
                   mol_type = other DNA
                   organism = synthetic construct
modified_base    order(1..4,5..20)
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base    4..5
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 410
tgtngtttt tttttttt                                         20

SEQ ID NO: 411      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
                   note = Synthetic oligonucleotide
modified_base    1
                   mod_base = OTHER
                   note = 5-iodo-2-prime-deoxyuridine
source           1..20

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modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..4,5..20)
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base      4..5
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 411
ngtcgtttt tttttttt                                         20

SEQ ID NO: 412      moltype = DNA length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
modified_base     note = Synthetic oligonucleotide
                  1
                  mod_base = OTHER
                  note = 5-iodo-2-prime-deoxyuridine
modified_base     3
                  mod_base = OTHER
                  note = 5-iodo-2-prime-deoxyuridine
source           1..20
                  mol_type = other DNA
                  organism = synthetic construct
modified_base     order(1..4,5..20)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base     4..5
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
SEQUENCE: 412
ngncgtttt tttttttt                                         20

SEQ ID NO: 413      moltype = DNA length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
modified_base     note = Synthetic oligonucleotide
                  7
                  mod_base = OTHER
                  note = 5-iodo-2-prime-deoxyuridine
source           1..20
                  mol_type = other DNA
                  organism = synthetic construct
modified_base     order(1..4,5..20)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base     4..5
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
SEQUENCE: 413
tgtcgtnntt tttttttt                                         20

SEQ ID NO: 414      moltype = DNA length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
modified_base     note = Synthetic oligonucleotide
                  3
                  mod_base = OTHER
                  note = a,a,a-trifluoro-dT
source           1..20
                  mol_type = other DNA
                  organism = synthetic construct
modified_base     order(1..4,5..20)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base     4..5
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
SEQUENCE: 414
tgncgtttt tttttttt                                         20

SEQ ID NO: 415      moltype = DNA length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
modified_base     note = Synthetic oligonucleotide
                  6

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source          mod_base = OTHER
                note = a,a,a-trifluoro-dT
1..20
mol_type = other DNA
organism = synthetic construct
modified_base   order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base   4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 415
tgtcgntttt tttttttttt                                         20

SEQ ID NO: 416      moltype = DNA length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide
modified_base     3
mod_base = OTHER
note = a,a,a-trifluoro-dT
modified_base     6
mod_base = OTHER
note = a,a,a-trifluoro-dT
source            1..20
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 416
tgnncgntttt tttttttttt                                         20

SEQ ID NO: 417      moltype = DNA length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide
modified_base     6
mod_base = OTHER
note = 5-chloro-2-prime-deoxyuridine
source            1..20
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..4,5..6,7..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 417
tgtcgntttt tttttttttt                                         20

SEQ ID NO: 418      moltype = DNA length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide
modified_base     3
mod_base = OTHER
note = 5-chloro-2-prime-deoxyuridine
modified_base     6
mod_base = OTHER
note = 5-chloro-2-prime-deoxyuridine
source            1..20
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..3,4..5,6..7,8..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     5..6
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 418
tgnncgntttt tttttttttt                                         20

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SEQ ID NO: 419      moltype = DNA length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide
modified_base
2
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source
1..20
mol_type = other DNA
organism = synthetic construct
order(1..3,4..20)
modified_base
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
3..4
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 419
tncgaaaa tttttttt          20

SEQ ID NO: 420      moltype = DNA length = 15
FEATURE
misc_feature
1..15
note = Synthetic oligonucleotide
modified_base
3
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source
1..15
mol_type = other DNA
organism = synthetic construct
order(1..4,5..12,13..15)
modified_base
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
order(4..5,12..13)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 420
tgcgtttt tcgttt          15

SEQ ID NO: 421      moltype = DNA length = 18
FEATURE
misc_feature
1..18
note = Synthetic oligonucleotide
modified_base
3
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source
1..18
mol_type = other DNA
organism = synthetic construct
order(1..4,5..7,8..12,13..15,16..18)
modified_base
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
order(4..5,7..8,12..13,15..16)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 421
ttncgtcgaa tcgtcgaa         18

SEQ ID NO: 422      moltype = DNA length = 15
FEATURE
misc_feature
1..15
note = Synthetic oligonucleotide
modified_base
1
mod_base = OTHER
note = 5-bromo-2-prime-deoxyuridine
source
1..15
mol_type = other DNA
organism = synthetic construct
order(1..2,13..15)
modified_base
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
2..13
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 422
ncgacgtcgt gggggg          15

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SEQ ID NO: 423      moltype = DNA  length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide
modified_base
3
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source
1..20
mol_type = other DNA
organism = synthetic construct
order(1..4,5..20)
modified_base
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 423
tgngctttt tttttttt          20

SEQ ID NO: 424      moltype = DNA  length = 22
FEATURE
misc_feature
1..22
note = Synthetic oligonucleotide
modified_base
1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source
1..22
mol_type = other DNA
organism = synthetic construct
order(1..2,3..22)
modified_base
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 424
ncgtcgttt cggcgccgcg cg          22

SEQ ID NO: 425      moltype = DNA  length = 22
FEATURE
misc_feature
1..22
note = Synthetic oligonucleotide
modified_base
4
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source
1..22
mol_type = other DNA
organism = synthetic construct
modified_base
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 425
tcgnctttt cggcgccgcg cg          22

SEQ ID NO: 426      moltype = DNA  length = 22
FEATURE
misc_feature
1..22
note = Synthetic oligonucleotide
modified_base
10
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source
1..22
mol_type = other DNA
organism = synthetic construct
modified_base
order(1..11,12..22)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base
11..12
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 426
tcgtcgttt cggcgccgcg cg          22

SEQ ID NO: 427      moltype = DNA  length = 21
FEATURE
Location/Qualifiers

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misc_feature          1..21
note = Synthetic oligonucleotide
modified_base         1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base         15
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source               1..21
mol_type = other DNA
organism = synthetic construct
modified_base         1..21
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 427
ncgtcgttt tcggncgtt t                                21

SEQ_ID NO: 428      moltype = DNA length = 21
FEATURE             Location/Qualifiers
misc_feature        1..21
note = Synthetic oligonucleotide
modified_base       4
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base       15
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source              1..21
mol_type = other DNA
organism = synthetic construct
modified_base       1..21
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 428
tcgnccgttt tcggncgtt t                                21

SEQ_ID NO: 429      moltype = DNA length = 20
FEATURE             Location/Qualifiers
misc_feature        1..20
note = Synthetic oligonucleotide
modified_base       3
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base       16
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source              1..20
mol_type = other DNA
organism = synthetic construct
order(1..4,5..17,18..20)
modified_base       mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base       order(4..5,17..18)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 429
tgcgttttt ttttgncgtt                                20

SEQ_ID NO: 430      moltype = DNA length = 20
FEATURE             Location/Qualifiers
misc_feature        1..20
note = Synthetic oligonucleotide
modified_base       3
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source              1..20
mol_type = other DNA
organism = synthetic construct
modified_base       1..20
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 430
tgcgttttt tttttttttt                                20

SEQ_ID NO: 431      moltype = DNA length = 15
FEATURE             Location/Qualifiers

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misc_feature          1..15
note = Synthetic oligonucleotide
modified_base         1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base         13
mod_base = OTHER
note = 7-deaza-dG
source                1..15
mol_type = other DNA
organism = synthetic construct
order(1..2,12..15)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base         2..12
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 431
ncgacgtcgt ggnngg                                15

SEQ ID NO: 432
FEATURE
misc_feature          1..20
note = Synthetic oligonucleotide
modified_base         2
mod_base = OTHER
note = 2-Prime-O-methyl nucleoside
modified_base         3
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source                1..20
mol_type = other DNA
organism = synthetic construct
order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base         4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 432
tgnccgtttt tttttttt                                20

SEQ ID NO: 433
FEATURE
misc_feature          1..20
note = Synthetic oligonucleotide
modified_base         3
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base         5
mod_base = OTHER
note = 2-Prime-O-methyl nucleoside
source                1..20
mol_type = other DNA
organism = synthetic construct
order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base         4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 433
tgnccgtttt tttttttt                                20

SEQ ID NO: 434
FEATURE
misc_feature          1..20
note = Synthetic oligonucleotide
modified_base         order(2,5)
mod_base = OTHER
note = 2-Prime-O-methyl nucleosides
modified_base         3
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source                1..20
mol_type = other DNA

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modified_base      organism = synthetic construct
                  order(1..4,5..20)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base      4..5
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
SEQUENCE: 434
tgcgtttt tttttttt                                         20

SEQ ID NO: 435      moltype = DNA length = 20
FEATURE
misc_feature        Location/Qualifiers
1..20
note = Synthetic oligonucleotide
modified_base       3
mod_base = OTHER
note = 5-proynyl-dU
source              1..20
mol_type = other DNA
organism = synthetic construct
modified_base       order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base       4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 435
tgcgtttt tttttttt                                         20

SEQ ID NO: 436      moltype = DNA length = 20
FEATURE
misc_feature        Location/Qualifiers
1..20
note = Synthetic oligonucleotide
modified_base       6
mod_base = OTHER
note = 5-proynyl-dU
source              1..20
mol_type = other DNA
organism = synthetic construct
modified_base       order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base       4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 436
tgtcgnttt tttttttt                                         20

SEQ ID NO: 437      moltype = DNA length = 21
FEATURE
misc_feature        Location/Qualifiers
1..21
note = Synthetic oligonucleotide
modified_base       3
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source              1..21
mol_type = other DNA
organism = synthetic construct
modified_base       order(1..4,5..21)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base       4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 437
tgcgtttc ggcgcgcgcc g                                         21

SEQ ID NO: 438      moltype = DNA length = 21
FEATURE
misc_feature        Location/Qualifiers
1..21
note = Synthetic oligonucleotide
modified_base       2
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source              1..21
mol_type = other DNA

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modified_base      organism = synthetic construct
                  order(1..3,4..21)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base      3..4
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
SEQUENCE: 438
tncgttttcg ggcgcgcgcg t                                21

SEQ ID NO: 439      moltype = DNA length = 20
FEATURE
misc_feature        Location/Qualifiers
1..20
note = Synthetic oligonucleotide
modified_base        2
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source              1..20
mol_type = other DNA
organism = synthetic construct
modified_base        order(1..3,4..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base        3..4
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 439
tnccgtttttt tttttttttt                                20

SEQ ID NO: 440      moltype = DNA length = 20
FEATURE
misc_feature        Location/Qualifiers
1..20
note = Synthetic oligonucleotide
modified_base        3
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source              1..20
mol_type = other DNA
organism = synthetic construct
modified_base        order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base        4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 440
tgcgtttttt tttttttttt                                20

SEQ ID NO: 441      moltype = DNA length = 21
FEATURE
misc_feature        Location/Qualifiers
1..21
note = Synthetic oligonucleotide
modified_base        1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source              1..21
mol_type = other DNA
organism = synthetic construct
modified_base        order(1..2,3..21)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base        2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 441
ncgtcgttt tcggtcgttt t                                21

SEQ ID NO: 442      moltype = DNA length = 24
FEATURE
misc_feature        Location/Qualifiers
1..24
note = Synthetic oligonucleotide
modified_base        1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source              1..24
mol_type = other DNA

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modified_base      organism = synthetic construct
                  order(1..2,3..24)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base      2..3
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
SEQUENCE: 442    ncgtcgttt acggcgccgt gccg                               24
SEQ ID NO: 443   moltype = DNA length = 24
FEATURE          Location/Qualifiers
misc_feature     1..24
                  note = Synthetic oligonucleotide
modified_base     4
                  mod_base = OTHER
                  note = 5-ethyl-2-prime-deoxyuridine
source           1..24
                  mol_type = other DNA
                  organism = synthetic construct
modified_base     order(1..5,6..24)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base     5..6
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
SEQUENCE: 443    tcgnccgtt acggcgccgt gccg                               24
SEQ ID NO: 444   moltype = DNA length = 23
FEATURE          Location/Qualifiers
misc_feature     1..23
                  note = Synthetic oligonucleotide
modified_base     1
                  mod_base = OTHER
                  note = 5-ethyl-2-prime-deoxyuridine
source           1..23
                  mol_type = other DNA
                  organism = synthetic construct
modified_base     order(1..2,3..23)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base     2..3
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
SEQUENCE: 444    ncgtcgacga tcggcgcgcg ccg                                23
SEQ ID NO: 445   moltype = DNA length = 17
FEATURE          Location/Qualifiers
misc_feature     1..17
                  note = Synthetic oligonucleotide
modified_base     1
                  mod_base = OTHER
                  note = 5-iodo-2-prime-deoxyuridine
source           1..17
                  mol_type = other DNA
                  organism = synthetic construct
modified_base     1..17
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
SEQUENCE: 445    nctttttttt tttttttt                                         17
SEQ ID NO: 446   moltype = DNA length = 22
FEATURE          Location/Qualifiers
misc_feature     1..22
                  note = Synthetic oligonucleotide
modified_base     1
                  mod_base = OTHER
                  note = 5-iodo-2-prime-deoxyuridine
source           1..22
                  mol_type = other DNA
                  organism = synthetic construct
modified_base     1..22
                  mod_base = OTHER

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SEQUENCE: 446          note = Phosphorothioate internucleotide linkages
nctttttttt cgttttttt tt                                22

SEQ ID NO: 447      moltype = DNA  length = 22
FEATURE
misc_feature        Location/Qualifiers
1..22
note = Synthetic oligonucleotide
modified_base       10
mod_base = OTHER
note = 5-ido-2-prime-deoxyuridine
source              1..22
mol_type = other DNA
organism = synthetic construct
modified_base       1..22
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 447          note = Phosphorothioate internucleotide linkages
tcttttttn cgttttttt tt                                22

SEQ ID NO: 448      moltype = DNA  length = 22
FEATURE
misc_feature        Location/Qualifiers
1..22
note = Synthetic oligonucleotide
modified_base       1
mod_base = OTHER
note = 5-ido-2-prime-deoxyuridine
modified_base       10
mod_base = OTHER
note = 5-ido-2-prime-deoxyuridine
source              1..22
mol_type = other DNA
organism = synthetic construct
modified_base       1..22
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 448          note = Phosphorothioate internucleotide linkages
ncttttttn cgttttttt tt                                22

SEQ ID NO: 449      moltype = DNA  length = 24
FEATURE
misc_feature        Location/Qualifiers
1..24
note = Synthetic oligonucleotide
modified_base       1
mod_base = OTHER
note = 5-ido-2-prime-deoxyuridine
source              1..24
mol_type = other DNA
organism = synthetic construct
modified_base       order(1..2,3..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base       2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 449          note = Phosphodiester internucleotide linkages
ncgtcgttc gtcgtttgt cgtt                                24

SEQ ID NO: 450      moltype = DNA  length = 24
FEATURE
misc_feature        Location/Qualifiers
1..24
note = Synthetic oligonucleotide
modified_base       20
mod_base = OTHER
note = 5-ido-2-prime-deoxyuridine
source              1..24
mol_type = other DNA
organism = synthetic construct
modified_base       order(1..21,22..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base       21..22
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 450          note = Phosphodiester internucleotide linkages
tcgtcgttc gtcgtttgn cgtt                                24

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SEQ ID NO: 451      moltype = DNA  length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
modified_base      note = Synthetic oligonucleotide
1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base      20
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source            1..24
mol_type = other DNA
organism = synthetic construct
order(1..2,3..21,22..24)
modified_base      mod_base = OTHER
note = Phosphorothioate internucleotide linkages
order(2..3,21..22)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 451
ncgtcgttc gtcgtttgn cgtt                                24

SEQ ID NO: 452      moltype = DNA  length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
modified_base      note = Synthetic oligonucleotide
3
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base      5
mod_base = OTHER
note = 7-deaza-dG
source             1..20
mol_type = other DNA
organism = synthetic construct
order(1..4,5..20)
modified_base      mod_base = OTHER
note = Phosphorothioate internucleotide linkages
4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 452
tgnCNTTTT tttttttt                                20

SEQ ID NO: 453      moltype = DNA  length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
modified_base      note = Synthetic oligonucleotide
3
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base      5
mod_base = i
source             1..20
mol_type = other DNA
organism = synthetic construct
modified_base      1..19
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 453
tgnCNTTTT tttttttt                                20

SEQ ID NO: 454      moltype = DNA  length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
modified_base      note = Synthetic oligonucleotide
3
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base      4
mod_base = m5c
source             1..20

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mol_type = other DNA
organism = synthetic construct
order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base
4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 454
tgmngrttt tttttttttt                                         20

SEQ ID NO: 455      moltype = DNA length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide
modified_base      8
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source            1..20
mol_type = other DNA
organism = synthetic construct
order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base      4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 455
tgtcgttntt tttttttttt                                         20

SEQ ID NO: 456      moltype = DNA length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide
modified_base      9
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source            1..20
mol_type = other DNA
organism = synthetic construct
order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base      4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 456
tgtcgttntt tttttttttt                                         20

SEQ ID NO: 457      moltype = DNA length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
note = Synthetic oligonucleotide
modified_base      1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source            1..23
mol_type = other DNA
organism = synthetic construct
order(1..2,3..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base      2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 457
ncgtcggtt cggcgcgccc gct                                         23

SEQ ID NO: 458      moltype = DNA length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
note = Synthetic oligonucleotide
modified_base      1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source            1..23

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mol_type = other DNA
organism = synthetic construct
order(1..2,3..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base
2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 458
ncgtcgttt cggcgcgcbc cgt 23

SEQ ID NO: 459      moltype = DNA length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
note = Synthetic oligonucleotide
modified_base      4
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source            1..23
mol_type = other DNA
organism = synthetic construct
order(1..2,3..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base      2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 459
tcgnccgtttt cggcgcgcbc cgt 23

SEQ ID NO: 460      moltype = DNA length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
note = Synthetic oligonucleotide
modified_base      10
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source            1..23
mol_type = other DNA
organism = synthetic construct
order(1..2,3..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base      2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 460
tcgtcggtttt cggcgcgcbc cgt 23

SEQ ID NO: 461      moltype = DNA length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
note = Synthetic oligonucleotide
modified_base      10
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source            1..23
mol_type = other DNA
organism = synthetic construct
order(1..2,3..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base      2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 461
tcgtcggtttt cggcgcgcbc cgt 23

SEQ ID NO: 462      moltype = DNA length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
note = Synthetic oligonucleotide
modified_base      1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
modified_base      10

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        mod_base = OTHER
        note = 5-ethyl-2-prime-deoxyuridine
1..23
source          mol_type = other DNA
                organism = synthetic construct
modified_base   order(1..2,3..23)
                mod_base = OTHER
note = Phosphorothioate internucleotide linkages
2..3
modified_base   mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 462
ncgtcgtnn cggcgcgccg cgt                                23

SEQ ID NO: 463      moltype = DNA length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
note = Synthetic oligonucleotide
modified_base     1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
modified_base     4
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source           1..23
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..2,3..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 463
ncgnncgtttt cggcgcgccg cgt                               23

SEQ ID NO: 464      moltype = DNA length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
note = Synthetic oligonucleotide
modified_base     1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base     4
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source           1..23
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..2,3..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 464
ncgnncgtttt cggcgcgccg cgt                                23

SEQ ID NO: 465      moltype = DNA length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
modified_base     1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source           1..24
mol_type = other DNA
organism = synthetic construct
modified_base     order(1..2,3..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 465
ncgtcgtnn gtcgtttgt cggt                                24

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SEQ ID NO: 466      moltype = DNA  length = 22
FEATURE
misc_feature
1..22
note = Synthetic oligonucleotide
modified_base
1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source
1..22
mol_type = other DNA
organism = synthetic construct
order(1..2,3..22)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base
2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 466
ncgtcgttt gtcgttttcg tt                                22

SEQ ID NO: 467      moltype = DNA  length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide
modified_base
3
mod_base = OTHER
note = 5-(d-bromo-vinyl)-uridine
source
1..20
mol_type = other DNA
organism = synthetic construct
order(1..3,5..6,7..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base
6..7
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 467
tgcgtttt tttttttt                                         20

SEQ ID NO: 468      moltype = DNA  length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide
modified_base
6
mod_base = OTHER
note = 5-(d-bromo-vinyl)-uridine
source
1..20
mol_type = other DNA
organism = synthetic construct
order(1..4,5..6,8..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base
4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 468
tgtcgnttt tttttttt                                         20

SEQ ID NO: 469      moltype = DNA  length = 13
FEATURE
misc_feature
1..13
note = Synthetic oligonucleotide
modified_base
1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source
1..13
mol_type = other DNA
organism = synthetic construct
modified_base
1..13
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 469
ncggcggccg ccg                                           13

SEQ ID NO: 470      moltype = DNA  length = 24
FEATURE
Location/Qualifiers

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misc_feature          1..24
note = Synthetic oligonucleotide
modified_base         1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base         24
mod_base = OTHER
note = 3-Prime-O-methyl-riboguanidine
source               1..24
mol_type = other DNA
organism = synthetic construct
modified_base         1..24
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 470
ncgtcgttt acggcgccgt gccn                                24

SEQ_ID NO: 471      moltype = DNA length = 24
FEATURE             Location/Qualifiers
misc_feature        1..24
note = Synthetic oligonucleotide
modified_base        1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
modified_base        24
mod_base = OTHER
note = 3-Prime-O-methyl-riboguanidine
source              1..24
mol_type = other DNA
organism = synthetic construct
modified_base        1..24
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 471
ncgtcgttt acggcgccgt gccn                                24

SEQ_ID NO: 472      moltype = DNA length = 24
FEATURE             Location/Qualifiers
misc_feature        1..24
note = Synthetic oligonucleotide
modified_base        1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
modified_base        4
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
modified_base        24
mod_base = OTHER
note = 3-Prime-O-methyl-riboguanidine
source              1..24
mol_type = other DNA
organism = synthetic construct
modified_base        1..24
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 472
ncgnctgttt acggcgccgt gccn                                24

SEQ_ID NO: 473      moltype = DNA length = 25
FEATURE             Location/Qualifiers
misc_feature        1..25
note = Synthetic oligonucleotide
modified_base        1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source              1..25
mol_type = other DNA
organism = synthetic construct
modified_base        1..25
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base        25
mod_base = OTHER
note = Inverse nucleotide ( 3-prime and 5-prime switched)
SEQUENCE: 473
ncgtcgttt acggcgccgt gcccgt                            25

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SEQ ID NO: 474      moltype = DNA  length = 22
FEATURE
misc_feature
1..22
note = Synthetic oligonucleotide
modified_base
1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base
22
mod_base = OTHER
note = 3-Prime-O-methyl-riboguanidine
source
1..22
mol_type = other DNA
organism = synthetic construct
modified_base
1..22
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 474
ncgtcgttt cggcgcgcc cn                                22

SEQ ID NO: 475      moltype = DNA  length = 22
FEATURE
misc_feature
1..22
note = Synthetic oligonucleotide
modified_base
1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
modified_base
22
mod_base = OTHER
note = 3-Prime-O-methyl-riboguanidine
source
1..22
mol_type = other DNA
organism = synthetic construct
modified_base
1..22
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 475
ncgtcgttt cggcgcgcc cn                                22

SEQ ID NO: 476      moltype = DNA  length = 22
FEATURE
misc_feature
1..22
note = Synthetic oligonucleotide
modified_base
1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
modified_base
4
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
modified_base
22
mod_base = OTHER
note = 3-Prime-O-methyl-riboguanidine
source
1..22
mol_type = other DNA
organism = synthetic construct
modified_base
1..22
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 476
ncgnctttt cggcgcgcc cn                                22

SEQ ID NO: 477      moltype = DNA  length = 22
FEATURE
misc_feature
1..22
note = Synthetic oligonucleotide
modified_base
1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
modified_base
10
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
modified_base
22
mod_base = OTHER
note = 3-Prime-O-methyl-riboguanidine
source
1..22
mol_type = other DNA

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modified_base      organism = synthetic construct
1..22
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 477
ncgtcgtnn cggcgccgc cn                                22

SEQ ID NO: 478      moltype = DNA length = 22
FEATURE          Location/Qualifiers
misc_feature     1..22
note = Synthetic oligonucleotide
modified_base     1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base     10
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
modified_base     22
mod_base = OTHER
note = 3-Prime-O-methyl-riboguanidine
source           1..22
mol_type = other DNA
organism = synthetic construct
modified_base     1..22
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 478
ncgtcgtnn cggcgccgc cn                                22

SEQ ID NO: 479      moltype = DNA length = 23
FEATURE          Location/Qualifiers
misc_feature     1..23
note = Synthetic oligonucleotide
modified_base     1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source           1..23
mol_type = other DNA
organism = synthetic construct
modified_base     1..23
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     23
mod_base = OTHER
note = Inverse nucleotide ( 3-prime and 5-prime switched)
SEQUENCE: 479
ncgtcgtnn cggcgccgc cgt                               23

SEQ ID NO: 480      moltype = DNA length = 23
FEATURE          Location/Qualifiers
misc_feature     1..23
note = Synthetic oligonucleotide
modified_base     1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source           1..23
mol_type = other DNA
organism = synthetic construct
modified_base     1..23
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base     23
mod_base = OTHER
note = Inverse nucleotide ( 3-prime and 5-prime switched)
SEQUENCE: 480
ncgtcgtnn cggcgccgc cgt                               23

SEQ ID NO: 481      moltype = DNA length = 24
FEATURE          Location/Qualifiers
misc_feature     1..24
note = Synthetic oligonucleotide
modified_base     1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
modified_base     24
mod_base = OTHER

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source          note = 3-Prime-O-methyl-riboguanidine
                1..24
                mol_type = other DNA
                organism = synthetic construct
modified_base   1..24
                mod_base = OTHER
                note = Phosphorothioate internucleotide linkages
SEQUENCE: 481  ncgtcgacgt tcggcgccgt gccn                                24

SEQ ID NO: 482      moltype = DNA length = 24
FEATURE
misc_feature       Location/Qualifiers
                    1..24
                    note = Synthetic oligonucleotide
modified_base      1
                    mod_base = OTHER
                    note = 5-iodo-2-prime-deoxyuridine
modified_base      24
                    mod_base = OTHER
                    note = 3-Prime-O-methyl-riboguanidine
source            1..24
                    mol_type = other DNA
                    organism = synthetic construct
modified_base      1..24
                    mod_base = OTHER
                    note = Phosphorothioate internucleotide linkages
SEQUENCE: 482  ncgtcgacgt tcggcgccgt gccn                                24

SEQ ID NO: 483      moltype = DNA length = 23
FEATURE
misc_feature       Location/Qualifiers
                    1..23
                    note = Synthetic oligonucleotide
modified_base      1
                    mod_base = OTHER
                    note = 5-iodo-2-prime-deoxyuridine
modified_base      23
                    mod_base = OTHER
                    note = 3-Prime-O-methyl-riboguanidine
source            1..23
                    mol_type = other DNA
                    organism = synthetic construct
modified_base      1..23
                    mod_base = OTHER
                    note = Phosphorothioate internucleotide linkages
SEQUENCE: 483  ncgtcgacga tcggcgcgcg ccn                                23

SEQ ID NO: 484      moltype = DNA length = 23
FEATURE
misc_feature       Location/Qualifiers
                    1..23
                    note = Synthetic oligonucleotide
modified_base      1
                    mod_base = OTHER
                    note = 5-ethyl-2-prime-deoxyuridine
modified_base      23
                    mod_base = OTHER
                    note = 3-Prime-O-methyl-riboguanidine
source            1..23
                    mol_type = other DNA
                    organism = synthetic construct
modified_base      1..23
                    mod_base = OTHER
                    note = Phosphorothioate internucleotide linkages
SEQUENCE: 484  ncgtcgacga tcggcgcgcg ccn                                23

SEQ ID NO: 485      moltype = DNA length = 25
FEATURE
misc_feature       Location/Qualifiers
                    1..25
                    note = Synthetic oligonucleotide
modified_base      1
                    mod_base = OTHER
                    note = 5-ethyl-2-prime-deoxyuridine
source            1..25
                    mol_type = other DNA

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modified_base      organism = synthetic construct
1..25
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
25
mod_base = OTHER
note = Inverse nucleotide ( 3-prime and 5-prime switched)
SEQUENCE: 485
ncgtcgacgt tcggcgccgt gccgt                                25

SEQ ID NO: 486      moltype = DNA length = 24
FEATURE
misc_feature        Location/Qualifiers
1..24
note = Synthetic oligonucleotide
1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
1..24
mol_type = other DNA
organism = synthetic construct
modified_base        1..24
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
24
mod_base = OTHER
note = Inverse nucleotide ( 3-prime and 5-prime switched)
SEQUENCE: 486
ncgtcgacga tcggcgcgcg ccgt                                24

SEQ ID NO: 487      moltype = DNA length = 20
FEATURE
misc_feature        Location/Qualifiers
1..20
note = Synthetic oligonucleotide
3
mod_base = OTHER
note = Nitroindol
source              1..20
mol_type = other DNA
organism = synthetic construct
modified_base        order(1..4,5..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
4..5
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 487
tgncgtttt tttttttttt                                         20

SEQ ID NO: 488      moltype = DNA length = 20
FEATURE
misc_feature        Location/Qualifiers
1..20
note = Synthetic oligonucleotide
3
mod_base = OTHER
note = Nitropyrrrole
source              1..20
mol_type = other DNA
organism = synthetic construct
modified_base        order(1..3,4..5,6..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
5..6
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 488
tgncgtttt tttttttttt                                         20

SEQ ID NO: 489      moltype = DNA length = 20
FEATURE
misc_feature        Location/Qualifiers
1..20
note = Synthetic oligonucleotide
3
mod_base = OTHER
note = 6-nitro-benzimidazole
source              1..20
mol_type = other DNA

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modified_base      organism = synthetic construct
                  order(1..4,5..20)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base      4..5
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
SEQUENCE: 489
tgcgtttt tttttttt                                         20

SEQ ID NO: 490      moltype = DNA length = 23
FEATURE
misc_feature        Location/Qualifiers
1..23
note = Synthetic oligonucleotide
modified_base       1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source              1..23
mol_type = other DNA
organism = synthetic construct
modified_base       1..23
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 490
ncgtcgacga tggcgccgccc gcc                                         23

SEQ ID NO: 491      moltype = DNA length = 23
FEATURE
misc_feature        Location/Qualifiers
1..23
note = Synthetic oligonucleotide
modified_base       1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source              1..23
mol_type = other DNA
organism = synthetic construct
modified_base       1..23
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 491
ncgtcgacga tggcgccgccc gcc                                         23

SEQ ID NO: 492      moltype = DNA length = 21
FEATURE
misc_feature        Location/Qualifiers
1..21
note = Synthetic oligonucleotide
source              1..21
mol_type = other DNA
organism = synthetic construct
modified_base       order(1..3,4..21)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base       3..4
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 492
ttcgtttcg ggcgcgcgct t                                         21

SEQ ID NO: 493      moltype = DNA length = 21
FEATURE
misc_feature        Location/Qualifiers
1..21
note = Synthetic oligonucleotide
modified_base       2
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source              1..21
mol_type = other DNA
organism = synthetic construct
modified_base       order(1..3,4..21)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base       3..4
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 493
tncgtttcg ggcgcgcgct t                                         21

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SEQ ID NO: 494      moltype = DNA  length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide
modified_base
1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source
1..20
mol_type = other DNA
organism = synthetic construct
order(1..2,3..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base
2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 494
ncgtttcgg cgcgcgcccgt                                         20

SEQ ID NO: 495      moltype = DNA  length = 21
FEATURE
misc_feature
1..21
note = Synthetic oligonucleotide
modified_base
1..2
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
source
1..21
mol_type = other DNA
organism = synthetic construct
order(1..3,4..21)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base
3..4
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 495
nmcgttttcg ggcgcgcgcgt t                                         21

SEQ ID NO: 496      moltype = DNA  length = 25
FEATURE
misc_feature
1..25
note = Synthetic oligonucleotide
modified_base
1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source
1..25
mol_type = other DNA
organism = synthetic construct
1..25
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 496
ncgtcggtt acggcgccgt gccgt                                         25

SEQ ID NO: 497      moltype = DNA  length = 23
FEATURE
misc_feature
1..23
note = Synthetic oligonucleotide
modified_base
2
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
source
1..23
mol_type = other DNA
organism = synthetic construct
1..23
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 497
tnccgtttac ggccgcgtgc cgt                                         23

SEQ ID NO: 498      moltype = DNA  length = 23
FEATURE
misc_feature
1..23
note = Synthetic oligonucleotide
modified_base
2

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source          mod_base = OTHER
                note = 5-iodo-2-prime-deoxyuridine
1..23
mol_type = other DNA
organism = synthetic construct
modified_base   1..23
                mod_base = OTHER
                note = Phosphorothioate internucleotide linkages
SEQUENCE: 498
tnrgtttac ggcgccgtgc cgt                                23

SEQ ID NO: 499      moltype = DNA length = 17
FEATURE           Location/Qualifiers
misc_feature      1..17
note = Synthetic oligonucleotide
modified_base     1
                mod_base = OTHER
                note = 5-iodo-2-prime-deoxyuridine
source          1..17
                mol_type = other DNA
                organism = synthetic construct
modified_base    order(1..11,12..13,14..15,16..17)
                mod_base = OTHER
                note = Phosphorothioate internucleotide linkages
modified_base    11..17
                mod_base = OTHER
                note = Ribonucleosides
SEQUENCE: 499
ncgctcgaaa gttgtgt                                17

SEQ ID NO: 500      moltype = DNA length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide
modified_base     1
                mod_base = OTHER
                note = 5-ethyl-2-prime-deoxyuridine
source          1..24
                mol_type = other DNA
                organism = synthetic construct
modified_base    order(1..2,3..24)
                mod_base = OTHER
                note = Phosphorothioate internucleotide linkages
modified_base    2..3
                mod_base = OTHER
                note = Phosphodiester internucleotide linkages
SEQUENCE: 500
ncgtcgaacaa tcggcgcccg ccgt                                24

SEQ ID NO: 501      moltype = DNA length = 116
FEATURE           Location/Qualifiers
misc_feature      1..116
note = Synthetic oligonucleotide
source          1..116
                mol_type = other DNA
                organism = synthetic construct
SEQUENCE: 501
aggtggtaac cccttaggggt taccacccatc attggaaaac gtttttcggg gcgttcttag  60
gttggtaaccctt atgggggtta ccacccatc tgaaaaacgt ttttcggggc gttttt      116

SEQ ID NO: 502      moltype = DNA length = 18
FEATURE           Location/Qualifiers
misc_feature      1..18
note = Synthetic oligonucleotide
source          1..18
                mol_type = other DNA
                organism = synthetic construct
modified_base    15..17
                mod_base = OTHER
                note = Phosphorothioate linkages
modified_base    2..14
                mod_base = OTHER
                note = Phosphodiester linkages
SEQUENCE: 502
ggggacgatc gtcggggg                                18

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SEQ ID NO: 503      moltype = DNA length = 23
FEATURE           Location/Qualifiers
misc_feature      1..23
source            note = Synthetic oligonucleotide
modified_base     1..23
                  mol_type = other DNA
                  organism = synthetic construct
order(1..2,19..22)
modified_base     mod_base = OTHER
                  note = Phosphodiester linkages
modified_base     3..18
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
SEQUENCE: 503
ggggtcgacg tacgtcgagg ggg                                23

SEQ ID NO: 504      moltype = DNA length = 19
FEATURE           Location/Qualifiers
misc_feature      1..19
source            note = Synthetic oligonucleotide
modified_base     1..19
                  mol_type = other DNA
                  organism = synthetic construct
15..18
modified_base     mod_base = OTHER
                  note = Phosphorothioate linkages
modified_base     2..14
                  mod_base = OTHER
                  note = Phosphodiester linkages
SEQUENCE: 504
ggggtcgtcg acgagggggg                                     19

SEQ ID NO: 505      moltype = DNA length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
source            note = Synthetic oligonucleotide
modified_base     1..21
                  mol_type = other DNA
                  organism = synthetic construct
order(1..2,16..20)
modified_base     mod_base = OTHER
                  note = Phosphorothioate linkages
modified_base     3..15
                  mod_base = OTHER
                  note = Phosphodiester linkages
SEQUENCE: 505
ggggacgacg tcgtcggggg g                                    21

SEQ ID NO: 506      moltype = DNA length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
source            note = Synthetic oligonucleotide
modified_base     1..21
                  mol_type = other DNA
                  organism = synthetic construct
order(1..2,17..20)
modified_base     mod_base = OTHER
                  note = Phosphorothioate linkages
modified_base     3..16
                  mod_base = OTHER
                  note = Phosphodiester linkages
SEQUENCE: 506
gggggacgacg ctcgtcggggg g                                21

SEQ ID NO: 507      moltype = DNA length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
source            note = Synthetic oligonucleotide
modified_base     1..20
                  mol_type = other DNA
                  organism = synthetic construct
16..19
modified_base     mod_base = OTHER
                  note = Phosphorothioate linkages
modified_base     2..15
                  mod_base = OTHER

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SEQUENCE: 507          note = Phosphodiester linkages
ggggacgagc tcgtcgaaaaa                               20

SEQ ID NO: 508          moltype = DNA  length = 19
FEATURE
misc_feature           Location/Qualifiers
1..19
note = Synthetic oligonucleotide
source
1..19
mol_type = other DNA
organism = synthetic construct
modified_base           16..18
mod_base = OTHER
note = Phosphorothioate linkages
modified_base           2..15
mod_base = OTHER
note = Phosphodiester linkages

SEQUENCE: 508          note = Phosphodiester linkages
ggggacgagc tcgtcgaaaaa                               19

SEQ ID NO: 509          moltype = DNA  length = 19
FEATURE
misc_feature           Location/Qualifiers
1..19
note = Synthetic oligonucleotide
source
1..19
mol_type = other DNA
organism = synthetic construct
modified_base           15..18
mod_base = OTHER
note = Phosphorothioate linkages
modified_base           2..14
mod_base = OTHER
note = Phosphodiester linkages

SEQUENCE: 509          note = Phosphodiester linkages
ggggacgatc gtcggggggg                               19

SEQ ID NO: 510          moltype = DNA  length = 21
FEATURE
misc_feature           Location/Qualifiers
1..21
note = Synthetic oligonucleotide
source
1..21
mol_type = other DNA
organism = synthetic construct
modified_base           order(1..2,17..20)
mod_base = OTHER
note = Phosphorothioate linkages
modified_base           3..16
mod_base = OTHER
note = Phosphodiester linkages

SEQUENCE: 510          note = Phosphodiester linkages
ggggacgatc gaacgtgggg g                               21

SEQ ID NO: 511          moltype = DNA  length = 20
FEATURE
misc_feature           Location/Qualifiers
1..20
note = Synthetic oligonucleotide
source
1..20
mol_type = other DNA
organism = synthetic construct
modified_base           17..19
mod_base = OTHER
note = Phosphorothioate linkages
modified_base           2..16
mod_base = OTHER
note = Phosphodiester linkages

SEQUENCE: 511          note = Phosphodiester linkages
ggggacgatc gaacgtgggg g                               20

SEQ ID NO: 512          moltype = DNA  length = 26
FEATURE
misc_feature           Location/Qualifiers
1..26
note = Synthetic oligonucleotide
source
1..26
mol_type = other DNA
organism = synthetic construct
modified_base           order(1..2,22..25)

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modified_base mod_base = OTHER
               note = Phosphorothioate linkages
3..21
modified_base mod_base = OTHER
               note = Phosphodiester linkages
SEQUENCE: 512
ggggtcgacg tcgacgtcga gggggg                                     26

SEQ ID NO: 513      moltype = DNA length = 25
FEATURE          Location/Qualifiers
misc_feature     1..25
note = Synthetic oligonucleotide
source           1..25
mol_type = other DNA
organism = synthetic construct
modified_base    22..24
mod_base = OTHER
note = Phosphorothioate linkages
modified_base    2..21
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 513
ggggtcgacg tcgacgtcga gggggg                                     25

SEQ ID NO: 514      moltype = DNA length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide
source           1..20
mol_type = other DNA
organism = synthetic construct
modified_base    order(1..2,16..19)
mod_base = OTHER
note = Phosphorothioate linkages
modified_base    3..15
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 514
ggggacgacg tcgtgggggg                                     20

SEQ ID NO: 515      moltype = DNA length = 19
FEATURE          Location/Qualifiers
misc_feature     1..19
note = Synthetic oligonucleotide
source           1..19
mol_type = other DNA
organism = synthetic construct
modified_base    16..18
mod_base = OTHER
note = Phosphorothioate linkages
modified_base    2..15
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 515
ggggacgacg tcgtggggg                                     19

SEQ ID NO: 516      moltype = DNA length = 18
FEATURE          Location/Qualifiers
misc_feature     1..18
note = Synthetic oligonucleotide
source           1..18
mol_type = other DNA
organism = synthetic construct
modified_base    order(1..2,14..17)
mod_base = OTHER
note = Phosphorothioate linkages
modified_base    3..13
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 516
gggtcgatcg cgaggggg                                     18

SEQ ID NO: 517      moltype = DNA length = 21
FEATURE          Location/Qualifiers
misc_feature     1..21
note = Synthetic oligonucleotide

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source          1..21
               mol_type = other DNA
               organism = synthetic construct
modified_base   order(1..2,17..20)
               mod_base = OTHER
               note = Phosphorothioate linkages
modified_base   3..16
               mod_base = OTHER
               note = Phosphodiester linkages
SEQUENCE: 517
gggggacgag ctgcgtcgaaaa g                               21

SEQ ID NO: 518      moltype = DNA  length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide
modified_base     11
mod_base = OTHER
note = 5-ido-2-prime-deoxyuridine
modified_base     14
mod_base = OTHER
note = 5-ido-2-prime-deoxyuridine
source            1..20
mol_type = other DNA
organism = synthetic construct
modified_base     16..18
mod_base = OTHER
note = Phosphorothioate linkages
modified_base     17
mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 518
ggggacgacg ncgnnggggg                                20

SEQ ID NO: 519      moltype = DNA  length = 30
FEATURE           Location/Qualifiers
misc_feature      1..30
note = Synthetic oligonucleotide
source            1..30
mol_type = other DNA
organism = synthetic construct
modified_base     1..30
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 519
tcgaacgttc gaacgttcga acgttcgaat                               30

SEQ ID NO: 520      moltype = DNA  length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide
source            1..20
mol_type = other DNA
organism = synthetic construct
modified_base     1..4,16..20
mod_base = OTHER
note = 2-Prime-O-methyl nucleosides
SEQUENCE: 520
ggggacgacg tcgtgggggg                                20

SEQ ID NO: 521      moltype = DNA  length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide
modified_base     20
mod_base = OTHER
note = 2-Prime-O-methyl nucleoside
source            1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 521
ggggacgacg tcgtgggggg                                20

SEQ ID NO: 522      moltype = DNA  length = 22
FEATURE           Location/Qualifiers
misc_feature      1..22

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source          note = Synthetic oligonucleotide
                1..22
                mol_type = other DNA
                organism = synthetic construct
SEQUENCE: 522 ggggacgacg tcgtgggggg tt                                22

SEQ ID NO: 523      moltype = DNA  length = 22
FEATURE          Location/Qualifiers
misc_feature     1..22
note = Synthetic oligonucleotide
modified_base    21..22
mod_base = OTHER
note = 2-Prime-O-methyl ribonucleosides
source           1..22
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 523 ggggacgacg tcgtgggggg tt                                22

SEQ ID NO: 524      moltype = DNA  length = 10
FEATURE          Location/Qualifiers
misc_feature     1..10
note = Synthetic oligonucleotide
source           1..10
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 524 tcgtcgacga                                         10

SEQ ID NO: 525      moltype = DNA  length = 10
FEATURE          Location/Qualifiers
misc_feature     1..10
note = Synthetic oligonucleotide
source           1..10
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 525 gacgatcgctc                                         10

SEQ ID NO: 526      moltype = DNA  length = 10
FEATURE          Location/Qualifiers
misc_feature     1..10
note = Synthetic oligonucleotide
source           1..10
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 526 acgacgctcggt                                         10

SEQ ID NO: 527      moltype = DNA  length = 20
FEATURE          Location/Qualifiers
misc_feature     1..20
note = Synthetic oligonucleotide
source           1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 527 gggggagcat gcctgggggg                                20

SEQ ID NO: 528      moltype = DNA  length = 27
FEATURE          Location/Qualifiers
misc_feature     1..27
note = Synthetic oligonucleotide
source           1..27
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 528 ggggggggac gatcgctcggt gggggggg                                27

SEQ ID NO: 529      moltype = DNA  length = 27
FEATURE          Location/Qualifiers
misc_feature     1..27
note = Synthetic oligonucleotide
source           1..27
mol_type = other DNA

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SEQUENCE: 529	organism = synthetic construct	
gggggggggg gacgatcgac ggggggg		27
SEQ ID NO: 530	moltype = DNA length = 24	
FEATURE	Location/Qualifiers	
misc_feature	1..24	
source	note = Synthetic oligonucleotide	
	1..24	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 530		
ggggggggggac gatcgatcgac ggggg		24
SEQ ID NO: 531	moltype = DNA length = 30	
FEATURE	Location/Qualifiers	
misc_feature	1..30	
source	note = Synthetic oligonucleotide	
	1..30	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 531		
gggggggggggg tcgtcgacga ggggggggggg		30
SEQ ID NO: 532	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
misc_feature	1..31	
source	note = Synthetic oligonucleotide	
	1..31	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 532		
gggggggggggg acgagctcgat cgggggggggg g		31
SEQ ID NO: 533	moltype = DNA length = 29	
FEATURE	Location/Qualifiers	
misc_feature	1..29	
source	note = Synthetic oligonucleotide	
	1..29	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 533		
gggggggggggg acgatcgatcgac ggggggggggg		29
SEQ ID NO: 534	moltype = DNA length = 36	
FEATURE	Location/Qualifiers	
misc_feature	1..36	
source	note = Synthetic oligonucleotide	
	1..36	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 534		
gggggggggggg tcgacgtcga cgtcgagggg ggggggg		36
SEQ ID NO: 535	moltype = DNA length = 30	
FEATURE	Location/Qualifiers	
misc_feature	1..30	
source	note = Synthetic oligonucleotide	
	1..30	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 535		
gggggggggggg acgacgtcgat ggggggggggg		30
SEQ ID NO: 536	moltype = DNA length = 32	
FEATURE	Location/Qualifiers	
misc_feature	1..32	
source	note = Synthetic oligonucleotide	
	1..32	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 536		
gggggggggggg aacgacgtcgat ttgggggggg gg		32
SEQ ID NO: 537	moltype = DNA length = 40	
FEATURE	Location/Qualifiers	

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misc_feature	1..40	
	note = Synthetic oligonucleotide	
source	1..40	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 537	ggggggggggg acgacgacga tcgtcgctgt gggggggggg	40
SEQ ID NO: 538	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
misc_feature	1..31	
	note = Synthetic oligonucleotide	
source	1..31	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 538	ggggggggggg cacgacgtcg tggggggggg g	31
SEQ ID NO: 539	moltype = DNA length = 34	
FEATURE	Location/Qualifiers	
misc_feature	1..34	
	note = Synthetic oligonucleotide	
source	1..34	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 539	ggggggggggg aacgttcgaa cgttgggggg gggg	34
SEQ ID NO: 540	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
	note = Synthetic oligonucleotide	
source	1..50	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 540	ggggggggggg aacgttcgaa cgttcgaacgtt ttcgaacgtt gggggggggg	50
SEQ ID NO: 541	moltype = DNA length = 34	
FEATURE	Location/Qualifiers	
misc_feature	1..34	
	note = Synthetic oligonucleotide	
source	1..34	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 541	ggggggggggg ttgcgaacgtt cgaagggggg gggg	34
SEQ ID NO: 542	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
misc_feature	1..31	
	note = Synthetic oligonucleotide	
source	1..31	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 542	ggggggggggg acgtcgacgt cggggggggg g	31
SEQ ID NO: 543	moltype = DNA length = 31	
FEATURE	Location/Qualifiers	
misc_feature	1..31	
	note = Synthetic oligonucleotide	
source	1..31	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 543	ggggggggggg tcgacgtcga cggggggggg g	31
SEQ ID NO: 544	moltype = DNA length = 40	
FEATURE	Location/Qualifiers	
misc_feature	1..40	
	note = Synthetic oligonucleotide	
source	1..40	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 544		

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ggggggggggg acgtcgacgt acgtcgacgt gggggggggg	40
SEQ ID NO: 545 moltype = DNA length = 32	
FEATURE Location/Qualifiers	
misc_feature 1..32	
note = Synthetic oligonucleotide	
source 1..32	
mol_type = other DNA	
organism = synthetic construct	
SEQUENCE: 545 gggggggggg tacgatatacg tagggggggg gg	32
SEQ ID NO: 546 moltype = DNA length = 32	
FEATURE Location/Qualifiers	
misc_feature 1..32	
note = Synthetic oligonucleotide	
source 1..32	
mol_type = other DNA	
organism = synthetic construct	
SEQUENCE: 546 gggggggggg tacgtatacg tagggggggg gg	32
SEQ ID NO: 547 moltype = DNA length = 30	
FEATURE Location/Qualifiers	
misc_feature 1..30	
note = Synthetic oligonucleotide	
source 1..30	
mol_type = other DNA	
organism = synthetic construct	
SEQUENCE: 547 gggggggggg cagcatgctg gggggggggg	30
SEQ ID NO: 548 moltype = DNA length = 10	
FEATURE Location/Qualifiers	
misc_feature 1..10	
note = Synthetic oligonucleotide	
source 1..10	
mol_type = other DNA	
organism = synthetic construct	
SEQUENCE: 548 acgacgacga	10
SEQ ID NO: 549 moltype = DNA length = 10	
FEATURE Location/Qualifiers	
misc_feature 1..10	
note = Synthetic oligonucleotide	
source 1..10	
mol_type = other DNA	
organism = synthetic construct	
SEQUENCE: 549 acgtcgacgt	10
SEQ ID NO: 550 moltype = DNA length = 24	
FEATURE Location/Qualifiers	
misc_feature 1..24	
note = Synthetic oligonucleotide	
source 1..24	
mol_type = other DNA	
organism = synthetic construct	
modified_base 1..24	
mod_base = OTHER	
note = Phosphorothioate internucleotide linkages	
SEQUENCE: 550 tcgtcgattc gtaacgacgt cgtt	24
SEQ ID NO: 551 moltype = DNA length = 18	
FEATURE Location/Qualifiers	
source 1..18	
mol_type = other DNA	
organism = synthetic construct	
SEQUENCE: 551 tttcgtcgtt tcgtcgtt	18
SEQ ID NO: 552 moltype = DNA length = 23	
FEATURE Location/Qualifiers	
source 1..23	

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mol_type = other DNA
organism = synthetic construct
SEQUENCE: 552
tcgtcgacga tcggcgcgcg ccg                                23

SEQ ID NO: 553      moltype = DNA  length = 27
FEATURE
source
1..27
mol_type = other DNA
organism = synthetic construct
modified_base
1..27
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 553
tcgtcgacga ttttcgtcg acgattt                               27

SEQ ID NO: 554      moltype = DNA  length = 22
FEATURE
source
1..22
mol_type = other DNA
organism = synthetic construct
modified_base
1..22
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 554
tcctgacgtt cggcgccgc cc                                    22

SEQ ID NO: 555      moltype = DNA  length = 27
FEATURE
source
1..27
mol_type = other DNA
organism = synthetic construct
modified_base
1..27
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 555
tcgcgtgcgt tttgtcgtt tgacgtt                               27

SEQ ID NO: 556      moltype = DNA  length = 27
FEATURE
source
1..27
mol_type = other DNA
organism = synthetic construct
modified_base
1..27
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 556
ggggacgacg tcgtggggcg gccgccc                               27

SEQ ID NO: 557      moltype = DNA  length = 20
FEATURE
source
1..20
mol_type = other DNA
organism = synthetic construct
modified_base
order(1..7,10..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base
7..10
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 557
tccatgacgt ttttgatgtt                                     20

SEQ ID NO: 558      moltype = DNA  length = 20
FEATURE
source
1..20
mol_type = other DNA
organism = synthetic construct
modified_base
order(1..17,19..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base
17..19
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 558
tccatgacgt ttttgatgtt                                     20

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SEQ ID NO: 559      moltype = DNA  length = 20
FEATURE
source
1..20
mol_type = other DNA
organism = synthetic construct
order(1..8,10..17,18..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
order(8..10,17..18)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 559
tccatgacgt ttttgatgtt                                20

SEQ ID NO: 560      moltype = DNA  length = 20
FEATURE
source
1..20
mol_type = other DNA
organism = synthetic construct
order(1..7,10..17,18..20)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
order(7..10,17..18)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 560
tccatgacgt ttttgatgtt                                20

SEQ ID NO: 561      moltype = DNA  length = 19
FEATURE
source
1..19
mol_type = other DNA
organism = synthetic construct
order(1..5,6..19)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
5..6
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 561
atgacgttt tgatgttgt                                19

SEQ ID NO: 562      moltype = DNA  length = 19
FEATURE
source
1..19
mol_type = other DNA
organism = synthetic construct
order(1..14,15..19)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
14..15
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 562
atgacgttt tgatgttgt                                19

SEQ ID NO: 563      moltype = DNA  length = 19
FEATURE
source
1..19
mol_type = other DNA
organism = synthetic construct
order(1..5,6..14,15..19)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
order(5..6,14..15)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 563
atgacgttt tgatgttgt                                19

SEQ ID NO: 564      moltype = DNA  length = 19
FEATURE
source
1..19
mol_type = other DNA
organism = synthetic construct

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modified_base      order(1..4,7..13,16..19)
modified_base      mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
modified_base      order(4..7,13..16)
modified_base      mod_base = OTHER
modified_base      note = Phosphodiester internucleotide linkages
SEQUENCE: 564
atgacgttt tcatgttgtt                                19

SEQ ID NO: 565      moltype = DNA length = 23
FEATURE          Location/Qualifiers
source           1..23
modified_base      mol_type = other DNA
modified_base      organism = synthetic construct
modified_base      order(1..11,14..23)
modified_base      mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
modified_base      11..14
modified_base      mod_base = OTHER
modified_base      note = Phosphodiester internucleotide linkages
SEQUENCE: 565
tcgatcgaaa ttccgtgcgtt ttt                                23

SEQ ID NO: 566      moltype = DNA length = 23
FEATURE          Location/Qualifiers
source           1..23
modified_base      mol_type = other DNA
modified_base      organism = synthetic construct
modified_base      order(1..10,15..23)
modified_base      mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
modified_base      10..15
modified_base      mod_base = OTHER
modified_base      note = Phosphodiester internucleotide linkages
SEQUENCE: 566
tcgatcgaaa ttccgtgcgtt ttt                                23

SEQ ID NO: 567      moltype = DNA length = 23
FEATURE          Location/Qualifiers
source           1..23
modified_base      mol_type = other DNA
modified_base      organism = synthetic construct
modified_base      order(1..9,16..23)
modified_base      mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
modified_base      9..16
modified_base      mod_base = OTHER
modified_base      note = Phosphodiester internucleotide linkages
SEQUENCE: 567
tcgatcgaaa ttccgtgcgtt ttt                                23

SEQ ID NO: 568      moltype = DNA length = 23
FEATURE          Location/Qualifiers
source           1..23
modified_base      mol_type = other DNA
modified_base      organism = synthetic construct
modified_base      order(1..7,13..23)
modified_base      mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
modified_base      7..13
modified_base      mod_base = OTHER
modified_base      note = Phosphodiester internucleotide linkages
SEQUENCE: 568
tcgatcgaaa ttccgtgcgtt ttt                                23

SEQ ID NO: 569      moltype = DNA length = 22
FEATURE          Location/Qualifiers
source           1..22
modified_base      mol_type = other DNA
modified_base      organism = synthetic construct
modified_base      order(1..9,14..22)
modified_base      mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
modified_base      9..14
modified_base      mod_base = OTHER
modified_base      note = Phosphodiester internucleotide linkages

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SEQUENCE: 569
tcgacgtttt cggcgccgc cg                                22

SEQ ID NO: 570      moltype = DNA  length = 25
FEATURE          Location/Qualifiers
source           1..25
                  mol_type = other DNA
                  organism = synthetic construct
modified_base    16..25
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base    1..16
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
modified_base    13..16
                  mod_base = OTHER
                  note = 1-Prime-2-prime-dideoxyribose (D spacer)

SEQUENCE: 570
acgacgtcgt cgnnnncggc cgccc                            25

SEQ ID NO: 571      moltype = DNA  length = 27
FEATURE          Location/Qualifiers
source           1..27
                  mol_type = other DNA
                  organism = synthetic construct
modified_base    1..27
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base    11..14
                  mod_base = OTHER
                  note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base    25..27
                  mod_base = OTHER
                  note = 1-Prime-2-prime-dideoxyribose (D spacer)

SEQUENCE: 571
acgacgtcgt nnnnacgacg tcgtnnn                           27

SEQ ID NO: 572      moltype = DNA  length = 30
FEATURE          Location/Qualifiers
source           1..30
                  mol_type = other DNA
                  organism = synthetic construct
modified_base    1..30
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base    1..3
                  mod_base = OTHER
                  note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base    14..17
                  mod_base = OTHER
                  note = 1-Prime-2-prime-dideoxyribose (D spacer)
modified_base    28..30
                  mod_base = OTHER
                  note = 1-Prime-2-prime-dideoxyribose (D spacer)

SEQUENCE: 572
nnnacgacgt cgtnnnnnacg acgtcgtnnn                      30

SEQ ID NO: 573      moltype = DNA  length = 27
FEATURE          Location/Qualifiers
source           1..27
                  mol_type = other DNA
                  organism = synthetic construct
modified_base    order(1..2,11..14,25..27)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base    order(2..11,14..25)
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages

SEQUENCE: 573
acgacgtcgt ttttacgacg tcgtttt                          27

SEQ ID NO: 574      moltype = DNA  length = 29
FEATURE          Location/Qualifiers
source           1..29
                  mol_type = other DNA
                  organism = synthetic construct

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modified_base      order(1..3,27..29)
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base      3..27
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 574
ccacgacgtc gtcgaagacg acgtcgtgg                                29

SEQ ID NO: 575          moltype = DNA  length = 22
FEATURE           Location/Qualifiers
source            1..22
                   mol_type = other DNA
                   organism = synthetic construct
modified_base     order(1..5,6..11,12..18,19..22)
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base     order(5..6,11..12,18..19)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 575
tcgacgttt cggcgccgcg cg                                         22

SEQ ID NO: 576          moltype = DNA  length = 22
FEATURE           Location/Qualifiers
source            1..22
                   mol_type = other DNA
                   organism = synthetic construct
modified_base     order(1..5,6..11,12..18,19..22)
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base     order(5..6,11..12,18..19)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 576
tcgacgttt cggcgccgcg cg                                         22

SEQ ID NO: 577          moltype = DNA  length = 22
FEATURE           Location/Qualifiers
source            1..22
                   mol_type = other DNA
                   organism = synthetic construct
modified_base     order(1..2,3..4,5..7,8..11,12..16,17..22)
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base     order(2..3,4..5,7..8,11..12,16..17)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 577
tcgcgacgtt cggcgccgcg cg                                         22

SEQ ID NO: 578          moltype = DNA  length = 22
FEATURE           Location/Qualifiers
source            1..22
                   mol_type = other DNA
                   organism = synthetic construct
modified_base     order(1..4,5..11,12..22)
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base     order(4..5,11..12)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 578
tcgcgacgtt cggcgccgcg cg                                         22

SEQ ID NO: 579          moltype = DNA  length = 22
FEATURE           Location/Qualifiers
source            1..22
                   mol_type = other DNA
                   organism = synthetic construct
modified_base     order(1..4,5..14,15..22)
                   mod_base = OTHER
                   note = Phosphorothioate internucleotide linkages
modified_base     order(4..5,14..15)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages

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SEQUENCE: 579
tcgcgacgtt cggcgcgccg cg                                22

SEQ ID NO: 580      moltype = DNA  length = 22
FEATURE          Location/Qualifiers
source           1..22
                  mol_type = other DNA
                  organism = synthetic construct
modified_base    order(1..4,5..16,17..22)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base    order(4..5,16..17)
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages

SEQUENCE: 580
tcgcgacgtt cggcgcgccg cg                                22

SEQ ID NO: 581      moltype = DNA  length = 22
FEATURE          Location/Qualifiers
source           1..22
                  mol_type = other DNA
                  organism = synthetic construct
modified_base    order(1..7,8..16,17..22)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base    order(7..8,16..17)
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages

SEQUENCE: 581
tcgcgacgtt cggcgcgccg cg                                22

SEQ ID NO: 582      moltype = DNA  length = 22
FEATURE          Location/Qualifiers
source           1..22
                  mol_type = other DNA
                  organism = synthetic construct
modified_base    order(1..7,8..14,15..22)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base    order(7..8,14..15)
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages

SEQUENCE: 582
tcgcgacgtt cggcgcgccg cg                                22

SEQ ID NO: 583      moltype = DNA  length = 22
FEATURE          Location/Qualifiers
source           1..22
                  mol_type = other DNA
                  organism = synthetic construct
modified_base    order(1..4,5..11,12..16,17..22)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base    order(4..5,11..12,16..17)
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages

SEQUENCE: 583
tcgcgacgtt cggcgcgccg cg                                22

SEQ ID NO: 584      moltype = DNA  length = 22
FEATURE          Location/Qualifiers
source           1..22
                  mol_type = other DNA
                  organism = synthetic construct
modified_base    order(1..7,8..11,12..16,17..22)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base    order(7..8,11..12,16..17)
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages

SEQUENCE: 584
tcgcgacgtt cggcgcgccg cg                                22

SEQ ID NO: 585      moltype = DNA  length = 25
FEATURE          Location/Qualifiers
source           1..25

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modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..5,6..13,14..25)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(5..6,13..14)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 585
tcgtcgaacg ttccggcgctg cgccg                                25

SEQ ID NO: 586      moltype = DNA length = 25
FEATURE           Location/Qualifiers
source            1..25
modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..5,6..13,14..16,17..25)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(5..6,13..14,16..17)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 586
tcgtcgaacg ttccggcgctg cgccg                                25

SEQ ID NO: 587      moltype = DNA length = 25
FEATURE           Location/Qualifiers
source            1..25
modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..5,6..13,14..21,22..25)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(5..6,13..14,21..22)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 587
tcgtcgaacg ttccggcgctg cgccg                                25

SEQ ID NO: 588      moltype = DNA length = 25
FEATURE           Location/Qualifiers
source            1..25
modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..9,10..16,17..25)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(9..10,16..17)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 588
tcgtcgaacg ttccggcgctg cgccg                                25

SEQ ID NO: 589      moltype = DNA length = 24
FEATURE           Location/Qualifiers
source            1..24
modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..7,8..16,17..24)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(7..8,16..17)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 589
tcgcgacgtt cgttgcgcbc gccc                                24

SEQ ID NO: 590      moltype = DNA length = 24
FEATURE           Location/Qualifiers
source            1..24
modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..2,3..11,12..18,19..24)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(2..3,11..12,18..19)

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mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 590
tcgcgacgtt cggtgcgcgc gccg                                24

SEQ ID NO: 591      moltype = DNA  length = 23
FEATURE          Location/Qualifiers
source           1..23
modified_base    mol_type = other DNA
                  organism = synthetic construct
                  order(1..5,6..11,12..16,17..23)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
                  order(5..6,11..12,16..17)
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
SEQUENCE: 591
tcgcgacgtt cggcgcgtcg ccg                                23

SEQ ID NO: 592      moltype = DNA  length = 23
FEATURE          Location/Qualifiers
source           1..23
modified_base    mol_type = other DNA
                  organism = synthetic construct
                  order(1..5,6..11,12..17,18..23)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
                  order(5..6,11..12,17..18)
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
SEQUENCE: 592
tcgcgacgtt cggcggtcg ccg                                23

SEQ ID NO: 593      moltype = DNA  length = 23
FEATURE          Location/Qualifiers
source           1..23
modified_base    mol_type = other DNA
                  organism = synthetic construct
                  order(1..3,4..11,12..16,17..23)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
                  order(3..4,11..12,16..17)
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
SEQUENCE: 593
tcgcgacgtt cggcgcgtcg ccg                                23

SEQ ID NO: 594      moltype = DNA  length = 23
FEATURE          Location/Qualifiers
source           1..23
modified_base    mol_type = other DNA
                  organism = synthetic construct
                  order(1..3,4..11,12..17,18..23)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
                  order(3..4,11..12,17..18)
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
SEQUENCE: 594
tcgcgacgtt cggcggtcg ccg                                23

SEQ ID NO: 595      moltype = DNA  length = 19
FEATURE          Location/Qualifiers
source           1..19
modified_base    mol_type = other DNA
                  organism = synthetic construct
                  order(1..2,3..5,6..8,9..19)
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
                  order(2..3,5..6,8..9)
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
SEQUENCE: 595
tcgacgtcga cgtgacggg                                    19

SEQ ID NO: 596      moltype = DNA  length = 19

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FEATURE	Location/Qualifiers
source	1..19
	mol_type = other DNA
	organism = synthetic construct
modified_base	1..19
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
SEQUENCE: 596	
tcgacgtcga cgtgacggg	19
SEQ ID NO: 597	moltype = DNA length = 20
FEATURE	Location/Qualifiers
source	1..20
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..4,5..6,8..11,12..13,14..15,16..17,18..19)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
modified_base	order(2..3,4..5,7..8,11..12,13..14,15..16,17..18,19..20)
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 597	
tcgcgacgtt cgccgcgcgcg	20
SEQ ID NO: 598	moltype = DNA length = 23
FEATURE	Location/Qualifiers
source	1..23
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..5,6..8,9..12,13..18,19..23)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
modified_base	order(2..3,5..6,8..9,12..13,18..19)
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 598	
tcgtcgaacga tcggcgcgcg	23
SEQ ID NO: 599	moltype = DNA length = 23
FEATURE	Location/Qualifiers
source	1..23
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..5,6..8,9..12,13..17,18..23)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
modified_base	order(2..3,5..6,8..9,12..13,17..18)
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 599	
tcgtcgaacga tcggcgcgcg	23
SEQ ID NO: 600	moltype = DNA length = 24
FEATURE	Location/Qualifiers
source	1..24
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..5,6..10,11..15,16..21,22..24)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
modified_base	order(2..3,5..6,10..11,15..16,21..22)
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 600	
tcgtcgttac gtaacgacga cgtt	24
SEQ ID NO: 601	moltype = DNA length = 24
FEATURE	Location/Qualifiers
source	1..24
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..5,6..10,11..15,16..24)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
modified_base	order(5..6,10..11,15..16)
	mod_base = OTHER

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SEQUENCE: 601          note = Phosphodiester internucleotide linkages
tcgtcgttac gtaacgacga cgtt                                24

SEQ ID NO: 602          moltype = DNA  length = 23
FEATURE
source
1..23
mol_type = other DNA
organism = synthetic construct
modified_base
1..23
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

SEQUENCE: 602          note = Phosphorothioate internucleotide linkages
tcgtcgacga tcggcgcgcg 23

SEQ ID NO: 603          moltype = DNA  length = 24
FEATURE
source
1..24
mol_type = other DNA
organism = synthetic construct
modified_base
order(1..5,6..8,9..12,13..18,19..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base
order(5..6,8..9,12..13,18..19)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 603          note = Phosphodiester internucleotide linkages
tcgtcgacga tcggcgccgt gccg                                24

SEQ ID NO: 604          moltype = DNA  length = 24
FEATURE
source
1..24
mol_type = other DNA
organism = synthetic construct
modified_base
order(1..5,6..12,13..18,19..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base
order(5..6,12..13,18..19)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 604          note = Phosphodiester internucleotide linkages
tcgtcgacga tcggcgccgt gccg                                24

SEQ ID NO: 605          moltype = DNA  length = 24
FEATURE
source
1..24
mol_type = other DNA
organism = synthetic construct
modified_base
order(1..10,12..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base
10..12
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 605          note = Phosphodiester internucleotide linkages
tcgtcgacga tcggcgccgt gccg                                24

SEQ ID NO: 606          moltype = DNA  length = 23
FEATURE
source
1..23
mol_type = other DNA
organism = synthetic construct
modified_base
order(1..5,6..8,9..12,13..17,18..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base
order(5..6,8..9,12..13,17..18)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 606          note = Phosphodiester internucleotide linkages
tcgtcgacga tcggcgcgcg ccg                                23

SEQ ID NO: 607          moltype = DNA  length = 23
FEATURE
source
1..23
mol_type = other DNA
organism = synthetic construct

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modified_base      order(1..5,6..12,13..17,18..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base      order(5..6,12..13,17..18)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 607
tcgtcgacga tcggcgcgccg ccg                                23

SEQ ID NO: 608      moltype = DNA length = 23
FEATURE
source
1..23
mol_type = other DNA
organism = synthetic construct
modified_base      order(1..10,12..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base      10..12
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 608
tcgtcgacga tcggcgcgccg ccg                                23

SEQ ID NO: 609      moltype = DNA length = 19
FEATURE
source
1..19
mol_type = other DNA
organism = synthetic construct
modified_base      order(1..9,11..19)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base      9..11
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 609
tcgacgtcga cgtgacgtt                                         19

SEQ ID NO: 610      moltype = DNA length = 19
FEATURE
source
1..19
mol_type = other DNA
organism = synthetic construct
modified_base      order(1..5,6..11,12..19)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base      order(5..6,11..12)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 610
tcgacgtcga cgtgacgtt                                         19

SEQ ID NO: 611      moltype = DNA length = 19
FEATURE
source
1..19
mol_type = other DNA
organism = synthetic construct
modified_base      order(1..5,6..13,14..19)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base      5..6
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 611
tcgacgtcga cgtgacgtt                                         19

SEQ ID NO: 612      moltype = DNA length = 19
FEATURE
source
1..19
mol_type = other DNA
organism = synthetic construct
modified_base      order(1..5,6..11,12..19)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base      order(5..6,11..12)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

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SEQUENCE: 612
tcgtcgacga cgtgtcgat                                19

SEQ ID NO: 613      moltype = DNA  length = 19
FEATURE
source
1..19
mol_type = other DNA
organism = synthetic construct
order(1..6,7..12,13..19)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
order(6..7,12..13)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 613
tcgacgtcga cgtgacgtt                                19

SEQ ID NO: 614      moltype = DNA  length = 19
FEATURE
source
1..19
mol_type = other DNA
organism = synthetic construct
order(1..4,5..9,10..14,15..19)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
order(4..5,9..10,14..15)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 614
tcgacgtcga cgtgacggtt                               19

SEQ ID NO: 615      moltype = DNA  length = 24
FEATURE
source
1..24
mol_type = other DNA
organism = synthetic construct
order(1..8,9..17,18..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
order(8..9,17..18)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 615
tcgtcgacga cggcgccgtg ccgt                           24

SEQ ID NO: 616      moltype = DNA  length = 23
FEATURE
source
1..23
mol_type = other DNA
organism = synthetic construct
order(1..7,8..14,15..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
order(7..8,14..15)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 616
tcgtcgacgc ggcgcccgtc cgt                           23

SEQ ID NO: 617      moltype = DNA  length = 24
FEATURE
source
1..24
mol_type = other DNA
organism = synthetic construct
order(1..8,9..15,16..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
order(8..9,15..16)
mod_base = OTHER
note = Phosphodiester internucleotide linkages

SEQUENCE: 617
tcgtcgacga tcggcgccgt gccg                          24

SEQ ID NO: 618      moltype = DNA  length = 24
FEATURE
source
1..24

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modified_base      mol_type = other DNA
                   organism = synthetic construct
                   order(1..7,8..13,14..17,18..24)
                   mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                   order(7..8,13..14,17..18)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 618     tcgtcgacga tcggcgccgt gccg                               24
SEQ ID NO: 619     moltype = DNA length = 25
FEATURE          Location/Qualifiers
source           1..25
modified_base    mol_type = other DNA
                   organism = synthetic construct
                   order(1..7,8..16,17..25)
                   mod_base = OTHER
modified_base    note = Phosphorothioate internucleotide linkages
                   order(7..8,16..17)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 619     tcgtcgacga tcggcgccgt gccgt                               25
SEQ ID NO: 620     moltype = DNA length = 24
FEATURE          Location/Qualifiers
source           1..24
modified_base    mol_type = other DNA
                   organism = synthetic construct
                   order(1..8,9..16,17..24)
                   mod_base = OTHER
modified_base    note = Phosphorothioate internucleotide linkages
                   order(8..9,16..17)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 620     tcgtcgacga cggcgccgtg ccgt                               24
SEQ ID NO: 621     moltype = DNA length = 24
FEATURE          Location/Qualifiers
source           1..24
modified_base    mol_type = other DNA
                   organism = synthetic construct
                   order(1..2,3..5,6..8,9..11,12..17,18..24)
                   mod_base = OTHER
modified_base    note = Phosphorothioate internucleotide linkages
                   order(2..3,5..6,8..9,11..12,17..18)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 621     tcgtcgacgt cggcgccgtg ccgt                               24
SEQ ID NO: 622     moltype = DNA length = 19
FEATURE          Location/Qualifiers
source           1..19
modified_base    mol_type = other DNA
                   organism = synthetic construct
                   1..19
                   mod_base = OTHER
modified_base    note = Phosphorothioate internucleotide linkages
SEQUENCE: 622     tcgtcgacga cgtgtcgat                               19
SEQ ID NO: 623     moltype = DNA length = 23
FEATURE          Location/Qualifiers
source           1..23
modified_base    mol_type = other DNA
                   organism = synthetic construct
                   order(1..2,3..5,6..8,9..12,13..17,18..23)
                   mod_base = OTHER
modified_base    note = Phosphorothioate internucleotide linkages
                   order(2..3,8..9,12..13,17..18)
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
SEQUENCE: 623

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tcgtcgacga tgccgcgcg ccg	23
SEQ ID NO: 624	moltype = DNA length = 23
FEATURE	Location/Qualifiers
source	1..23
	mol_type = other DNA
	organism = synthetic construct
modified_base	1..23
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
SEQUENCE: 624	
tcgtcgacga tgccgcgcg ggc	23
SEQ ID NO: 625	moltype = DNA length = 23
FEATURE	Location/Qualifiers
source	1..23
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..2,3..23)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
modified_base	2..3
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
modified_base	23
	mod_base = OTHER
	note = Butyrate appended
SEQUENCE: 625	
tcgtcgacga tgccgcgcg ggc	23
SEQ ID NO: 626	moltype = DNA length = 23
FEATURE	Location/Qualifiers
source	1..23
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..5,6..23)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
modified_base	5..6
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 626	
tcgtcgacga tgccgcgcg ggc	23
SEQ ID NO: 627	moltype = DNA length = 23
FEATURE	Location/Qualifiers
source	1..23
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..11,12..23)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
modified_base	11..12
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 627	
tcgtcgacga tgccgcgcg ggc	23
SEQ ID NO: 628	moltype = DNA length = 23
FEATURE	Location/Qualifiers
source	1..23
	mol_type = other DNA
	organism = synthetic construct
modified_base	order(1..11,13..23)
	mod_base = OTHER
	note = Phosphorothioate internucleotide linkages
modified_base	11..13
	mod_base = OTHER
	note = Phosphodiester internucleotide linkages
SEQUENCE: 628	
tcgtcgacga tgccgcgcg ggc	23
SEQ ID NO: 629	moltype = DNA length = 24
FEATURE	Location/Qualifiers
source	1..24
	mol_type = other DNA

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modified_base      organism = synthetic construct
                  order(1..2,3..23)
                  mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                  order(2..3,23..24)
                  mod_base = OTHER
modified_base      note = Phosphodiester internucleotide linkages
                  24
                  mod_base = OTHER
SEQUENCE: 629     note = Inverse nucleotide ( 3-prime and 5-prime switched)
tcgtcgacga tcggcgcgcg ccgt                                24

SEQ ID NO: 630      moltype = DNA length = 24
FEATURE          Location/Qualifiers
source           1..24
                  mol_type = other DNA
                  organism = synthetic construct
modified_base      order(1..12,13..23)
                  mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
                  order(12..13,23..24)
                  mod_base = OTHER
modified_base      note = Phosphodiester internucleotide linkages
                  24
                  mod_base = OTHER
SEQUENCE: 630     note = Inverse nucleotide ( 3-prime and 5-prime switched)
tcgtcgacga tcggcgcgcg ccgt                                24

SEQ ID NO: 631      moltype = DNA length = 18
FEATURE          Location/Qualifiers
source           1..18
                  mol_type = other DNA
                  organism = synthetic construct
modified_base      1..18
                  mod_base = OTHER
modified_base      note = Phosphodiester internucleotide linkages
SEQUENCE: 631     note = Phosphorothioate internucleotide linkages
tcgacgtcga cgtcgacg                                18

SEQ ID NO: 632      moltype = DNA length = 18
FEATURE          Location/Qualifiers
source           1..18
                  mol_type = other DNA
                  organism = synthetic construct
modified_base      1..18
                  mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
SEQUENCE: 632     note = Phosphorothioate internucleotide linkages
tcgacgtcga cgtcgacg                                18

SEQ ID NO: 633      moltype = DNA length = 25
FEATURE          Location/Qualifiers
source           1..25
                  mol_type = other DNA
                  organism = synthetic construct
modified_base      order(1..5,6..24)
                  mod_base = OTHER
modified_base      note = Phosphorothioate internucleotide linkages
modified_base      order(5..6,24..25)
                  mod_base = OTHER
modified_base      note = Phosphodiester internucleotide linkages
                  25
                  mod_base = OTHER
SEQUENCE: 633     note = Inverse nucleotide ( 3-prime and 5-prime switched)
tcgtcgacgt tcggcgccgt gcccgt                                25

SEQ ID NO: 634      moltype = DNA length = 25
FEATURE          Location/Qualifiers
source           1..25
                  mol_type = other DNA
                  organism = synthetic construct
modified_base      order(1..11,13..24)
                  mod_base = OTHER

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modified_base          note = Phosphorothioate internucleotide linkages
                      order(11..13,24..25)
modified_base          mod_base = OTHER
                      note = Phosphodiester internucleotide linkages
                      25
modified_base          mod_base = OTHER
                      note = Inverse nucleotide ( 3-prime and 5-prime switched)
SEQUENCE: 634          25
tcgtcgacgt tcggcgccgt gccgt

SEQ ID NO: 635          moltype = DNA length = 23
FEATURE
source
1..23
mol_type = other DNA
organism = synthetic construct
order(1..18,19..23)
modified_base          mod_base = OTHER
note = Phosphorothioate internucleotide linkages
18..19
modified_base          mod_base = OTHER
note = Phosphodiester internucleotide linkages
13..23
modified_base          mod_base = OTHER
note = Inverse nucleotide (inverse orientation: 3-prime and
5-prime switched)
SEQUENCE: 635          23
gcgcgcgcg gctagcagct gct

SEQ ID NO: 636          moltype = DNA length = 23
FEATURE
source
1..23
mol_type = other DNA
organism = synthetic construct
order(1..18,19..23)
modified_base          mod_base = OTHER
note = Phosphorothioate internucleotide linkages
18..19
modified_base          mod_base = OTHER
note = Phosphodiester internucleotide linkages
13..23
modified_base          mod_base = OTHER
note = Inverse nucleotide (inverse orientation: 3-prime and
5-prime switched)
SEQUENCE: 636          23
cggcgcgcg cgttagcagct gct

SEQ ID NO: 637          moltype = DNA length = 25
FEATURE
source
1..25
mol_type = other DNA
organism = synthetic construct
order(1..19,20..24)
modified_base          mod_base = OTHER
note = Phosphorothioate internucleotide linkages
19..20
modified_base          mod_base = OTHER
note = Phosphodiester internucleotide linkages
14..25
modified_base          mod_base = OTHER
note = Inverse nucleotide (inverse orientation: 3-prime and
5-prime switched)
SEQUENCE: 637          25
cggcgccgtg ccgnnttgca ctgtc

SEQ ID NO: 638          moltype = DNA length = 24
FEATURE
source
1..24
mol_type = other DNA
organism = synthetic construct
order(1..19,20..24)
modified_base          mod_base = OTHER
note = Phosphorothioate internucleotide linkages
19..20
modified_base          mod_base = OTHER
note = Phosphodiester internucleotide linkages
14..24
modified_base          mod_base = OTHER
note = Inverse nucleotide (inverse orientation: 3-prime and
5-prime switched)

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mod_base = OTHER
note = Inverse nucleotide (inverse orientation: 3-prime and
      5-prime switched)
SEQUENCE: 638
gccgtgcgcg ggcttgca cgtc                               24

SEQ ID NO: 639          moltype = DNA  length = 25
FEATURE
source
1..25
mol_type = other DNA
organism = synthetic construct
order(1..20,21..25)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
20..21
mod_base = OTHER
note = Phosphodiester internucleotide linkages
15..25
mod_base = OTHER
note = Inverse nucleotide (inverse orientation: 3-prime and
      5-prime switched)
SEQUENCE: 639
tcggcgccgc ccgatagc cgtc                               25

SEQ ID NO: 640          moltype = DNA  length = 23
FEATURE
source
1..23
mol_type = other DNA
organism = synthetic construct
order(3..5,6..8,9..12,13..17,18..23)
mod_base = OTHER
note = Stabilized internucleotide linkages
1..2
mod_base = OTHER
note = Phosphodiester internucleotide linkages
order(2..3,5..6,8..9,12..13,17..18)
mod_base = OTHER
note = Phosphodiester or phosphodiester-like
      internucleotide linkages
SEQUENCE: 640
tcgtcgacgt tcggcgccgc ccg                               23

SEQ ID NO: 641          moltype = DNA  length = 21
FEATURE
source
1..21
mol_type = other DNA
organism = synthetic construct
order(1..3,16..21)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
3..16
mod_base = OTHER
note = Phosphodiester internucleotide linkages
SEQUENCE: 641
ggggacgacg tcgtgggggg g                               21

SEQ ID NO: 642          moltype = DNA  length = 24
FEATURE
source
1..24
mol_type = other DNA
organism = synthetic construct
1..24
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 642
tcgtcgacga tcggcgccgt gccg                               24

SEQ ID NO: 643          moltype = DNA  length = 20
FEATURE
source
1..20
mol_type = other DNA
organism = synthetic construct
16..19
mod_base = OTHER
note = Phosphorothioate linkages
2..15
mod_base = OTHER
note = Phosphorothioate linkages

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mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 643
ggggacgacg tcgtgggggg 20

SEQ ID NO: 644 moltype = DNA length = 22
FEATURE Location/Qualifiers
source 1..22
mol_type = other DNA
organism = synthetic construct
modified_base 1..22
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 644
tcgtcgttt cggcgccgcg cg 22

SEQ ID NO: 645 moltype = DNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other DNA
organism = synthetic construct
modified_base order(1..5,6..8,9..12,13..17,18..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base order(5..6,8..9,12..13,17..18)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
modified_base order(6..7,9..10,13..14,16,18,20,23)
mod_base = OTHER
note = 2-Prime-O-methyl nucleosides
SEQUENCE: 645
tcgtcgacga tcggcgccgc ccg 23

SEQ ID NO: 646 moltype = DNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other DNA
organism = synthetic construct
modified_base order(1..2,3..5,6..8,9..12,13..17,18..23)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base order(2..3,5..6,8..9,12..13,17..18)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
modified_base order(3..6..7,9..10,13..14,16,18,20,23)
mod_base = OTHER
note = 2-Prime-O-methyl nucleosides
SEQUENCE: 646
tcgtcgacga tcggcgccgc ccg 23

SEQ ID NO: 647 moltype = DNA length = 22
FEATURE Location/Qualifiers
source 1..22
mol_type = other DNA
organism = synthetic construct
modified_base order(1..2,3..11,12..22)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base order(2..3,11..12)
mod_base = OTHER
note = Phosphodiester internucleotide linkages
modified_base 1
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
SEQUENCE: 647
ncttttttgt cgtttttttt tt 22

SEQ ID NO: 648 moltype = DNA length = 23
FEATURE Location/Qualifiers
source 1..23
mol_type = other DNA
organism = synthetic construct
modified_base 1..23
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base 1

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mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
SEQUENCE: 648
ncgacgtcga tcggcgcgcg ccg                                23

SEQ ID NO: 649      moltype = DNA  length = 24
FEATURE          Location/Qualifiers
source           1..24
                  mol_type = other DNA
                  organism = synthetic construct
modified_base    1..24
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base    1
                  mod_base = OTHER
                  note = 5-iodo-2-prime-deoxyuridine
SEQUENCE: 649
ncgacgtcga tcggcgcgcg ccgt                                24

SEQ ID NO: 650      moltype = DNA  length = 23
FEATURE          Location/Qualifiers
source           1..23
                  mol_type = other DNA
                  organism = synthetic construct
modified_base    1..23
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base    1
                  mod_base = OTHER
                  note = 5-ethyl-2-prime-deoxyuridine
SEQUENCE: 650
ncgacgtcga tcggcgcgcg ccg                                23

SEQ ID NO: 651      moltype = DNA  length = 24
FEATURE          Location/Qualifiers
source           1..24
                  mol_type = other DNA
                  organism = synthetic construct
modified_base    1..24
                  mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base    1
                  mod_base = OTHER
                  note = 5-iodo-2-prime-deoxyuridine
SEQUENCE: 651
ncgtcgacga tcggcgccgc ccgt                                24

SEQ ID NO: 652      moltype = DNA  length = 21
FEATURE          Location/Qualifiers
source           1..21
                  mol_type = other DNA
                  organism = synthetic construct
order(1..2,3..21)
modified_base    mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base    2..3
                  mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
modified_base    1
                  mod_base = OTHER
                  note = 5-iodo-2-prime-deoxyuridine
modified_base    4
                  mod_base = OTHER
                  note = 5-iodo-2-prime-deoxyuridine
SEQUENCE: 652
ncgncttt tcggtcgtt t                                     21

SEQ ID NO: 653      moltype = DNA  length = 21
FEATURE          Location/Qualifiers
source           1..21
                  mol_type = other DNA
                  organism = synthetic construct
order(1..5,6..21)
modified_base    mod_base = OTHER
                  note = Phosphorothioate internucleotide linkages
modified_base    5..6

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modified_base      mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
1
modified_base      mod_base = OTHER
                  note = 5-iodo-2-prime-deoxyuridine
4
modified_base      mod_base = OTHER
                  note = 5-iodo-2-prime-deoxyuridine
SEQUENCE: 653
ncgncgttt tcggtcgtt t                                21

SEQ ID NO: 654      moltype = DNA  length = 15
FEATURE
source           Location/Qualifiers
1..15
mol_type = other DNA
organism = synthetic construct
order(1..2,12..15)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
2..13
modified_base      mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
1
modified_base      mod_base = OTHER
                  note = 5-bromo-2-prime-deoxyuridine
SEQUENCE: 654
ncgacgtcgt ggggg                                15

SEQ ID NO: 655      moltype = DNA  length = 21
FEATURE
source           Location/Qualifiers
1..21
mol_type = other DNA
organism = synthetic construct
order(1..2,3..21)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
2..3
modified_base      mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
1
modified_base      mod_base = OTHER
                  note = 5-iodo-2-prime-deoxyuridine
SEQUENCE: 655
ncgtcggtt tcggtcgtt t                                21

SEQ ID NO: 656      moltype = DNA  length = 24
FEATURE
source           Location/Qualifiers
1..24
mol_type = other DNA
organism = synthetic construct
order(1..2,3..24)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
2..3
modified_base      mod_base = OTHER
                  note = Phosphodiester internucleotide linkages
1
modified_base      mod_base = OTHER
                  note = 5-ethyl-2-prime-deoxyuridine
24
modified_base      mod_base = OTHER
                  note = 3-Prime-O-methyl-riboguanidine
4
modified_base      mod_base = OTHER
                  note = 5-ethyl-2-prime-deoxyuridine
SEQUENCE: 656
ncgncgttt acggcgccgt gccn                                24

SEQ ID NO: 657      moltype = DNA  length = 22
FEATURE
source           Location/Qualifiers
1..22
mol_type = other DNA
organism = synthetic construct
order(1..2,3..22)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages

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modified_base      2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
modified_base      22
mod_base = OTHER
note = 3-Prime-O-methyl-riboguanidine
modified_base      1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
SEQUENCE: 657
ncgtcgttt cggcgccgc cn                                22

SEQ ID NO: 658      moltype = DNA length = 22
FEATURE
source             Location/Qualifiers
1..22
mol_type = other DNA
organism = synthetic construct
modified_base      order(1..2,3..22)
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base      2..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
modified_base      1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
modified_base      4
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
modified_base      22
mod_base = OTHER
note = 3-Prime-O-methyl-riboguanidine
SEQUENCE: 658
ncgnccgttt cggcgccgc cn                                22

SEQ ID NO: 659      moltype = DNA length = 21
FEATURE
source             Location/Qualifiers
1..21
mol_type = other DNA
organism = synthetic construct
modified_base      1..21
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base      1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
SEQUENCE: 659
ncgtcggtt tcggtcgtt t                                21

SEQ ID NO: 660      moltype = DNA length = 21
FEATURE
source             Location/Qualifiers
1..21
mol_type = other DNA
organism = synthetic construct
modified_base      1..21
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base      2
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
SEQUENCE: 660
tnccgtttcg ggcggccgc t                                21

SEQ ID NO: 661      moltype = DNA length = 24
FEATURE
source             Location/Qualifiers
1..24
mol_type = other DNA
organism = synthetic construct
modified_base      1..24
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
modified_base      1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
SEQUENCE: 661
ncgtcgacga tcggcgccgc ccgt                                24

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SEQ ID NO: 662      moltype = DNA  length = 23
FEATURE
source
1..23
mol_type = other DNA
organism = synthetic construct
3..23
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
1..3
mod_base = OTHER
note = Phosphodiester internucleotide linkages
modified_base
1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
SEQUENCE: 662
ncgacgtcga tcggcgcgccg ccg                                23

SEQ ID NO: 663      moltype = DNA  length = 23
FEATURE
source
1..23
mol_type = other DNA
organism = synthetic construct
2..23
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
1..2
mod_base = OTHER
note = Phosphodiester internucleotide linkages
modified_base
1
mod_base = OTHER
note = 5-ethyl-2-prime-deoxyuridine
SEQUENCE: 663
ncgacgtcga tcggcgcgccg ccg                                23

SEQ ID NO: 664      moltype = DNA  length = 20
FEATURE
source
1..20
mol_type = other DNA
organism = synthetic construct
1..20
mod_base = OTHER
note = Phosphorothioate internucleotide linkages
SEQUENCE: 664
tgtcgaaaaa tttttttttt                                20

SEQ ID NO: 665      moltype = DNA  length = 21
FEATURE
source
1..21
mol_type = other DNA
organism = synthetic construct
17..20
mod_base = OTHER
note = Phosphorothioate linkages
2..16
mod_base = OTHER
note = Phosphodiester linkages
modified_base
9
mod_base = OTHER
note = 5-iodo-2-prime-deoxyuridine
SEQUENCE: 665
ggggacganc gaacgtgggg g                                21

SEQ ID NO: 666      moltype = DNA  length = 26
FEATURE
source
1..26
mol_type = other DNA
organism = synthetic construct
modified_base
22..25
mod_base = OTHER
note = Phosphorothioate linkages
2..21
mod_base = OTHER
note = Phosphodiester linkages
modified_base
5
mod_base = OTHER

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SEQUENCE: 666          note = 5-ido-2-prime-deoxyuridine
ggggncgacg tcgacgtcga gggggg                                26

SEQ ID NO: 667          moltype = DNA  length = 26
FEATURE                                         Location/Qualifiers
source                                           1..26
modified_base                                     mol_type = other DNA
                                                 organism = synthetic construct
                                                 22..25
                                                 mod_base = OTHER
                                                 note = Phosphorothioate linkages
modified_base                                     2..21
                                                 mod_base = OTHER
                                                 note = Phosphodiester linkages
modified_base                                     5
                                                 mod_base = OTHER
                                                 note = 5-ido-2-prime-deoxyuridine
modified_base                                     11
                                                 mod_base = OTHER
                                                 note = 5-ido-2-prime-deoxyuridine
SEQUENCE: 667          note = 5-ido-2-prime-deoxyuridine
ggggncgacg ncgacgtcga gggggg                                26

SEQ ID NO: 668          moltype = DNA  length = 26
FEATURE                                         Location/Qualifiers
source                                           1..26
modified_base                                     mol_type = other DNA
                                                 organism = synthetic construct
                                                 22..25
                                                 mod_base = OTHER
                                                 note = Phosphorothioate linkages
modified_base                                     2..21
                                                 mod_base = OTHER
                                                 note = Phosphodiester linkages
modified_base                                     5
                                                 mod_base = OTHER
                                                 note = 5-ido-2-prime-deoxyuridine
modified_base                                     17
                                                 mod_base = OTHER
                                                 note = 5-ido-2-prime-deoxyuridine
SEQUENCE: 668          note = 5-ido-2-prime-deoxyuridine
ggggncgacg tcgacgnca gggggg                                26

SEQ ID NO: 669          moltype = DNA  length = 26
FEATURE                                         Location/Qualifiers
source                                           1..26
modified_base                                     mol_type = other DNA
                                                 organism = synthetic construct
                                                 22..25
                                                 mod_base = OTHER
                                                 note = Phosphorothioate linkages
modified_base                                     2..21
                                                 mod_base = OTHER
                                                 note = Phosphodiester linkages
modified_base                                     5
                                                 mod_base = OTHER
                                                 note = 5-ido-2-prime-deoxyuridine
modified_base                                     11
                                                 mod_base = OTHER
                                                 note = 5-ido-2-prime-deoxyuridine
modified_base                                     17
                                                 mod_base = OTHER
                                                 note = 5-ido-2-prime-deoxyuridine
SEQUENCE: 669          note = 5-ido-2-prime-deoxyuridine
ggggncgacg ncgacgnca gggggg                                26

SEQ ID NO: 670          moltype = DNA  length = 21
FEATURE                                         Location/Qualifiers
source                                           1..21
modified_base                                     mol_type = other DNA
                                                 organism = synthetic construct
                                                 17..20
                                                 mod_base = OTHER
                                                 note = Phosphorothioate linkages
modified_base                                     2..16

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modified_base      mod_base = OTHER
                  note = Phosphodiester linkages
9
modified_base      mod_base = OTHER
                  note = 5-ido-2-prime-deoxyuridine
16
modified_base      mod_base = OTHER
                  note = 5-ido-2-prime-deoxyuridine
SEQUENCE: 670
ggggacganc gaacgngggg g                                21

SEQ ID NO: 671      moltype = DNA  length = 27
FEATURE
source           Location/Qualifiers
1..27
mol_type = other DNA
organism = synthetic construct
modified_base      mod_base = OTHER
note = Phosphorothioate linkages
22..26
modified_base      mod_base = OTHER
note = Phosphorothioate linkages
2..21
modified_base      mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 671
ggggtcgacg tcgacgtcga gggggggg                                27

SEQ ID NO: 672      moltype = DNA  length = 21
FEATURE
source           Location/Qualifiers
1..21
mol_type = other DNA
organism = synthetic construct
modified_base      mod_base = OTHER
note = Phosphorothioate linkages
16..20
modified_base      mod_base = OTHER
note = Phosphorothioate linkages
2..15
modified_base      mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 672
ggggacgacg tcgtgggggg g                                21

SEQ ID NO: 673      moltype = DNA  length = 22
FEATURE
source           Location/Qualifiers
1..22
mol_type = other DNA
organism = synthetic construct
modified_base      mod_base = OTHER
note = Phosphorothioate linkages
17..21
modified_base      mod_base = OTHER
note = Phosphorothioate linkages
2..16
modified_base      mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 673
ggggacgatc gaacgtgggg gg                                22

SEQ ID NO: 674      moltype = DNA  length = 21
FEATURE
source           Location/Qualifiers
1..21
mol_type = other DNA
organism = synthetic construct
modified_base      mod_base = OTHER
note = Phosphorothioate linkages
17..20
modified_base      mod_base = OTHER
note = Phosphorothioate linkages
2..16
modified_base      mod_base = OTHER
note = Phosphodiester linkages
SEQUENCE: 674
ggggacgatc gaacgtgggg g                                21

SEQ ID NO: 675      moltype = DNA  length = 26
FEATURE
source           Location/Qualifiers
1..26
mol_type = other DNA
organism = synthetic construct
modified_base      mod_base = OTHER
note = Phosphorothioate linkages
22..25
modified_base      mod_base = OTHER
note = Phosphorothioate linkages
2..21

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SEQUENCE: 675          mod_base = OTHER
                      note = Phosphodiester linkages
gggggtcgacg tcgacgtcga gggggg                                26

SEQ_ID NO: 676          moltype = DNA  length = 20
FEATURE           Location/Qualifiers
source            1..20
modified_base      mol_type = other DNA
                      organism = synthetic construct
                     16..18
                     mod_base = OTHER
                     note = Phosphorothioate linkages
                     order(2..15,19..20)
                     mod_base = OTHER
                     note = Phosphodiester linkages
SEQUENCE: 676          mod_base = OTHER
ggggacgacg tcgtgggggg                                20

SEQ_ID NO: 677          moltype = DNA  length = 11
FEATURE           Location/Qualifiers
source            1..11
modified_base      mol_type = other DNA
                      organism = synthetic construct
                     1..2
                     mod_base = OTHER
                     note = Phosphorothioate linkages
                     2..11
                     mod_base = OTHER
                     note = Phosphodiester linkages
                     10
                     mod_base = OTHER
                     note = Vitamin E appended
                     11
                     mod_base = OTHER
                     note = Triethylene glycol
SEQUENCE: 677          tcgacgtcgt n                                11

SEQ_ID NO: 678          moltype = DNA  length = 11
FEATURE           Location/Qualifiers
source            1..11
modified_base      mol_type = other DNA
                      organism = synthetic construct
                     1..11
                     mod_base = OTHER
                     note = Phosphodiester internucleotide linkages
                     11
                     mod_base = OTHER
                     note = Doubler2 (Chemgenes)
                     11
                     mod_base = OTHER
                     note = Butyrate appended
SEQUENCE: 678          tcgacgtcgt t                                11

SEQ_ID NO: 679          moltype = DNA  length = 11
FEATURE           Location/Qualifiers
source            1..11
modified_base      mol_type = other DNA
                      organism = synthetic construct
                     1..11
                     mod_base = OTHER
                     note = Phosphodiester internucleotide linkages
                     11
                     mod_base = OTHER
                     note = Doubler2 (Chemgenes)
                     11
                     mod_base = OTHER
                     note = Cholesterol appended
SEQUENCE: 679          tcgacgtcgt t                                11

SEQ_ID NO: 680          moltype = DNA  length = 12
FEATURE           Location/Qualifiers
source            1..12

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modified_base      mol_type = other DNA
                   organism = synthetic construct
                   1..12
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
modified_base      12
                   mod_base = OTHER
                   note = Doubler2 (Chemgenes)
modified_base      12
                   mod_base = OTHER
                   note = Cholesterol appended
SEQUENCE: 680
tcgacgtcgt tt          12

SEQ ID NO: 681      moltype = DNA length = 24
FEATURE           Location/Qualifiers
source            1..24
                   mol_type = other DNA
                   organism = synthetic construct
modified_base      1..24
                   mod_base = OTHER
                   note = Phosphodiester internucleotide linkages
modified_base      12..13
                   mod_base = OTHER
                   note = Cholesterol appended
modified_base      24
                   mod_base = OTHER
                   note = Butyrate appended
SEQUENCE: 681
tcgacgtcgt tttcgacgt cgtt          24

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**1-22.** (canceled)

**23.** A method of treating cancer in a subject, said method comprising

- (a) administering to the subject at least dose of a composition comprising a TLR9 agonist and
- (b) administering to the subject at least one dose of a composition comprising a CPI, wherein the composition comprising the TLR9 agonist is administered in a volume of greater than 4 mL, a volume of between 5 and 20 mL, a volume of between 5 and 10 mL, a volume of 5 mL, or a volume of 7 mL.

**24-27.** (canceled)

**28.** The method of claim **23**, wherein the TLR9 agonist induces IFN- $\alpha$ .

**29.** The method of claim **23**, wherein the TLR9 agonist is CpG DNA, an A-class CpG DNA, or an A-class CpG DNA having a sequence of GGGGGGGGGGGAC-GATCGTCGGGGGGGGGG (SEQ ID NO:82).

**30-33.** (canceled)

**34.** The method of claim **23**, wherein the composition comprising the TLR9 agonist is formulated as a virus-like particle (VLP).

**35.** The method of claim **34**, wherein the TLR9 agonist is an A-class CpG DNA.

**36.** (canceled)

**37.** The method of claim **23**, wherein the composition comprising the TLR9 agonist is administered via intratumoral, peritumoral, systemic, intravenous, intraperitoneal, enteric, oral, intramuscular, subcutaneous, transmucosal, topical and/or transdermal routes.

**38.** (canceled)

**39.** The method of claim **23**, wherein the cancer is associated with a cancerous tumor,

optionally wherein the cancerous tumor is a lymphoma, a melanoma, or a cancerous tumor of a tissue or organ selected from the group consisting of skin, head and

neck, esophagus, stomach, liver, colon, rectum, pancreas, lung, breast, cervix, ovary, kidney, bladder, prostate, thyroid, brain, muscle, and bone.

**40-43.** (canceled)

**44.** The method of claim **23**, wherein the subject is a human.

**45.** The method of claim **23**, wherein the composition comprising the CPI is administered via intratumoral, peritumoral, systemic, intravenous, intraperitoneal, enteric, oral, intramuscular, subcutaneous, transmucosal, topical and/or transdermal routes.

**46.** The method of claim **23**, wherein the CPI is an antibody or antigen-binding fragment thereof which binds specifically to an antigen selected from the group consisting of PD-1, PD-L1, and CTLA-4.

**47-49.** (canceled)

**50.** The method of claim **23**, wherein the composition comprising the CPI comprises a combination of CPIs selected from the group consisting of:

(a) a first antibody or antigen-binding fragment thereof which binds specifically to CTLA-4, and a second antibody or antigen-binding fragment thereof which binds specifically to PD-1;

(b) a first antibody or antigen-binding fragment thereof which binds specifically to CTLA-4, and a second antibody or antigen-binding fragment thereof which binds specifically to PD-L1;

(c) a first antibody or antigen-binding fragment thereof which binds specifically to PD-1, and a second antibody or antigen-binding fragment thereof which binds specifically to PD-L1.

**51.** The method of claim **23**, wherein the composition comprising the TLR9 agonist is administered prior to administration of the composition comprising the CPI,

the composition comprising the TLR9 agonist and the composition comprising the CPI are administered substantially at the same time, or

wherein the composition comprising the CPI is administered prior to administration of the composition comprising the TLR9 agonist.

**52.** (canceled)

**53.** The method of claim **23**, wherein the composition comprising the TLR9 agonist and the composition comprising the CPI are administered via different routes or the same route.

**54.** (canceled)

**55.** The method of claim **23**, wherein at least two doses of the composition comprising the TLR9 agonist are administered or wherein at least two doses of the composition comprising the CPI are administered.

**56.** The method of claim **23**, wherein (a) two doses; (b) three doses; (c) four doses; or (d) five doses of the composition comprising the TLR9 agonist are administered.

**57.** The method of claim **23**, wherein two doses of the composition comprising the TLR9 agonist are administered prior to administration of the composition comprising the CPI.

**58.** (canceled)

**59.** The method of claim **23**, wherein the composition comprising the TLR9 agonist and the composition comprising the CPI are administered concurrently and at least two doses of each composition are administered, or

wherein the composition comprising the TLR9 agonist and the composition comprising the CPI are administered sequentially and at least two doses of each composition are administered.

**60.** (canceled)

**61.** The method of claim **23**, wherein the composition comprising the TLR9 agonist and the composition comprising the CPI are administered sequentially and by the same route, or

wherein the composition comprising the TLR9 agonist and the composition comprising the CPI are administered sequentially and by different routes.

**62.** (canceled)

**63.** The method of claim **23** where the composition comprising the TLR9 agonist is administered 1 to 3 weeks before the composition comprising the CPI.

**64.** The method of claim **23**, further comprising administering one or more additional therapeutic agents or treatments;

wherein the one or more additional therapeutic agents or treatments is selected from the group consisting of an immune checkpoint inhibitor, an antibody that activates a co-stimulatory pathway, a cancer chemotherapy, and radiation therapy.

**65.** (canceled)

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