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(54) Title: RNA ANTAGONIST COMPOUNDS FOR THE MODULATION OF PIK3CA EXPRESSION

(57) Abstract: The present invention relates to oligomer compounds (oligomers), which target PIK3CA mRNA in a cell, leading to reduced expression of PIK3CA. Reduction of PIK3CA expression is beneficial for the treatment of certain medical disorders, such as hyperproliferative diseases such as cancer.

RNA ANTAGONIST COMPOUNDS FOR THE MODULATION OF PIK3CA EXPRESSION.

FIELD OF INVENTION

The present invention relates to oligomeric compounds (oligomers) that target PIK3CA
5 mRNA in a cell, leading to reduced expression of PIK3CA. In particular, this invention relates
to oligomeric compounds (oligomers), which target the PIK3CA kinase mRNA in a cell,
leading to reduced expression of the PIK3CA kinase. Reduction of PIK3CA expression is
beneficial for a range of medical disorders, such as hyperproliferative diseases such as
cancer.

10 RELATED CASES

This application claims the benefit under 35 U.S.C. § 119(e) of U.S. Provisional Application
Serial No. 60/992,050, filed December 3, 2007, the disclosure of which is incorporated
herein by reference in its entirety.

BACKGROUND

15 Phosphatidylinositol 3-kinase (PI3K) is a ubiquitous lipid kinase involved in receptor
signal transduction by tyrosine kinase receptors. PI3K comprises a large and complex
family that includes 3 classes with multiple subunits and isoforms. The class I PI3Ks are
composed of a Src homology-2 domain-containing an 85 kDa regulatory subunit (p85) and a
100-kDa catalytic subunit (p110), which catalyses the phosphorylation of phosphoinositol 4-
20 phosphate and phosphoinositol 4,5-phosphate at their D3 positions. The PI3K regulatory
subunits include p85alpha and its truncated splice variants p50alpha and p55alpha, as well
as p85beta and p55gamma; the catalytic subunits include p110alpha, p110beta, and
p110delta. The human catalytic subunit p110alpha is encoded by the PIK3CA gene, located
on the human chromosome 3 [Chr 3: 180.35 - 180.44 M bp] specifically [chr3:180,349,005-
25 180,435,191 bp](NCBI reference sequence annotation) (3q26.3), which is frequently
mutated in a variety of human cancers; PIK3CA has been shown to be mutated in 32% of
colorectal cancer, 27% of glioblastomas, 25% of gastric cancers, 36% of hepatocellular
carcinomas, 18-40% of breast cancers, 4-12% of ovarian cancers and 4% of lung cancers
(Samuels et al., 2006). Most of the mutations found map to three mutational hotspots within

the PIK3CA coding sequence, known as E542K, E545K and H1047R (Kang et al., 2005). A comprehensive map of detected PIK3CA mutations and their prevalence in different human tissues can be found on

<http://www.sanger.ac.uk/perl/genetics/CGP/cosmic?action=gene&ln=PIK3CA> (hereby
5 incorporated by reference).

PI3K has been indicated in a wide range of cancers, such as colorectal carcinoma, where it has been shown that the activation of PI3K/Akt is associated with colorectal carcinoma and can convert differentiated human gastric or colonic carcinoma cells to a less differentiated and more malignant phenotype (Rychahou et al 2006).

10 The effects of PI3K on tumor growth and progression are thought to be mediated by Akt, a downstream effector of PI3K. In humans there are three members of the Akt gene family, Akt 1, Akt 2 and Akt3. Akt is overexpressed in a number of cancers, including colon, pancreatic, ovarian and some steroid hormone-insensitive breast cancers.

Inhibitors of proteins that are involved in the PI3K/Akt signalling which have been
15 suggested as potential therapeutic agents include both siRNAs and antisense oligonucleotides (US2006030536A), however to date most research in this area appears to have focused on the use of siRNAs:

WO2005/091849 refers to antisense down-regulation of PI3K, however no specific antisense oligonucleotides are disclosed.

20 Zhang et al., 2004 (Cancer Biology and Therapy 3:12 1283-1289) disclose siRNAs targeting p110alpha and suggest its use in gene therapy in ovarian cancer.

Rychahou et al 2006 (Annals of Surgery 243833 – 844) discloses siRNA complexes targeting p85alpha and p110alpha which were found to decrease *in vitro* colon cell cancer survival and increase apoptosis in human colon cancer cells, and decreased liver metastasis
25 in *in vivo* experiments.

Meng et al., 2006 (Cellular Signalling 18 2262-2271) disclose siRNAs targeting p110alpha for inhibiting PI3K activity in ovarian cancer cells. The authors determined that inhibition of AKT1 is sufficient to affect cell migration, invasion and proliferation.

Hsieh et al., 2004 (NAR 32 893-901) reports on the use of 148 siRNA duplexes
30 targeting 30 genes within the PI3K pathway.

US 2005/0272682 discloses siRNA complexes targeting a phosphoinositide 3-kinase (PI3K) signal transduction pathway.

In an exemplary aspect, the present invention provides highly efficient antisense oligonucleotides which target the PI3K pathway, specifically the PIK3CA mRNA, and in

particular a new class of PIK3CA antagonists which have been selected based on LNA chemistry, and/or by the selection of particularly effective target sites on the PIK3CA mRNA.

SUMMARY OF INVENTION

5 The invention provides an oligomer of between 10 – 50, such as 10 - 30 nucleotides in length which comprises a contiguous nucleotide sequence of a total of between 10 – 30 nucleotides, wherein said contiguous nucleotide sequence is at least 80% (e.g., 85%, 90%, 95%, 98%, or 99%) homologous to a region corresponding to the reverse complement of a mammalian PIK3CA gene or mRNA, such as SEQ ID NO: 1 or naturally occurring variants
10 thereof.

 The invention provides an oligomer of 10 – 50 monomers, such as 10 - 30 monomers which comprises a first region of 10 – 30 monomers, wherein the sequence of the first region is at least 80% (e.g., 85%, 90%, 95%, 98%, or 99%) identical to the reverse complement of a target region of a nucleic acid which encodes a mammalian PIK3CA, such as a
15 mammalian PIK3CA gene or mRNA, such as a nucleic acid have the sequence set forth in SEQ ID NO: 1 or naturally occurring variants thereof.

 The invention provides for a conjugate comprising the oligomer according to the invention, and at least one non-nucleotide or non-polynucleotide moiety (“conjugated moiety”) covalently attached to said oligomer.

20 The invention provides for a pharmaceutical composition comprising an oligomer or a conjugate according to the invention, and a pharmaceutically acceptable diluent, carrier, salt or adjuvant.

 The invention provides an oligomer of between 10-50 nucleobases in length which comprises a contiguous nucleobase sequence of a total of between 10-50 nucleobases,
25 wherein said contiguous nucleobase sequence is at least 80% identical to the reverse complement of a target region of a nucleic acid which encodes mammalian PIK3CA.

 The invention provides for the oligomer or the conjugate according to invention, for use as a medicament, such as for the treatment of hyperproliferative diseases such as cancer.

30 The invention provides for the use of an oligomer or the conjugate according to the invention, for the manufacture of a medicament for the treatment of hyperproliferative diseases such as cancer.

 The invention provides for a method of treating hyperproliferative diseases such as cancer, said method comprising administering an oligomer, a conjugate or a pharmaceutical

composition according to the invention, to a patient suffering from, or likely to suffer from said hyperproliferative disease such as cancer.

The invention provides for a method for the inhibition of both PIK3CA and beta-catenin in a cell which is expressing both PIK3CA and beta-catenin, said method comprising
5 administering an oligomer, or a conjugate according to the invention to said cell so as to effect the inhibition of PIK3CA and beta-catenin in said cell. Suitably the oligomer which is capable of inhibiting or down-regulating both PI3CA and beta-catenin in a cell has significantly homology to, or is capable of hybridising to the reverse complement of both target nucleic acids, such as an oligomer with a sequence of nucleobases of SEQ ID 82.

10 The invention further provides for an oligomer according to the invention, for use in medicine.

The invention further provides for an oligomer according to the invention, for use for the treatment of one or more of the diseases referred to herein, such as a disease selected from the group consisting of: hyperproliferative diseases such as cancer,

15 Further provided are methods of down-regulating the expression of PIK3CA in a cell, cells or tissues comprising contacting said cells or tissues, *in vitro* or *in vivo*, with one or more of the oligomers, conjugates or compositions of the invention.

Also disclosed are methods of treating an animal, such as a non-human animal, or a human, suspected of having or being prone (susceptible) to a hyperproliferative disease
20 such as cancer and/or diseases or conditions, associated with expression, or over-expression, of PIK3CA, by administering to said animal or human a therapeutically or prophylactically effective amount of one or more of the oligomers, conjugates or pharmaceutical compositions of the invention. Further, methods of using oligomers for the inhibition of expression of PIK3CA, and for treatment of diseases associated with activity of
25 PIK3CA are provided.

The invention provides for a method for treating a disease selected from the group consisting of hyperproliferative diseases such as cancer; the method comprising administering an (effective amount of) one or more oligomers of the invention, conjugates, or pharmaceutical compositions thereof, to a patient in need thereof.

30 The invention provides for a method of inhibiting or reducing the expression of PIK3CA (and optionally beta-catenin) in a cell or a tissue, such as by down-regulation, the method comprising the step of contacting said cell or tissue with an (effective amount of) one or more oligomers of the invention, conjugates, or pharmaceutical compositions thereof so that expression of PIK3CA (and optionally beta-catenin) is inhibited or reduced.

In some aspects, the oligomer of the invention is selected from the group consisting of

5' A_sG_s^{Me}C_sC_sa_st_st_sC_sa_st_st_sC_sC_sA_s^{Me}C_s^{Me}C -3' (SEQ ID NO: 67); and

5' - T_sT_sA_st_st_sg_st_sg_sc_sa_st_sc_st_s^{Me}C_sA_sG -3' (SEQ ID NO: 77),

wherein uppercase letters denote beta-D-oxy-LNA monomers and lowercase letters
 5 denote DNA monomers, the subscript "s" denotes a phosphorothioate linkage, and ^{Me}C
 denotes a beta-D-oxy-LNA monomer containing a 5-methylcytosine base.

BRIEF DESCRIPTION OF FIGURES

Figure 1. Oligonucleotides presented in Table 3 were evaluated for their potential to
 knockdown the PIK3CA mRNA at concentrations of 0.8, 4 and 20 nM in MCF7 cells 24
 10 hours after transfection using Real-time PCR. All results were normalised to GAPDH and
 inhibition of PIK3CA mRNA is shown as percent of mock-transfected control. Results shown
 are average of three independent experiments.

Figure 2. Oligonucleotides presented in Table 3 were evaluated for their potential to
 knockdown the PIK3CA mRNA at concentrations of 0.8, 4 and 20 nM in PC3 cells 24 hours
 15 after transfection using Real-time PCR. All results were normalised to GAPDH and inhibition
 of PIK3CA mRNA is shown as percent of mock-transfected control. Results shown are
 average of three independent experiments.

Figure 3. Sequence alignment of the human PIK3CA mRNA sequence (Genbank Accession
 No: NM_006218) and the mouse PIK3CA mRNA sequence (Genbank Accession No:
 20 NM_008839).

Figure 4. Location of target sequences on the human PIK3CA mRNA sequence (Genbank
 Accession No: NM_006218). Positions marked in grey are mutation hotspots – 1781, 1790
 and 3297.

Figure 5. SEQ ID NO: 1 *Homo sapiens* phosphoinositide-3-kinase, catalytic, alpha
 25 polypeptide (PIK3CA) mRNA, (Genbank Accession No: NM_006218) 3724 bp.

Figure 6. SEQ ID NO 105. *Homo sapiens* phosphoinositide-3-kinase catalytic, alpha
 polypeptide protein sequence (PIK3CA) (Genbank Accession No: NP_006209).

Figure 7. SEQ ID NO 106. *Mus musculus* phosphatidylinositol 3-kinase, catalytic, alpha
 polypeptide (Pik3ca), mRNA. (Genbank Accession No: NM_008839).

30 **Figure 8.** SEQ ID NO 107. *Mus musculus* phosphoinositide-3-kinase catalytic, alpha
 polypeptide protein sequence (PIK3CA) Accession number NP_032865.

Figure 9. SEQ ID NO 108. *Macaca mulatta* phosphatidylinositol 3-kinase, catalytic, alpha polypeptide (Pik3ca), mRNA. (Genbank Accession No: XM_001109162).

Figure 10. SEQ ID NO 109. *Macaca mulatta* phosphoinositide-3-kinase catalytic, alpha polypeptide protein sequence (PIK3CA) (Genbank Accession No: XP_001109162).

5 **Figure 11.** Cell proliferation assay (MTS assay) in MCF7 cells. Four independent experiments were performed. The results from the experiment best representing the average activity of each oligo is shown.

Figure 12. Cell proliferation assay (MTS) in PC3 cells. Two independent experiments were performed. The results from the experiment best representing the average activity of each
10 oligo is shown.

Figure 13. Caspase 3/7 activity in PC3 cells after transfection with PIK3CA oligonucleotides. Data are expressed as fold induction compared to mock.

Figure 14. Cell proliferation assay (MTS) in HCT116 cells.

Figure 15. Caspase 3/7 activity in HCT116 cells after transfection with PIK3CA oligos. Data
15 are expressed as fold induction compared to mock.

Figure 16. Plasma stability of PIK3CA oligonucleotides. The LNA oligonucleotides were incubated with mouse plasma at 37 °C and aliquots were taken at 0, 24, 48 and 120 h. The results are visualized by gel electrophoresis using an SDS-PAGE gel.

Figure 17. T_m determination of PIK3CA oligonucleotides hybridised to a target region of a
20 target nucleic acid. Bold, uppercase letters with a superscript "o" to the right represent β -D-oxy LNA monomers. ^mC represent LNA monomers with 5-methylcytosine bases. Subscript "s" represents a phosphorothioate linkage. Lowercase letters represent DNA monomers.

Figure 18. Down-regulation of PIK3CA protein and pAkt in A549 cells

Figure 19. Down-regulation of PIK3CA protein and pAkt in 15PC3 cells

25 **Figure 20.** Analysis of knock down of PIK3CA mRNA in liver.

Figure 21. *In vivo* knock down of PIK3CA mRNA in mouse liver. Data are expressed as % down-regulation compared to saline (100%) \pm stdev. There were 5 animals in each group.

Figure 22. The most potent oligonucleotides were evaluated for their potential to knock
30 down the PIK3CA mRNA at concentrations of 0.04 nM, 0.2 nM, 0.8 nM, 4 nM, 10 nM and 20 nM in PC3 cells 24 hours after transfection using Real-time PCR. All results were normalised to GAPDH and inhibition of PIK3CA mRNA is shown as percent of mock-transfected control. Results shown are the average of two independent experiments.

Figure 23. The most potent oligonucleotides were evaluated for their potential to knock
down the PIK3CA mRNA at concentrations of 0.04 nM, 0.2 nM, 0.8 nM, 4 nM, 10 nM and 20

nM in MCF7 cells 24 hours after transfection using Real-time PCR. All results were normalised to GAPDH and inhibition of PIK3CA mRNA is shown as percent of mock-transfected control. Results shown are the average of two independent experiments.

DETAILED DESCRIPTION OF INVENTION

5 **The Oligomer**

The present invention employs oligomeric compounds (referred herein as oligomers), for use in modulating the function of nucleic acid molecules encoding mammalian PIK3CA, such as the PIK3CA nucleic acid shown in SEQ ID 1, and naturally occurring variants of such nucleic acid molecules encoding mammalian PIK3CA. The term "oligomer" in the
10 context of the present invention, refers to a molecule formed by covalent linkage of two or more nucleotides (*i.e.* an oligonucleotide). Herein, each single nucleotide, such as the nucleotides present in the oligomer of the invention, may also be referred to as a "monomer" or "unit". In some embodiments, the oligomer may consist or comprises of a contiguous nucleotide sequence of between 10 – 30 nucleotides in length (*i.e.* comprises or consists of
15 from 10 – 30 covalently linked monomers).

In various embodiments, the compounds according to the invention are linear molecules or are synthesised as a linear molecule. The oligomer, in such embodiments, is a single stranded molecule, and typically does not comprise short regions of, for example, at least 3, 4 or 5 contiguous nucleotides, which are complementary to another region within the
20 same oligomer (*i.e.* duplexes) - in this regards, In some embodiments, the oligomer is not (essentially) double stranded. In some embodiments, the oligomer is essentially not double stranded, such as is not a siRNA. In various embodiments, the oligomer of the invention may consist entirely of the contiguous nucleotide region. Thus, the oligomer is not substantially self-complementary. siRNAs comprise of 2 complementary short RNA (or
25 equivalent nucleobase units) sequences, such as between 21 and 23nts long, with, typically a 2nt 3' overhang on either end. In order to enhance *in vivo* uptake, the siRNAs may be conjugated, such as conjugated to a sterol, such as a cholesterol group (typically at the 3' or 5' termini of one or both of the strands).

The Target

30 Suitably the oligomer of the invention is capable of down-regulating expression of the PIK3CA gene. In this regards, the oligomer of the invention can effect the inhibition of PIK3CA, typically in a mammalian such as a human cell. In some embodiments, the

oligomers of the invention bind to the target nucleic acid and effect inhibition of expression of at least 10% or 20% compared to the normal expression level, more preferably at least a 30%, 40%, 50%, 60%, 70%, 80%, 90% or 95% inhibition as compared to the normal expression level (such as immediately prior to dosing of the oligomer). In some
5 embodiments, such modulation is seen when using between 0.04 and 25nM, such as between 0.8 and 20nM concentration of the compound of the invention. In the same or a different embodiment, the inhibition of expression is less than 100%, such as less than 98% inhibition, less than 95% inhibition, less than 90% inhibition, less than 80% inhibition, such as less than 70% inhibition. Modulation of expression level may be determined by measuring
10 protein levels, e.g. by the methods such as SDS-PAGE followed by western blotting using suitable antibodies raised against the target protein. Alternatively, modulation of expression levels can be determined by measuring levels of mRNA, e.g. by northern blotting or quantitative RT-PCR. When measuring via mRNA levels, the level of down-regulation when using an appropriate dosage, such as between 0.04 and 25nM, such as between 0.8 and
15 20nM concentration, is, in some embodiments, typically to a level of between 10-20% the normal levels in the absence of the compound of the invention.

The PIK3CA gene is likely to be a naturally occurring gene, and therefore in relation to the human gene it will have the sequence of SEQ ID NO 1 or a natural variant thereof, whether a "silent" (e.g. not associated with a disease or other alteration in PIK3CA kinase
20 properties) or "functional" (e.g. disease-associated) variant. The target sequence from the PIK3CA gene will be DNA or RNA, preferably mRNA. The oligomer hybridizes, such as specifically hybridises or hybridises under stringent conditions, to a single stranded nucleic acid molecule having the sequence of a portion of SEQ ID NO: 1.

It will be noted that, in some embodiment, some oligomers are capable of targeting
25 both PIK3CA and beta-catenin. Therefore in some embodiments, the target may be PIK3CA and beta-catenin.

The invention therefore, in some embodiments, provides a method of down-regulating or inhibiting the expression of PIK3CA protein and/or mRNA in a cell which is expressing PIK3CA protein and/or mRNA, said method comprising administering or contacting the
30 oligomer or conjugate according to the invention (suitably in an effective amount) to said cell to down-regulating or inhibiting the expression of PIK3CA protein and/or mRNA in said cell. Suitably the cell is a mammalian cell such as a human cell. The administration may occur, in some embodiments, *in vitro*. The administration may occur in some embodiments, *in vivo*.

The term "target nucleic acid", as used herein refers to the DNA or RNA encoding mammalian PIK3CA polypeptide, such as human PIK3CA, such as SEQ ID NO: 1. PIK3CA encoding nucleic acids or naturally occurring variants thereof, and RNA nucleic acids derived therefrom, preferably mRNA, such as pre-mRNA, although preferably mature mRNA. In some embodiments, for example when used in research or diagnostics the "target nucleic acid" may be a cDNA or a synthetic oligonucleotide derived from the above DNA or RNA nucleic acid targets. The oligomer according to the invention is preferably capable of hybridising to the target nucleic acid. It will be recognised that SEQ ID NO: 1 is a cDNA sequences, and as such, corresponds to the mature mRNA target sequence, although uracil is replaced with thymidine in the cDNA sequences.

The mammalian PIK3CA kinase is preferably selected from the group consisting of human or mouse PIK3CA kinase. Preferably the mammalian PIK3CA kinase is human PIK3CA kinase, such as the PIK3CA Kinase encoded by the nucleic acid as shown in SEQ ID NO 1. The nucleic acid which encodes the mammalian PIK3CA kinase is, in a preferable embodiment, the human PIK3CA kinase cDNA sequence is shown as SEQ ID NO 1 and/or the mouse PIK3CA kinase cDNA sequence is shown as SEQ ID NO 106, or allelic variants thereof, such as the PIK3CA mutations listed on <http://www.sanger.ac.uk/perl/genetics/CGP/cosmic?action=gene&ln=PIK3CA> (hereby incorporated by reference).

The term "naturally occurring variant thereof" refers to variants of the PIK3CA polypeptide of nucleic acid sequence which exist naturally within the defined taxonomic group, such as mammalian, such as mouse, monkey, and preferably human. Typically, when referring to "naturally occurring variants" of a polynucleotide the term also may encompass any allelic variant of the PIK3CA encoding genomic DNA which are found at the Chromosome 3 [Chr 3: 180.35 - 180.44 M bp] specifically [chr3:180,349,005-180,435,191 bp](NCBI reference sequence annotation) (3q26.3) by chromosomal translocation or duplication, and the RNA, such as mRNA derived therefrom. "Naturally occurring variants" may also include variants derived from alternative splicing of the PIK3CA mRNA. When referenced to a specific polypeptide sequence, e.g., the term also includes naturally occurring forms of the protein which may therefore be processed, e.g. by co- or post-translational modifications, such as signal peptide cleavage, proteolytic cleavage, glycosylation, etc. Variant sequences, may have at least 60%, more preferably at least 70%, more preferably at least 80%, more preferably at least 85%, more preferably at least 90%, more preferably at least 95% sequence homology to a target sequence in PIK3CA.

Typically, an oligomer of the invention corresponding to said variant sequences is still capable of down-regulating PIK3CA.

Particularly relevant variants of PIK3CA which may be targeted by the oligomers of the invention are spontaneous point mutations which are related to hyperproliferative diseases such as cancer – in this regards, point mutations which cause amino acid substitutions at positions E542, E545 or H1047, such as point mutations which cause the substitutions E542K, E545K and H1047R are particularly relevant. By designing oligomers which target PIK3CA mRNA which comprises such a spontaneous mutation, oligomers can be created which have a preferential activity (down-regulation) on the mRNA of variant (mutated) form of PIK3CA, which, as in the case of point mutations which cause amino acid substitutions at positions E542, E545 or H1047 are associated with a cancer phenotype.

In some embodiments, the PIK3CA gene or mRNA target comprises a single base substitution at a position which corresponds to position 1781, 1790 or 3297 of SEQ ID NO 1. In such embodiments, the nucleotide present at position 1781 may be other than G, such as A, C or T/U, the nucleotide present at position 1790 may be other than G, such as A, C or T/U, or the nucleotide present at position 3297 may be other than A, such as G, C or T/U. (T refers to DNA target, U to mRNA target).

In some embodiments, the contiguous nucleotide sequence of the oligomer according to the invention may comprise a nucleobase which corresponds to position 1781 of SEQ ID NO 1, wherein the nucleobases which corresponds to position 1781 is not a C, such is selected from A, G or T. Suitably, in some embodiments, the remaining nucleobases of such a contiguous nucleotide sequence may be fully complementary to the corresponding region of SEQ ID NO 1.

In some embodiments, the contiguous nucleotide sequence of the oligomer according to the invention may comprise a nucleobase which corresponds to position 1790 of SEQ ID NO 1, wherein the nucleobases which corresponds to position 1790 is not a C, such is selected from A, G or T. Suitably, in some embodiments, the remaining nucleobases of such a contiguous nucleotide sequence may be fully complementary to the corresponding region of SEQ ID NO 1.

In some embodiments, the contiguous nucleotide sequence of the oligomer according to the invention may comprise a nucleobase which corresponds to position 3297 of SEQ ID NO 1, wherein the nucleobases which corresponds to position 3297 is not a T, such is selected from A, G or C. Suitably, some embodiments, the remaining nucleobases of such a contiguous nucleotide sequence may be fully complementary to the corresponding region of

SEQ ID NO 1.

Oligomer Sequences

The oligomers comprise or consist of a contiguous nucleotide sequence which corresponds to the reverse complement of a nucleotide sequence present in SEQ ID NO: 1.

5 Thus, the oligomer can comprise or consist of, or a sequence selected from the group consisting of SEQ ID NOS: 2 - 16 or 17 - 28 or 110 - 124 or 125 - 136 or 149 - 160, wherein said oligomer (or contiguous nucleotide portion thereof) may optionally have one, two, or three mismatches against said selected sequence.

10 The oligomer may comprise or consist of a contiguous nucleotide sequence which is fully complementary (perfectly complementary) to the equivalent region of a nucleic acid which encodes a mammalian PIK3CA (e.g., SEQ ID NO: 1). Thus, the oligomer can comprise or consist of an antisense nucleotide sequence.

15 However, in some embodiments, the oligomer may tolerate 1, 2, 3, or 4 (or more) mismatches, when hybridising to the target sequence and still sufficiently bind to the target to show the desired effect, *i.e.* down-regulation of the target. Mismatches may, for example, be compensated by increased length of the oligomer nucleotide sequence and/or an increased number of nucleotide analogues, such as LNA, present within the nucleotide sequence.

20 In some embodiments, the contiguous nucleotide sequence comprises no more than 3, such as no more than 2 mismatches when hybridizing to the target sequence, such as to the corresponding region of a nucleic acid which encodes a mammalian PIK3CA.

In some embodiments, the contiguous nucleotide sequence comprises no more than a single mismatch when hybridizing to the target sequence, such as the corresponding region of a nucleic acid which encodes a mammalian PIK3CA.

25 The nucleotide sequence of the oligomers of the invention or the contiguous nucleotide sequence is preferably at least 80% homologous to a corresponding sequence selected from the group consisting of SEQ ID NOS: 2 - 16 or 17 - 28 or 110 - 124 or 125 - 136 or 149 - 160, such as at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96% homologous, at least 97%, at least 98%, at
30 least 99%, such as 100% homologous (identical).

The nucleotide sequence of the oligomers of the invention or the contiguous nucleotide sequence is preferably at least 80% homologous to the reverse complement of a corresponding sequence present in SEQ ID NO: 1, such as at least 85%, at least 90%, at

least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96% homologous, at least 97%, at least 98%, at least 99%, such as 100% homologous (identical).

The nucleotide sequence of the oligomers of the invention or the contiguous nucleotide sequence is preferably at least 80% complementary to a sub-sequence present in
5 SEQ ID NO: 1, such as at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96% complementary, at least 97%, at least 98%, at least 99%, such as 100% complementary (perfectly complementary).

In some embodiments the oligomer (or contiguous nucleotide portion thereof) is selected from, or comprises, one of the sequences selected from the group consisting of
10 SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26 and 28 or a sub-sequence of at least 10 contiguous nucleotides thereof, wherein said oligomer (or contiguous nucleotide portion thereof) may optionally comprise one, two, or three mismatches when compared to the sequence.

In some embodiments the oligomer (or contiguous nucleotide portion thereof) is
15 selected from, or comprises, one of the sequences selected from the group consisting of SEQ ID NOS: 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 28, 129, 130, 131, 132, 133, 134, 135 and 136 or a sub-sequence of at least 10 contiguous nucleotides thereof, wherein said oligomer (or contiguous nucleotide portion thereof) may optionally comprise one, two, or three mismatches when compared to the
20 sequence.

In some embodiments the oligomer (or contiguous nucleotide portion thereof) is selected from, or comprises, one of the sequences selected from the group consisting of SEQ ID NOS: 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159 and 160 or a sub-sequence of at least 10 contiguous nucleotides thereof, wherein said oligomer (or
25 contiguous nucleotide portion thereof) may optionally comprise one, two, or three mismatches when compared to the sequence.

In some embodiments the sub-sequence may consist of 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29 contiguous nucleotides, such as between 12 -22, such as between 12-18 nucleotides. Suitably, in some embodiments, the sub-sequence is
30 of the same length as the contiguous nucleotide sequence of the oligomer of the invention.

However, it is recognised that, in some embodiments the nucleotide sequence of the oligomer may comprise additional 5' or 3' nucleotides, such as, independently, 1, 2, 3, 4 or 5 additional nucleotides 5' and/or 3', which are non-complementary to the target sequence. In this respect the oligomer of the invention, may, in some embodiments, comprise a

contiguous nucleotide sequence which is flanked 5' and or 3' by additional nucleotides. In some embodiments the additional 5' or 3' nucleotides are naturally occurring nucleotides, such as DNA or RNA. In some embodiments, the additional 5' or 3' nucleotides may represent region D as referred to in the context of gapmer oligomers herein.

5 In some embodiments the oligomer (or contiguous nucleotide portion thereof) is selected from, or comprises, one of the sequences selected from the group consisting of SEQ ID NO 111, 112, 114, 115, 116, 118, 119, 122, 131, 132 and 136, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof, wherein said oligomer (or contiguous nucleotide portion thereof) may
10 optionally comprise one, two, or three mismatches against said selected sequence.

In some embodiments the oligomer (or contiguous nucleotide portion thereof) is selected from, or comprises, one of the sequences selected from the group consisting of SEQ ID NO 149, 150, 153, 154, 157, and 158; or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof, wherein
15 said oligomer (or contiguous nucleotide portion thereof) may optionally comprise one, two, or three mismatches against said selected sequence.

In some embodiments the oligomer (or contiguous nucleotide portion thereof) is selected from, or comprises, one of the sequences selected from the group consisting of SEQ ID NO 3, 4, 6, 7, 8, 10, 11, 14, 23, 24 and 28, or a sub-sequence of at least 10
20 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof, wherein said oligomer (or contiguous nucleotide portion thereof) may optionally comprise one, two, or three mismatches against said selected sequence.

In some embodiments the oligomer (or contiguous nucleotide portion thereof) is selected from, or comprises, one of the sequences selected from the group consisting of
25 SEQ ID NO 151, 152, 155, 156, 159 and 160; or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof, wherein said oligomer (or contiguous nucleotide portion thereof) may optionally comprise one, two, or three mismatches against said selected sequence.

In some embodiments the oligomer (or contiguous nucleotide portion thereof) is
30 selected from, or comprises, one of the sequences selected from the group consisting of SEQ ID NO: 57, 60, 64, 67, 70, 74, 77, 82, 87, 90 and 96, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof, wherein said oligomer (or contiguous nucleotide portion thereof) may optionally comprise one, two, or three mismatches against said selected sequence.

In some embodiments the oligomer (or contiguous nucleotide portion thereof) is selected from, or comprises, one of the sequences selected from the group consisting of SEQ ID NO: 87, 90 and 96, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof, wherein said oligomer (or
5 contiguous nucleotide portion thereof) may optionally comprise one, two, or three mismatches against said selected sequence.

In some embodiments the oligomer (or contiguous nucleotide portion thereof) is selected from, or comprises, one of the sequences selected from the group consisting of SEQ ID NO: 99, 100, 101, 102, 103, or 104, or a sub-sequence of at least 10 contiguous
10 nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof, wherein said oligomer (or contiguous nucleotide portion thereof) may optionally comprise one, two, or three mismatches against said selected sequence.

In some embodiments the oligomer (or contiguous nucleotide portion thereof) is selected from, or comprises, one of the sequences selected from the group consisting of
15 SEQ ID NO: 99, 100 or 104, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof, wherein said oligomer (or contiguous nucleotide portion thereof) may optionally comprise one, two, or three mismatches against said selected sequence.

In some embodiments the oligomer according to the invention consists or comprises of
20 a nucleotide sequence according to SEQ ID NO 2, such as SEQ ID NO 56, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 3, such as SEQ ID 57, 58 or 59, or a sub-
25 sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 4, such as SEQ ID NO 60, 61 and 62, or a sub-
30 sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 5, such as SEQ ID NO 63, or a sub-sequence
of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 6, such as SEQ ID NO 64, 65 and 66, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

5 In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 7, such as SEQ ID NO 67, 68 or 69, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

10 In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 8, such as SEQ ID 70, 71 or 72, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

15 In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 9, such as SEQ ID 73, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

20 In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 10, such as SEQ ID 74, 75 or 76, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 11, such as SEQ ID 77, 78 or 79, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

25 In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 12, such as SEQ ID 80, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

30 In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 13, such as SEQ ID 81 or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 14, such as SEQ ID 82, 83, or 84, or a sub-

sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 15, such as SEQ ID 85, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 16, such as SEQ ID 86, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 17, such as SEQ ID 87, 88 or 89, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 18, such as SEQ ID 90, 91 or 92, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 19, such as SEQ ID 93, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 20, such as SEQ ID 94, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 21, such as SEQ ID 95, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 22, such as SEQ ID 96, 97 or 98, or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 23, such as SEQ ID 99, 137 or 138 or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

5 In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 24, such as SEQ ID 100, 139 or 140 or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

10 In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 25, such as SEQ ID 101, 141 or 142 or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

15 In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 26, such as SEQ ID 102, 143 or 144 or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

20 In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 27, such as SEQ ID 103, 145 or 146 or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence according to SEQ ID 28, such as SEQ ID 104, 147 or 148 or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

25 In some embodiments the oligomer according to the invention consists or comprises of a nucleotide sequence selected from the group consisting of SEQ ID 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159 or 160 or a sub-sequence of at least 10 contiguous nucleotides thereof, such as 11, 12, 13, 14, 15 or 16 contiguous nucleotides thereof.

SEQ ID NO: 149*	GCTCAGTGATTTXAGAGAGAGGAT
SEQ ID NO: 150*	TTTCTCCTGCTXAGTGATTTCAGA
SEQ ID NO: 151*	GATTTXAGAGAGAGGA
SEQ ID NO: 152*	AGTGATTTXAGAGAGA
SEQ ID NO: 153*	ATCTTTCTCCTGCTXAGTGATTTC

SEQ ID NO: 154*	CAGTGATTTXAGAGAGAGGATCTC
SEQ ID NO: 155*	TCCTGCTXAGTGATTT
SEQ ID NO: 156*	TTCTCCTGCTXAGTGA
SEQ ID NO: 157†	AGCCACCATGAXGTGCATCATTCA
SEQ ID NO: 158†	TCCAGCCACCATGAXGTGCATCAT
SEQ ID NO: 159†	GCCACCATGAXGTGCA
SEQ ID NO: 160†	ACCATGAXGTGCATCA

*Where X is either a nucleobases other than C, such as A, G or T, preferably T.

† Where X is either a nucleobases other than T, such as A, G or C, preferably C.

In some embodiments, the oligomer according to the invention consists or comprises a nucleobase sequence selected from the following (5' – 3'):

5 (G)(A)(T)TTXAG(A)(G)(A)(G), wherein the nucleobases in brackets are optional, and wherein X is a nucleobases other than C, such as A, G or T, preferably T. See SEQ ID NOs 149 - 152, for example.

10 (C)(T)(G)CTXAG(T)(G)(G), wherein the nucleobases in brackets are optional, and wherein X is a nucleobases other than C, such as A, G or T, preferably T. See SEQ ID NOs 153 - 156, for example.

(C)(A)(T)GAXGT(G)(C)(A), wherein the nucleobases in brackets are optional, and wherein X is a nucleobases other than T, such as A, G or C, preferably C. See SEQ ID NOs 157 - 160, for example.

15 In some embodiments in the above embodiments X is a nucleobases in region B (gapmer or shortmer), such as a DNA nucleotide. Suitably X may be positioned as the middle nucleobases of region B, or has at least one, two, three or four other nucleobases of region B either 5' and/or at least one, two, three or four other nucleobases of region B 3' to X. Therefore, in some embodiments, X is not part of regions A, C or, where present D, or in some embodiments, is not a nucleobase of region B which is immediately adjacent to
20 regions A or C.

However, it is considered that, in some embodiments, the oligomer or contiguous nucleobase sequence may comprise one or more mismatches when compared to the nucleic acid which encodes the PIK3CA kinase polypeptide.

25 The oligomer of the invention, preferably, does not comprise more than four, such as not more than three, such as not more than two, such as not more than one mismatch, with the corresponding region of the sequence present in the nucleic acid which encodes the

PIK3CA kinase polypeptide, such as SEQ ID NO 1 or naturally occurring variants thereof, such as a allelic variants and spontaneous variants, such as the nucleic acids which encode the E524K, E545K and H1047R mutants, such as the G1781A, G1790A or A3297G spontaneous mutants of SEQ ID NO 1 (the residue letter before the position refers to the WT version, the letter after refers to the preferred mutant residue).

In one aspect the invention provides a method for the preparation of an oligomer for the down-regulation of a target mRNA associated with cancer cells, such as a PIK3CA mRNA target, said method comprising the steps of:

a) Identifying a single point mutation present in the target mRNA associated with cancer, wherein the single point mutation is present in said cancer cells but is absent in non-cancer cells.

b) Preparing an oligomer which is consists or comprises of a contiguous nucleobase sequence which is complimentary to said target mRNA associated with cancer, wherein said contiguous nucleobase sequence corresponds to a region of the target mRNA which comprises said single point mutation.

Suitably the single point mutation is associated to indicated with said cancer, such as the PIK3CA point mutations referred to herein.

Suitably the oligomer is a gapmer or shortmer oligonucleotide as described herein (although not limited necessarily to the oligomers targeting PIK3CA). As referred to herein, in some embodiments, the nucleobase residue present in such an oligomer which corresponds to the single point mutation is in region B.

In one aspect, it may be advantageous to specifically target regions of the mRNA target which comprise a point mutation associated to a cancer phenotype as it allows the design of oligomers which have a lower efficacy against the target in non-cancerous cells, as to those in cancerous cells, thereby allowing a differentiation between the effective treatment of cancerous cells and (reduced) negative effects on non-cancerous cells.

When determining "homology" between the oligomers of the invention (or contiguous nucleotide sequence) and the nucleic acid which encodes the mammalian PIK3CA or the reverse complement thereof, such as those disclosed herein, the determination of homology may be made by a simple alignment with the corresponding nucleotide sequence of the compound of the invention and the corresponding region of the nucleic acid which encodes the mammalian PIK3CA (or target nucleic acid), or the reverse complement thereof, and the homology is determined by counting the number of bases which align and dividing by the total number of contiguous nucleotides in the compound of the invention, and multiplying by

100. In such a comparison, if gaps exist, it is preferable that such gaps are merely mismatches rather than areas where the number of nucleotides within the gap differ between the nucleotide sequence of the invention and the target nucleic acid.

The terms "corresponding to" and "corresponds to" refer to the comparison between
5 the nucleotide sequence of the oligomer or contiguous nucleotide sequence (a first sequence) and the equivalent contiguous nucleotide sequence of a further sequence selected from either i) a sub-sequence of the reverse complement of the nucleic acid target, such as the mRNA which encodes the PIK3CA protein, such as SEQ ID NO: 1, and/or ii) the sequence of nucleotides provided herein such as the group consisting of SEQ ID NOS: 2 -
10 16 or 17 - 28 or 110 - 124 or 125 - 136 or 149 - 160, or sub-sequence thereof. Nucleotide analogues are compared directly to their equivalent or corresponding nucleotides. A first sequence which corresponds to a further sequence under i) or ii) typically is identical to that sequence over the length of the first sequence (such as the contiguous nucleotide sequence) or, as described herein may, in some embodiments, is at least 80% homologous
15 to a corresponding sequence, such as at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96% homologous, such as 100% homologous (identical).

The terms "corresponding nucleotide analogue" and "corresponding nucleotide" are intended to indicate that the nucleotide in the nucleotide analogue and the naturally
20 occurring nucleotide are identical. For example, when the 2-deoxyribose unit of the nucleotide is linked to an adenine, the "corresponding nucleotide analogue" contains a pentose unit (different from 2-deoxyribose) linked to an adenine.

Length

The oligomers comprise or consist of a contiguous nucleotide sequence of a total of
25 between 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 contiguous nucleotides in length.

In some embodiments, the oligomers comprise or consist of a contiguous nucleotide sequence of a total of between 10 - 22, such as 12 - 18, such as 13 - 17 or 12 - 16, such as 13, 14, 15, 16 contiguous nucleotides in length.

30 In some embodiments, the oligomers comprise or consist of a contiguous nucleotide sequence of a total of 10, 11, 12, 13, or 14 contiguous nucleotides in length.

In some embodiments, the oligomer according to the invention consists of no more than 22 nucleotides, such as no more than 20 nucleotides, such as no more than 18

nucleotides, such as 15, 16 or 17 nucleotides. In some embodiments the oligomer of the invention comprises less than 20 nucleotides.

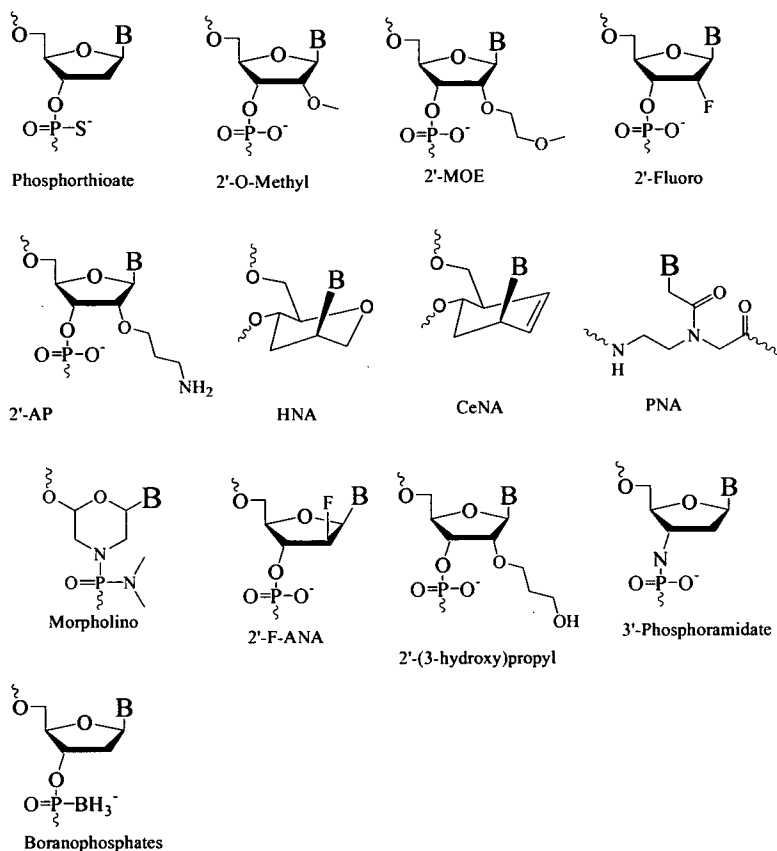
Nucleotide analogues

5 The term "nucleotide" as used herein, refers to a glycoside comprising a sugar moiety, a base moiety and a covalently linked phosphate group and covers both naturally occurring nucleotides, such as DNA or RNA, preferably DNA, and non-naturally occurring nucleotides comprising modified sugar and/or base moieties, which are also referred to as "nucleotide analogues" herein.

10 Non-naturally occurring nucleotides include nucleotides which have modified sugar moieties, such as bicyclic nucleotides or 2' modified nucleotides, such as 2' substituted nucleotides.

"Nucleotide analogues" are variants of natural nucleotides, such as DNA or RNA nucleotides, by virtue of modifications in the sugar and/or base moieties. Analogues could in principle be merely "silent" or "equivalent" to the natural nucleotides in the context of the oligonucleotide, *i.e.* have no functional effect on the way the oligonucleotide works to inhibit target gene expression. Such "equivalent" analogues may nevertheless be useful if, for example, they are easier or cheaper to manufacture, or are more stable to storage or manufacturing conditions, or represent a tag or label. Preferably, however, the analogues will have a functional effect on the way in which the oligomer works to inhibit expression; for example by producing increased binding affinity to the target and/or increased resistance to intracellular nucleases and/or increased ease of transport into the cell. Specific examples of nucleoside analogues are described by *e.g.* Freier & Altmann; *Nucl. Acid Res.*, 1997, 25, 4429-4443 and Uhlmann; *Curr. Opinion in Drug Development*, 2000, 3(2), 293-213, and in Scheme 1:

20



Scheme 1

The oligomer may thus comprise or consist of a simple sequence of natural occurring nucleotides – preferably 2'-deoxynucleotides (referred to here generally as “DNA”), but also possibly ribonucleotides (referred to here generally as “RNA”), or a combination of such naturally occurring nucleotides and one or more non-naturally occurring nucleotides, *i.e.* nucleotide analogues. Such nucleotide analogues may suitably enhance the affinity of the oligomer for the target sequence.

Examples of suitable and preferred nucleotide analogues are provided by

PCT/DK2006/000512 or are referenced therein.

Incorporation of affinity-enhancing nucleotide analogues in the oligomer, such as LNA or 2'-substituted sugars, can allow the size of the specifically binding oligomer to be reduced, and may also reduce the upper limit to the size of the oligomer before non-specific or aberrant binding takes place.

In some embodiments the oligomer comprises at least 2 nucleotide analogues. In some embodiments, the oligomer comprises from 3-8 nucleotide analogues, *e.g.* 6 or 7 nucleotide analogues. In the by far most preferred embodiments, at least one of said nucleotide analogues is a locked nucleic acid (LNA); for example at least 3 or at least 4, or

at least 5, or at least 6, or at least 7, or 8, of the nucleotide analogues may be LNA. In some embodiments all the nucleotides analogues may be LNA.

It will be recognised that when referring to a preferred nucleotide sequence motif or nucleotide sequence, which consists of only nucleotides, the oligomers of the invention which are defined by that sequence may comprise a corresponding nucleotide analogue in place of one or more of the nucleotides present in said sequence, such as LNA units or other nucleotide analogues, which raise the duplex stability/ T_m of the oligomer/target duplex (*i.e.* affinity enhancing nucleotide analogues).

In some embodiments, any mismatches between the nucleotide sequence of the oligomer and the target sequence are preferably found in regions outside the affinity enhancing nucleotide analogues, such as region B as referred to herein, and/or region D as referred to herein, and/or at the site of non modified such as DNA nucleotides in the oligonucleotide, and/or in regions which are 5' or 3' to the contiguous nucleotide sequence.

Examples of such modification of the nucleotide include modifying the sugar moiety to provide a 2'-substituent group or to produce a bridged (locked nucleic acid) structure which enhances binding affinity and may also provide increased nuclease resistance.

A preferred nucleotide analogue is LNA, such as oxy-LNA (such as beta-D-oxy-LNA, and alpha-L-oxy-LNA), and/or amino-LNA (such as beta-D-amino-LNA and alpha-L-amino-LNA) and/or thio-LNA (such as beta-D-thio-LNA and alpha-L-thio-LNA) and/or ENA (such as beta-D-ENA and alpha-L-ENA). Most preferred is beta-D-oxy-LNA.

In some embodiments the nucleotide analogues present within the oligomer of the invention (such as in regions A and C mentioned herein) are independently selected from, for example: 2'-O-alkyl-RNA units, 2'-amino-DNA units, 2'-fluoro-DNA units, LNA units, arabino nucleic acid (ANA) units, 2'-fluoro-ANA units, HNA units, INA (intercalating nucleic acid -Christensen, 2002. Nucl. Acids. Res. 2002 30: 4918-4925, hereby incorporated by reference) units and 2'MOE units. In some embodiments there is only one of the above types of nucleotide analogues present in the oligomer of the invention, or contiguous nucleotide sequence thereof.

In some embodiments the nucleotide analogues are 2'-O-methoxyethyl-RNA (2'MOE), 2'-fluoro-DNA monomers or LNA nucleotide analogues, and as such the oligonucleotide of the invention may comprise nucleotide analogues which are independently selected from these three types of analogue, or may comprise only one type of analogue selected from the three types. In some embodiments at least one of said nucleotide analogues is 2'-MOE-RNA, such as 2, 3, 4, 5, 6, 7, 8, 9 or 10 2'-MOE-RNA nucleotide units. In some

embodiments at least one of said nucleotide analogues is 2'-fluoro DNA, such as 2, 3, 4, 5, 6, 7, 8, 9 or 10 2'-fluoro-DNA nucleotide units.

In some embodiments, the oligomer according to the invention comprises at least one Locked Nucleic Acid (LNA) unit, such as 1, 2, 3, 4, 5, 6, 7, or 8 LNA units, such as between 3 – 7 or 4 to 8 LNA units, or 3, 4, 5, 6 or 7 LNA units. In some embodiments, all the nucleotide analogues are LNA. In some embodiments, the oligomer may comprise both beta-D-oxy-LNA, and one or more of the following LNA units: thio-LNA, amino-LNA, oxy-LNA, and/or ENA in either the beta-D or alpha-L configurations or combinations thereof. In some embodiments all LNA cytosine units are 5'methyl-Cytosine. In some embodiments of the invention, the oligomer may comprise both LNA and DNA units. Preferably the combined total of LNA and DNA units is 10-25, preferably 10-20, even more preferably 12-16. In some embodiments of the invention, the nucleotide sequence of the oligomer, such as the contiguous nucleotide sequence consists of at least one LNA and the remaining nucleotide units are DNA units. In some embodiments the oligomer comprises only LNA nucleotide analogues and naturally occurring nucleotides (such as RNA or DNA, most preferably DNA nucleotides), optionally with modified internucleotide linkages such as phosphorothioate.

The term "nucleobase" refers to the base moiety of a nucleotide and covers both naturally occurring as well as non-naturally occurring variants. Thus, "nucleobase" covers not only the known purine and pyrimidine heterocycles but also heterocyclic analogues and tautomers thereof.

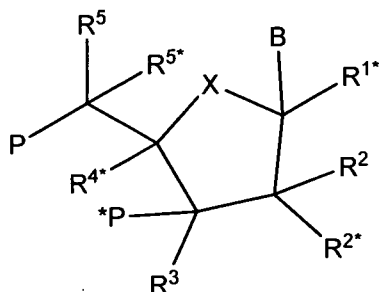
Examples of nucleobases include, but are not limited to adenine, guanine, cytosine, thymidine, uracil, xanthine, hypoxanthine, 5-methylcytosine, isocytosine, pseudoisocytosine, 5-bromouracil, 5-propynyluracil, 6-aminopurine, 2-aminopurine, inosine, diaminopurine, and 2-chloro-6-aminopurine.

In some embodiments, at least one of the nucleobases present in the oligomer is a modified nucleobase selected from the group consisting of 5-methylcytosine, isocytosine, pseudoisocytosine, 5-bromouracil, 5-propynyluracil, 6-aminopurine, 2-aminopurine, inosine, diaminopurine, and 2-chloro-6-aminopurine.

LNA

The term "LNA" refers to a bicyclic nucleotide analogue, known as "Locked Nucleic Acid". It may refer to an LNA monomer, or, when used in the context of an "LNA oligonucleotide" refers to an oligonucleotide containing one or more such bicyclic nucleotide analogues.

The LNA used in the oligonucleotide compounds of the invention preferably has the structure of the general formula I



wherein X is selected from -O-, -S-, -N(R^{N*})-, -C(R⁶R^{6*})-;

- 5 B is selected from hydrogen, optionally substituted C₁₋₄-alkoxy, optionally substituted C₁₋₄-alkyl, optionally substituted C₁₋₄-acyloxy, nucleobases, DNA intercalators, photochemically active groups, thermochemically active groups, chelating groups, reporter groups, and ligands;

- 10 P designates the radical position for an internucleotide linkage to a succeeding monomer, or a 5'-terminal group, such internucleotide linkage or 5'-terminal group optionally including the substituent R⁵ or equally applicable the substituent R^{5*};

P* designates an internucleotide linkage to a preceding monomer, or a 3'-terminal group;

- 15 R^{4*} and R^{2*} together designate a biradical consisting of 1-4 groups/atoms selected from -C(R^aR^b)-, -C(R^a)=C(R^b)-, -C(R^a)=N-, -O-, -Si(R^a)₂-, -S-, -SO₂-, -N(R^a)-, and >C=Z,

- 20 wherein Z is selected from -O-, -S-, and -N(R^a)-, and R^a and R^b each is independently selected from hydrogen, optionally substituted C₁₋₁₂-alkyl, optionally substituted C₂₋₁₂-alkenyl, optionally substituted C₂₋₁₂-alkynyl, hydroxy, C₁₋₁₂-alkoxy, C₂₋₁₂-alkoxyalkyl, C₂₋₁₂-alkenyloxy, carboxy, C₁₋₁₂-alkoxycarbonyl, C₁₋₁₂-alkylcarbonyl, formyl, aryl, aryloxy-carbonyl, aryloxy, arylcarbonyl, heteroaryl, heteroaryloxy-carbonyl, heteroaryloxy, heteroarylcarbonyl, amino, mono- and di(C₁₋₆-alkyl)amino, carbamoyl, mono- and di(C₁₋₆-alkyl)-amino-carbonyl, amino-C₁₋₆-alkyl-aminocarbonyl, mono- and di(C₁₋₆-alkyl)amino-C₁₋₆-alkyl-aminocarbonyl, C₁₋₆-alkyl-carbonylamino, carbamido, C₁₋₆-alkanoyloxy, sulphono, C₁₋₆-alkylsulphonyloxy, nitro, azido, sulphanyl, C₁₋₆-alkylthio, halogen, DNA intercalators, photochemically active groups, thermochemically active groups, chelating groups, reporter groups, and ligands, where aryl and heteroaryl may be optionally substituted and where two geminal substituents R^a and R^b together may designate optionally substituted methylene (=CH₂), and each of the substituents R^{1*}, R², R³, R⁵, R^{5*}, R⁶ and R^{6*}, which are present is independently selected
- 25

from hydrogen, optionally substituted C₁₋₁₂-alkyl, optionally substituted C₂₋₁₂-alkenyl, optionally substituted C₂₋₁₂-alkynyl, hydroxy, C₁₋₁₂-alkoxy, C₂₋₁₂-alkoxyalkyl, C₂₋₁₂-alkenyloxy, carboxy, C₁₋₁₂-alkoxycarbonyl, C₁₋₁₂-alkylcarbonyl, formyl, aryl, aryloxy-carbonyl, aryloxy, arylcarbonyl, heteroaryl, heteroaryloxy-carbonyl, heteroaryloxy, heteroarylcarbonyl, amino, 5 mono- and di(C₁₋₆-alkyl)amino, carbamoyl, mono- and di(C₁₋₆-alkyl)-amino-carbonyl, amino-C₁₋₆-alkyl-aminocarbonyl, mono- and di(C₁₋₆-alkyl)amino-C₁₋₆-alkyl-aminocarbonyl, C₁₋₆-alkyl-carbonylamino, carbamido, C₁₋₆-alkanoyloxy, sulphono, C₁₋₆-alkylsulphonyloxy, nitro, azido, sulphanyl, C₁₋₆-alkylthio, halogen, DNA intercalators, photochemically active groups, thermochemically active groups, chelating groups, reporter groups, and ligands, where aryl 10 and heteroaryl may be optionally substituted, and where two geminal substituents together may designate oxo, thioxo, imino, or optionally substituted methylene, or together may form a spiro biradical consisting of a 1-5 carbon atom(s) alkylene chain which is optionally interrupted and/or terminated by one or more heteroatoms/groups selected from -O-, -S-, and -(NR^N)- where R^N is selected from hydrogen and C₁₋₄-alkyl, and where two adjacent 15 (non-geminal) substituents may designate an additional bond resulting in a double bond; and R^{N*}, when present and not involved in a biradical, is selected from hydrogen and C₁₋₄-alkyl; and basic salts and acid addition salts thereof;

In some embodiments R^{5*} is selected from H, -CH₃, -CH₂-CH₃, -CH₂-O-CH₃, and -CH=CH₂.

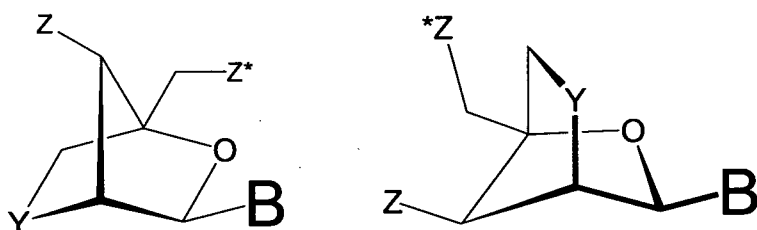
20 In some embodiments, R^{4*} and R^{2*} together designate a biradical selected from -C(R^aR^b)-O-, -C(R^aR^b)-C(R^cR^d)-O-, -C(R^aR^b)-C(R^cR^d)-C(R^eR^f)-O-, -C(R^aR^b)-O-C(R^cR^d)-, -C(R^aR^b)-O-C(R^cR^d)-O-, -C(R^aR^b)-C(R^cR^d)-, -C(R^aR^b)-C(R^cR^d)-C(R^eR^f)-, -C(R^a)=C(R^b)-C(R^cR^d)-, -C(R^aR^b)-N(R^c)-, -C(R^aR^b)-C(R^cR^d)-N(R^e)-, -C(R^aR^b)-N(R^c)-O-, and -C(R^aR^b)-S-, -C(R^aR^b)-C(R^cR^d)-S-, wherein R^a, R^b, R^c, R^d, R^e, and R^f each is independently 25 selected from hydrogen, optionally substituted C₁₋₁₂-alkyl, optionally substituted C₂₋₁₂-alkenyl, optionally substituted C₂₋₁₂-alkynyl, hydroxy, C₁₋₁₂-alkoxy, C₂₋₁₂-alkoxyalkyl, C₂₋₁₂-alkenyloxy, carboxy, C₁₋₁₂-alkoxycarbonyl, C₁₋₁₂-alkylcarbonyl, formyl, aryl, aryloxy-carbonyl, aryloxy, arylcarbonyl, heteroaryl, heteroaryloxy-carbonyl, heteroaryloxy, heteroarylcarbonyl, amino, mono- and di(C₁₋₆-alkyl)amino, carbamoyl, mono- and di(C₁₋₆-alkyl)-amino-carbonyl, amino- 30 C₁₋₆-alkyl-aminocarbonyl, mono- and di(C₁₋₆-alkyl)amino-C₁₋₆-alkyl-aminocarbonyl, C₁₋₆-alkyl-carbonylamino, carbamido, C₁₋₆-alkanoyloxy, sulphono, C₁₋₆-alkylsulphonyloxy, nitro, azido, sulphanyl, C₁₋₆-alkylthio, halogen, DNA intercalators, photochemically active groups, thermochemically active groups, chelating groups, reporter groups, and ligands, where aryl

and heteroaryl may be optionally substituted and where two geminal substituents R^a and R^b together may designate optionally substituted methylene ($=CH_2$),

In a further embodiment R^{4*} and R^{2*} together designate a biradical (bivalent group) selected from $-CH_2-O-$, $-CH_2-S-$, $-CH_2-NH-$, $-CH_2-N(CH_3)-$, $-CH_2-CH_2-O-$, $-CH_2-CH(CH_3)-$, $-CH_2-CH_2-S-$, $-CH_2-CH_2-NH-$, $-CH_2-CH_2-CH_2-$, $-CH_2-CH_2-CH_2-O-$, $-CH_2-CH_2-CH(CH_3)-$, $-CH=CH-CH_2-$, $-CH_2-O-CH_2-O-$, $-CH_2-NH-O-$, $-CH_2-N(CH_3)-O-$, $-CH_2-O-CH_2-$, $-CH(CH_3)-O-$, $-CH(CH_2-O-CH_3)-O-$.

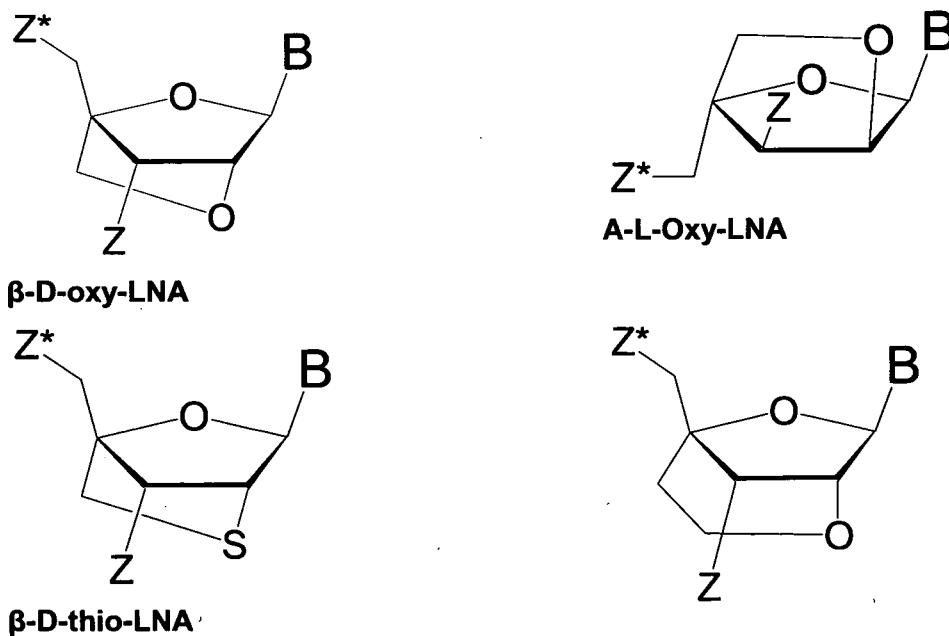
For all chiral centers, asymmetric groups may be found in either *R* or *S* orientation.

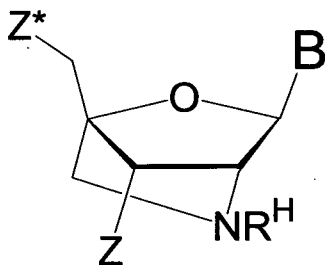
10 Preferably, the LNA used in the oligomer of the invention comprises at least one LNA unit according to any of the formulas



wherein Y is $-O-$, $-O-CH_2-$, $-S-$, $-NH-$, or $N(R^H)$; Z and Z^* are independently selected among an internucleotide linkage, a terminal group or a protecting group; B constitutes a natural or non-natural nucleotide base moiety, and R^H is selected from hydrogen and C_{1-4} -alkyl.

Specifically preferred LNA units are shown in scheme 2:



B-D-ENA **β -D-amino-LNA****Scheme 2**

The term "thio-LNA" comprises a locked nucleotide in which Y in the general formula above is selected from S or $-\text{CH}_2\text{-S-}$. Thio-LNA can be in both beta-D and alpha-L-configuration.

- 5 The term "amino-LNA" comprises a locked nucleotide in which Y in the general formula above is selected from $-\text{N}(\text{H})-$, $\text{N}(\text{R})-$, $\text{CH}_2\text{-N}(\text{H})-$, and $-\text{CH}_2\text{-N}(\text{R})-$ where R is selected from hydrogen and C_{1-4} -alkyl. Amino-LNA can be in both beta-D and alpha-L-configuration.

- 10 The term "oxy-LNA" comprises a locked nucleotide in which Y in the general formula above represents $-\text{O-}$ or $-\text{CH}_2\text{-O-}$. Oxy-LNA can be in both beta-D and alpha-L-configuration.

The term "ENA" comprises a locked nucleotide in which Y in the general formula above is $-\text{CH}_2\text{-O-}$ (where the oxygen atom of $-\text{CH}_2\text{-O-}$ is attached to the 2'-position relative to the base B).

- 15 In a preferred embodiment LNA is selected from beta-D-oxy-LNA, alpha-L-oxy-LNA, beta-D-amino-LNA and beta-D-thio-LNA, in particular beta-D-oxy-LNA.

RNase recruitment

- 20 It is recognised that an oligomeric compound may function via non RNase mediated degradation of target mRNA, such as by steric hindrance of translation, or other methods, however, the preferred oligomers of the invention are capable of recruiting an endoribonuclease (RNase), such as RNase H.

- 25 It is preferable that the oligomer, or contiguous nucleotide sequence, comprises of a region of at least 6, such as at least 7 consecutive nucleotide units, such as at least 8 or at least 9 consecutive nucleotide units (residues), including 7, 8, 9, 10, 11, 12, 13, 14, 15 or 16 consecutive nucleotides, which, when formed in a duplex with the complementary target RNA is capable of recruiting RNase. The contiguous sequence which is capable of

recruiting RNase may be region B as referred to in the context of a gapmer as described herein. In some embodiments the size of the contiguous sequence which is capable of recruiting RNase, such as region B, may be higher, such as 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 nucleotide units.

5 EP 1 222 309 provides *in vitro* methods for determining RNaseH activity, which may be used to determine the ability to recruit RNaseH. A oligomer is deemed capable of recruiting RNase H if, when provided with the complementary RNA target, it has an initial rate, as measured in pmol//min, of at least 1 %, such as at least 5%, such as at least 10% or less than 20% of the equivalent DNA only oligonucleotide, with no 2' substitutions, with
10 phosphorothioate linkage groups between all nucleotides in the oligonucleotide, using the methodology provided by Example 91 - 95 of EP 1 222 309.

In some embodiments, an oligomer is deemed essentially incapable of recruiting RNaseH if, when provided with the complementary RNA target, and RNaseH, the RNaseH initial rate, as measured in pmol//min, is less than 1%, such as less than 5%, such as less
15 than 10% or less than 20% of the initial rate determined using the equivalent DNA only oligonucleotide, with no 2' substitutions, with phosphorothioate linkage groups between all nucleotides in the oligonucleotide, using the methodology provided by Example 91 - 95 of EP 1 222 309.

In other embodiments, an oligomer is deemed capable of recruiting RNaseH if, when
20 provided with the complementary RNA target, and RNaseH, the RNaseH initial rate, as measured in pmol//min, is at least 20%, such as at least 40 %, such as at least 60 %, such as at least 80 % of the initial rate determined using the equivalent DNA only oligonucleotide, with no 2' substitutions, with phosphorothioate linkage groups between all nucleotides in the oligonucleotide, using the methodology provided by Example 91 - 95 of EP 1 222 309.

25 Typically the region of the oligomer which forms the consecutive nucleotide units which, when formed in a duplex with the complementary target RNA is capable of recruiting RNase consists of nucleotide units which form a DNA/RNA like duplex with the RNA target – and include both DNA units and LNA units which are in the alpha-L configuration, particularly preferred being alpha-L-oxy LNA.

30 The oligomer of the invention may comprise a nucleotide sequence which comprises both nucleotides and nucleotide analogues, and may be in the form of a gapmer, a headmer or a mixmer.

A headmer is defined by a contiguous stretch of non-RNase recruiting nucleotide analogues at the 5'-end followed by a contiguous stretch of DNA or modified nucleotide units

recognizable and cleavable by the RNase towards the 3'-end (such as at least 7 such nucleotides), and a tailmer is defined by a contiguous stretch of DNA or modified nucleotides recognizable and cleavable by the RNase at the 5'-end (such as at least 7 such nucleotides), followed by a contiguous stretch of non-RNase recruiting nucleotide analogues towards the 3'-end. Other chimeras according to the invention, called mixmers consisting of an alternate composition of DNA or modified nucleotides recognizable and cleavable by RNase and non-RNase recruiting nucleotide analogues. Some nucleotide analogues may also be able to mediate RNaseH binding and cleavage. Since α -L-LNA recruits RNaseH activity to a certain extent, smaller gaps of DNA or modified nucleotides recognizable and cleavable by the RNaseH for the gapmer construct might be required, and more flexibility in the mixmer construction might be introduced.

Gapmer Design

Preferably, the oligomer of the invention is a gapmer. A gapmer oligomer is an oligomer which comprises a contiguous stretch of nucleotides which is capable of recruiting an RNase, such as RNaseH, such as a region of at least 6 or 7 DNA nucleotides, referred to herein in as region B, wherein region B is flanked both 5' and 3' by regions of affinity enhancing nucleotide analogues, such as between 1 – 6 nucleotide analogues 5' and 3' to the contiguous stretch of nucleotides which is capable of recruiting RNase – these regions are referred to as regions A and C respectively.

Preferably the gapmer comprises a (poly)nucleotide sequence of formula (5' to 3'), A-B-C, or optionally A-B-C-D or D-A-B-C, wherein; region A (5' region) consists or comprises of at least one nucleotide analogue, such as at least one LNA unit, such as between 1-6 nucleotide analogues, such as LNA units, and; region B consists or comprises of at least five consecutive nucleotides which are capable of recruiting RNase (when formed in a duplex with a complementary RNA molecule, such as the mRNA target), such as DNA nucleotides, and; region C (3' region) consists or comprises of at least one nucleotide analogue, such as at least one LNA unit, such as between 1-6 nucleotide analogues, such as LNA units, and; region D, when present consists or comprises of 1, 2 or 3 nucleotide units, such as DNA nucleotides.

In some embodiments, region A consists of 1, 2, 3, 4, 5 or 6 nucleotide analogues, such as LNA units, such as between 2-5 nucleotide analogues, such as 2-5 LNA units, such as 3 or 4 nucleotide analogues, such as 3 or 4 LNA units; and/or region C consists of 1, 2, 3, 4, 5 or 6 nucleotide analogues, such as LNA units, such as between 2-5 nucleotide

analogues, such as 2-5 LNA units, such as 3 or 4 nucleotide analogues, such as 3 or 4 LNA units.

In some embodiments B consists or comprises of 5, 6, 7, 8, 9, 10, 11 or 12 consecutive nucleotides which are capable of recruiting RNase, or between 6-10, or
5 between 7-9, such as 8 consecutive nucleotides which are capable of recruiting RNase. In some embodiments region B consists or comprises at least one DNA nucleotide unit, such as 1-12 DNA units, preferably between 4-12 DNA units, more preferably between 6-10 DNA units, such as between 7-10 DNA units, most preferably 8, 9 or 10 DNA units.

In some embodiments region A consist of 3 or 4 nucleotide analogues, such as LNA,
10 region B consists of 7, 8, 9 or 10 DNA units, and region C consists of 3 or 4 nucleotide analogues, such as LNA. Such designs include (A-B-C) 3-10-3, 3-10-4, 4-10-3, 3-9-3, 3-9-4, 4-9-3, 3-8-3, 3-8-4, 4-8-3, 3-7-3, 3-7-4, 4-7-3, and may further include region D, which may have one or 2 nucleotide units, such as DNA units.

Further gapmer designs are disclosed in WO2004/046160 and are hereby
15 incorporated by reference.

US provisional application, 60/977409, hereby incorporated by reference, refers to 'shortmer' gapmer oligomers, which, in some embodiments may be the gapmer oligomer according to the present invention.

In some embodiments the oligomer is consisting of a contiguous nucleotide sequence
20 of a total of 10, 11, 12, 13 or 14 nucleotide units, wherein the contiguous nucleotide sequence is of formula (5' – 3'), A-B-C, or optionally A-B-C-D or D-A-B-C, wherein; A consists of 1, 2 or 3 nucleotide analogue units, such as LNA units; B consists of 7, 8 or 9 contiguous nucleotide units which are capable of recruiting RNase when formed in a duplex with a complementary RNA molecule (such as a mRNA target); and C consists of 1, 2 or 3
25 nucleotide analogue units, such as LNA units. When present, D consists of a single DNA unit.

In some embodiments A consists of 1 LNA unit. In some embodiments A consists of 2 LNA units. In some embodiments A consists of 3 LNA units. In some embodiments C consists of 1 LNA unit. In some embodiments C consists of 2 LNA units. In some
30 embodiments C consists of 3 LNA units. In some embodiments B consists of 7 nucleotide units. In some embodiments B consists of 8 nucleotide units. In some embodiments B consists of 9 nucleotide units. In some embodiments B comprises of between 1 – 9 DNA units, such as 2, 3, 4, 5, 6, 7 or 8 DNA units. In some embodiments B consists of DNA units. In some embodiments B comprises of at least one LNA unit which is in the alpha-L

configuration, such as 2, 3, 4, 5, 6, 7, 8 or 9 LNA units in the alpha-L-configuration. In some embodiments B comprises of at least one alpha-L-oxy LNA unit or wherein all the LNA units in the alpha-L- configuration are alpha-L-oxy LNA units. In some embodiments the number of nucleotides present in A-B-C are selected from the group consisting of (nucleotide analogue units – region B – nucleotide analogue units): 1-8-1, 1-8-2, 2-8-1, 2-8-2, 3-8-3, 2-8-3, 3-8-2, 4-8-1, 4-8-2, 1-8-4, 2-8-4, or; 1-9-1, 1-9-2, 2-9-1, 2-9-2, 2-9-3, 3-9-2, 1-9-3, 3-9-1, 4-9-1, 1-9-4, or; 1-10-1, 1-10-2, 2-10-1, 2-10-2, 1-10-3, 3-10-1. In some embodiments the number of nucleotides in A-B-C are selected from the group consisting of: 2-7-1, 1-7-2, 2-7-2, 3-7-3, 2-7-3, 3-7-2, 3-7-4, and 4-7-3. In some embodiments both A and C consists of two LNA units each, and B consists of 8 or 9 nucleotide units, preferably DNA units.

Internucleotide Linkages

The terms "linkage group" or "internucleotide linkage" are intended to mean a group capable of covalently coupling together two nucleotides, two nucleotide analogues, and a nucleotide and a nucleotide analogue, etc. Specific and preferred examples include phosphate groups and phosphorothioate groups.

The nucleotides of the oligomer of the invention or contiguous nucleotides sequence thereof are coupled together via linkage groups. Suitably each nucleotide is linked to the 3' adjacent nucleotide via a linkage group.

Suitable internucleotide linkages include those listed within PCT/DK2006/000512, for example the internucleotide linkages listed on the first paragraph of page 34 of PCT/DK2006/000512 (hereby incorporated by reference).

It is, in some embodiments, preferred to modify the internucleotide linkage from its normal phosphodiester to one that is more resistant to nuclease attack, such as phosphorothioate or boranophosphate – these two, being cleavable by RNase H, also allow that route of antisense inhibition in reducing the expression of the target gene.

Suitable sulphur (S) containing internucleotide linkages as provided herein may be preferred. Phosphorothioate internucleotide linkages are also preferred, particularly for the gap region (B) of gapmers. Phosphorothioate linkages may also be used for the flanking regions (A and C, and for linking A or C to D, and within region D, as appropriate).

Regions A, B and C, may however comprise internucleotide linkages other than phosphorothioate, such as phosphodiester linkages, particularly, for instance when the use of nucleotide analogues protects the internucleotide linkages within regions A and C from endo-nuclease degradation – such as when regions A and C comprise LNA nucleotides.

The internucleotide linkages in the oligomer may be phosphodiester, phosphorothioate or boranophosphate so as to allow RNase H cleavage of targeted RNA. Phosphorothioate is preferred, for improved nuclease resistance and other reasons, such as ease of manufacture.

5 In one aspect of the oligomer of the invention, the nucleotides and/or nucleotide analogues are linked to each other by means of phosphorothioate groups.

It is recognised that the inclusion of phosphodiester linkages, such as one or two linkages, into an otherwise phosphorothioate oligomer, particularly between or adjacent to nucleotide analogue units (typically in region A and or C) can modify the bioavailability and/or bio-distribution of an oligomer – see WO2008/053314, hereby incorporated by
10 reference.

In some embodiments, such as the embodiments referred to above, where suitable and not specifically indicated, all remaining linkage groups are either phosphodiester or phosphorothioate, or a mixture thereof.

15 In some embodiments all the internucleotide linkage groups are phosphorothioate.

When referring to specific gapmer oligonucleotide sequences, such as those provided herein it will be understood that, in various embodiments, when the linkages are phosphorothioate linkages, alternative linkages, such as those disclosed herein may be used, for example phosphate (phosphodiester) linkages may be used, particularly for linkages between
20 nucleotide analogues, such as LNA, units. Likewise, when referring to specific gapmer oligonucleotide sequences, such as those provided herein, when the C residues are annotated as 5'methyl modified cytosine, in various embodiments, one or more of the Cs present in the oligomer may be unmodified C residues. in some embodiments in some embodiments

25 ***Oligomeric Compounds***

The oligomers of the invention may, for example, be selected from the group consisting of: 29 – 55 or 56 – 148. Particularly preferred compounds include, but are not necessarily limited to, SEQ ID NOs 67 and 77.

Conjugates

30 In the context the term "conjugate" is intended to indicate a heterogenous molecule formed by the covalent attachment ("conjugation") of the oligomer as described herein to one or more non-nucleotide, or non-polynucleotide moieties. Examples of non-nucleotide or non- polynucleotide moieties include macromolecular agents such as proteins, fatty acid

chains, sugar residues, glycoproteins, polymers, or combinations thereof. Typically proteins may be antibodies for a target protein. Typical polymers may be polyethylene glycol.

Therefore, in various embodiments, the oligomer of the invention may comprise both a polynucleotide region which typically consists of a contiguous sequence of nucleotides, and
5 a further non-nucleotide region. When referring to the oligomer of the invention consisting of a contiguous nucleotide sequence, the compound may comprise non-nucleotide components, such as a conjugate component.

In some embodiments of the invention the oligomer (compound) is linked to a ligand or conjugate. For example in order to increase the cellular uptake of the oligomer. In some
10 embodiments the conjugate is a sterols, such as cholesterol.

The oligomers of the invention may also be conjugated to active drug substances, for example, aspirin, ibuprofen, a sulfa drug, an antidiabetic, an antibacterial or an antibiotic.

In various embodiments of the invention the oligomeric compound is linked to ligands/conjugates, which may be used, e.g. to increase the cellular uptake of oligomeric
15 compounds. WO2007/031091 provides suitable ligands and conjugates, which are hereby incorporated by reference.

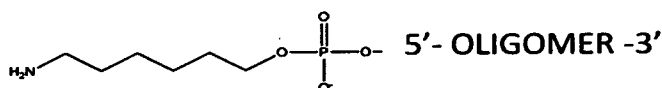
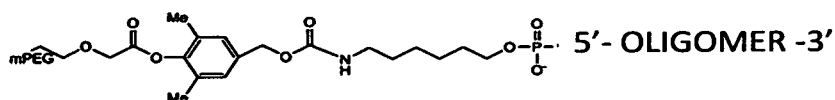
The invention also provides for a conjugate comprising the compound according to the invention as herein described, and at least one non-nucleotide or non-polynucleotide moiety covalently attached to said compound. Therefore, in various embodiments where the
20 compound of the invention consists of a specified nucleic acid or nucleotide sequence, as herein disclosed, the compound may also comprise at least one non-nucleotide or non-polynucleotide moiety (e.g. not comprising one or more nucleotides or nucleotide analogues) covalently attached to said compound.

Conjugation (to a conjugate moiety) may enhance the activity, cellular distribution or
25 cellular uptake of the oligomer of the invention. Such moieties include, but are not limited to, antibodies, polypeptides, lipid moieties such as a cholesterol moiety, cholic acid, a thioether, e.g. Hexyl-s-tritylthiol, a thiocholesterol, an aliphatic chain, e.g., dodecandiol or undecyl residues, a phospholipids, e.g., di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-o-hexadecyl-rac-glycero-3-h-phosphonate, a polyamine or a polyethylene glycol chain, an
30 adamantane acetic acid, a palmityl moiety, an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety.

The oligomers of the invention may also be conjugated to active drug substances, for example, aspirin, ibuprofen, a sulfa drug, an antidiabetic, an antibacterial or an antibiotic.

In certain embodiments the conjugated moiety is a sterol, such as cholesterol.

In various embodiments, the conjugated moiety comprises or consists of a positively charged polymer, such as a positively charged peptides of, for example between 1 -50, such as 2 – 20 such as 3 – 10 amino acid residues in length, and/or polyalkylene oxide such as polyethylglycol(PEG) or polypropylene glycol – see WO 2008/034123, hereby incorporated by reference. Suitably the positively charged polymer, such as a polyalkylene oxide may be attached to the oligomer of the invention via a linker such as the releasable inker described in WO 2008/034123. By way of example, the following conjugate moieties may be used in the conjugates of the invention:



10 **Activated oligomers**

The term “activated oligomer,” as used herein, refers to an oligomer of the invention that is covalently linked (i.e., functionalized) to at least one functional moiety that permits covalent linkage of the oligomer to one or more conjugated moieties, i.e., moieties that are not themselves nucleic acids or monomers, to form the conjugates herein described.

15 Typically, a functional moiety will comprise a chemical group that is capable of covalently bonding to the oligomer via, e.g., a 3'-hydroxyl group or the exocyclic NH₂ group of the adenine base, a spacer that is preferably hydrophilic and a terminal group that is capable of binding to a conjugated moiety (e.g., an amino, sulfhydryl or hydroxyl group). In some embodiments, this terminal group is not protected, e.g., is an NH₂ group. In other

20 embodiments, the terminal group is protected, for example, by any suitable protecting group such as those described in “Protective Groups in Organic Synthesis” by Theodora W Greene and Peter G M Wuts, 3rd edition (John Wiley & Sons, 1999). Examples of suitable hydroxyl protecting groups include esters such as acetate ester, aralkyl groups such as benzyl, diphenylmethyl, or triphenylmethyl, and tetrahydropyranyl. Examples of suitable

25 amino protecting groups include benzyl, alpha-methylbenzyl, diphenylmethyl, triphenylmethyl, benzyloxycarbonyl, tert-butoxycarbonyl, and acyl groups such as trichloroacetyl or trifluoroacetyl. In some embodiments, the functional moiety is self-cleaving. In other embodiments, the functional moiety is biodegradable. See e.g., U.S. Patent No. 7,087,229, which is incorporated by reference herein in its entirety.

In some embodiments, oligomers of the invention are functionalized at the 5' end in order to allow covalent attachment of the conjugated moiety to the 5' end of the oligomer. In other embodiments, oligomers of the invention can be functionalized at the 3' end. In still other embodiments, oligomers of the invention can be functionalized along the backbone or on the heterocyclic base moiety. In yet other embodiments, oligomers of the invention can be functionalized at more than one position independently selected from the 5' end, the 3' end, the backbone and the base.

In some embodiments, activated oligomers of the invention are synthesized by incorporating during the synthesis one or more monomers that is covalently attached to a functional moiety. In other embodiments, activated oligomers of the invention are synthesized with monomers that have not been functionalized, and the oligomer is functionalized upon completion of synthesis. In some embodiments, the oligomers are functionalized with a hindered ester containing an aminoalkyl linker, wherein the alkyl portion has the formula $(\text{CH}_2)_w$, wherein w is an integer ranging from 1 to 10, preferably about 6, wherein the alkyl portion of the alkylamino group can be straight chain or branched chain, and wherein the functional group is attached to the oligomer via an ester group $(-\text{O}-\text{C}(\text{O})-(\text{CH}_2)_w\text{NH})$.

In other embodiments, the oligomers are functionalized with a hindered ester containing a $(\text{CH}_2)_w$ -sulfhydryl (SH) linker, wherein w is an integer ranging from 1 to 10, preferably about 6, wherein the alkyl portion of the alkylamino group can be straight chain or branched chain, and wherein the functional group attached to the oligomer via an ester group $(-\text{O}-\text{C}(\text{O})-(\text{CH}_2)_w\text{SH})$

In some embodiments, sulfhydryl-activated oligonucleotides are conjugated with polymer moieties such as polyethylene glycol or peptides (via formation of a disulfide bond).

Activated oligomers containing hindered esters as described above can be synthesized by any method known in the art, and in particular by methods disclosed in PCT Publication No. WO 2008/034122 and the examples therein, which is incorporated herein by reference in its entirety.

In still other embodiments, the oligomers of the invention are functionalized by introducing sulfhydryl, amino or hydroxyl groups into the oligomer by means of a functionalizing reagent substantially as described in U.S. Patent Nos. 4,962,029 and 4,914,210, i.e., a substantially linear reagent having a phosphoramidite at one end linked through a hydrophilic spacer chain to the opposing end which comprises a protected or unprotected sulfhydryl, amino or hydroxyl group. Such reagents primarily react with hydroxyl

groups of the oligomer. In some embodiments, such activated oligomers have a functionalizing reagent coupled to a 5'-hydroxyl group of the oligomer. In other embodiments, the activated oligomers have a functionalizing reagent coupled to a 3'-hydroxyl group. In still other embodiments, the activated oligomers of the invention have a functionalizing reagent coupled to a hydroxyl group on the backbone of the oligomer. In yet further embodiments, the oligomer of the invention is functionalized with more than one of the functionalizing reagents as described in U.S. Patent Nos. 4,962,029 and 4,914,210, incorporated herein by reference in their entirety. Methods of synthesizing such functionalizing reagents and incorporating them into monomers or oligomers are disclosed in U.S. Patent Nos. 4,962,029 and 4,914,210.

In some embodiments, the 5'-terminus of a solid-phase bound oligomer is functionalized with a dienyl phosphoramidite derivative, followed by conjugation of the deprotected oligomer with, e.g., an amino acid or peptide via a Diels-Alder cycloaddition reaction.

In various embodiments, the incorporation of monomers containing 2'-sugar modifications, such as a 2'-carbamate substituted sugar or a 2'-(O-pentyl-N-phthalimido)-deoxyribose sugar into the oligomer facilitates covalent attachment of conjugated moieties to the sugars of the oligomer. In other embodiments, an oligomer with an amino-containing linker at the 2'-position of one or more monomers is prepared using a reagent such as, for example, 5'-dimethoxytrityl-2'-O-(e-phthalimidylaminopentyl)-2'-deoxyadenosine-3'-N,N-diisopropyl-cyanoethoxy phosphoramidite. See, e.g., Manoharan, et al., Tetrahedron Letters, 1991, 34, 7171.

In still further embodiments, the oligomers of the invention may have amine-containing functional moieties on the nucleobase, including on the N6 purine amino groups, on the exocyclic N2 of guanine, or on the N4 or 5 positions of cytosine. In various embodiments, such functionalization may be achieved by using a commercial reagent that is already functionalized in the oligomer synthesis.

Some functional moieties are commercially available, for example, heterobifunctional and homobifunctional linking moieties are available from the Pierce Co. (Rockford, Ill.). Other commercially available linking groups are 5'-Amino-Modifier C6 and 3'-Amino-Modifier reagents, both available from Glen Research Corporation (Sterling, Va.). 5'-Amino-Modifier C6 is also available from ABI (Applied Biosystems Inc., Foster City, Calif.) as Aminolink-2, and 3'-Amino-Modifier is also available from Clontech Laboratories Inc. (Palo Alto, Calif.). In some embodiments in some embodiments

Compositions

The oligomer of the invention may be used in pharmaceutical formulations and compositions. Suitably, such compositions comprise a pharmaceutically acceptable diluent, carrier, salt or adjuvant. PCT/DK2006/000512 provides suitable and preferred
5 pharmaceutically acceptable diluent, carrier and adjuvants - which are hereby incorporated by reference. Suitable dosages, formulations, administration routes, compositions, dosage forms, combinations with other therapeutic agents, pro-drug formulations are also provided in PCT/DK2006/000512 - which are also hereby incorporated by reference.

Applications

10 The oligomers of the invention may be utilized as research reagents for, for example, diagnostics, therapeutics and prophylaxis.

In research, such oligomers may be used to specifically inhibit the synthesis of PIK3CA protein (typically by degrading or inhibiting the mRNA and thereby prevent protein formation) in cells and experimental animals thereby facilitating functional analysis of the
15 target or an appraisal of its usefulness as a target for therapeutic intervention.

In diagnostics the oligomers may be used to detect and quantitate PIK3CA expression in cell and tissues by northern blotting, *in-situ* hybridisation or similar techniques.

For therapeutics, an animal or a human, suspected of having a disease or disorder, which can be treated by modulating the expression of PIK3CA kinase is treated by
20 administering antisense compounds in accordance with this invention. Such disorders include hyperproliferative disorders such as cancer. Further provided are methods of treating a mammal, such as treating a human, suspected of having or being prone to a disease or condition, associated with expression of PIK3CA kinase by administering a therapeutically or prophylactically effective amount of one or more of the oligomers or
25 compositions of the invention.

It has been suggested by leading scientists in the field that pharmaceutical intervention with PIK3CA will result in therapeutic options against cancer, such as those referred to herein.

30 The invention also relates to an oligomer, a composition or a conjugate as defined herein for use as a medicament.

The oligomers and other compositions according to the invention can be used for the treatment of conditions associated with over expression or expression of mutated version of the PIK3CA.

The invention further provides use of a compound of the invention in the manufacture of a medicament for the treatment of a disease, disorder or condition as referred to herein.

Generally stated, in some aspects, the invention is directed to a method of treating a mammal suffering from or susceptible to conditions associated with abnormal levels of
5 PIK3CA, comprising administering to the mammal and therapeutically effective amount of an oligomer targeted to PIK3CA that comprises one or more LNA units. The methods of the invention are preferably employed for treatment or prophylaxis against diseases caused by abnormal levels of PIK3CA. Alternatively stated, In some embodiments, the invention is furthermore directed to a method for treating abnormal levels of PIK3CA, said method
10 comprising administering a oligomer of the invention, or a conjugate of the invention or a pharmaceutical composition of the invention to a patient in need thereof.

The oligomers and other compositions according to the invention can be used for the treatment of conditions associated with over expression or expression of PIK3CA or mutated versions of the PIK3CA.

15 The disease or disorder, as referred to herein, may, in some embodiments be associated with a mutation in the PIK3CA gene or a gene whose protein product is associated with or interacts with PIK3CA. Therefore, in some embodiments, the target mRNA is a mutated form of the PIK3CA sequence.

The oligomer, a conjugate or a pharmaceutical composition according to the invention
20 is typically administered in an effective amount.

An interesting aspect of the invention is directed to the use of an oligomer (compound) as defined herein or a conjugate as defined herein for the preparation of a medicament for the treatment of a disease, disorder or condition as referred to herein.

The invention further relates to use of a compound, composition, or a conjugate as
25 defined herein for the manufacture of a medicament for the treatment of abnormal levels of PIK3CA or expression of mutant forms of PIK3CA (such as allelic variants, such as those associated with one of the diseases referred to herein).

Moreover, the invention relates to a method of treating a subject suffering from a disease or condition such as those referred to herein.

30 A patient who is in need of treatment is a patient (subject) suffering from or likely to suffer from the disease or disorder.

In some embodiments, the term 'treatment' as used herein refers to both treatment of an existing disease (e.g. a disease or disorder as herein referred to), or prevention of a

disease, *i.e.* prophylaxis. It will therefore be recognised that treatment as referred to herein may, in some embodiments, be prophylactic.

The oligomer, a conjugate or a pharmaceutical composition according to the invention is typically administered in an effective amount.

5 The invention also provides for the use of the compound or conjugate of the invention as described for the manufacture of a medicament for the treatment of a disorder as referred to herein, or for a method of the treatment of as a disorder as referred to herein.

10 The invention also provides for a method for treating a disorder as referred to herein said method comprising administering a compound according to the invention as herein described, and/or a conjugate according to the invention, and/or a pharmaceutical composition according to the invention to a patient in need thereof. The pharmaceutical composition according to the invention may be used for the treatment of conditions associated with abnormal levels of PIK3CA kinase, such as hyperproliferative diseases and cancer. The invention also provides for a method for treating cancer, said method
15 comprising administering a compound according to the invention as herein described, and/or a conjugate according to the invention, and/or a pharmaceutical composition according to the invention to a patient in need thereof. The invention also provides for the use of the compound or conjugate of the invention as described for the manufacture of a medicament for the treatment of cancer, or for a method of the treatment of cancer.

20 Suitable dosages, formulations, administration routes, compositions, dosage forms, combinations with other therapeutic agents, pro-drug formulations are also provided in PCT/DK2006/000512 - which are hereby incorporated by reference., although it should be recognised that the aspects of PCT/DK2006/000512 which are only specifically applicable to the treatment of cancer may not be appropriate in the therapeutic/pharmaceutical
25 compositions and methods of the present invention.

The invention also provides for a pharmaceutical composition comprising a compound or a conjugate as herein described or a conjugate, and a pharmaceutically acceptable diluent, carrier or adjuvant. PCT/DK2006/000512 provides suitable and preferred pharmaceutically acceptable diluent, carrier and adjuvants - which are hereby incorporated
30 by reference.

In some embodiments, the term 'treatment' as used herein refers to both treatment of an existing disease (e.g. a cancer as herein referred to), or prevention of a disease, *i.e.* prophylaxis. It will therefore be recognised that treatment as referred to herein may, in some embodiments, be prophylactic.

The invention further provides use of a compound of the invention in the manufacture of a medicament for the treatment of any and all conditions disclosed herein.

Generally stated, in some aspects, the invention is directed to a method of treating a mammal suffering from or susceptible to conditions associated with abnormal, typically elevated, levels of PIK3CA kinase, comprising administering to the mammal and therapeutically effective amount of an oligomer targeted to PIK3CAK that comprises one or more LNA units.

An interesting aspect of the invention is directed to the use of an oligomer (compound) as defined herein or as conjugate as defined herein for the preparation of a medicament for the treatment of a condition according to above.

The methods of the invention may, in some embodiments, be employed for treatment or prophylaxis against diseases caused by abnormal levels of PIK3CA kinase.

Furthermore, the invention described herein encompasses a method of preventing or treating a disease comprising a therapeutically effective amount of a PIK3CA kinase modulating oligomer to a human in need of such therapy. The invention further encompasses the use of a short period of administration of a PIK3CA kinase modulating oligonucleotide compound.

Alternatively stated, the invention is, in some embodiments, furthermore directed to a method for treating abnormal levels of PIK3CA kinase, said method comprising administering a oligomer of the invention, or a conjugate of the invention or a pharmaceutical composition of the invention to a patient in need thereof and further comprising the administration of a further chemotherapeutic agent. Said further administration may be such that the further chemotherapeutic agent is conjugated to the compound of the invention, is present in the pharmaceutical composition, or is administered in a separate formulation.

The invention also, in some aspects, relates to an oligomer, a composition or a conjugate as defined herein for use as a medicament.

The invention further relates to use of a compound, composition, or a conjugate as defined herein for the manufacture of a medicament for the treatment of abnormal levels of PIK3CA kinase or expression of mutant forms of PIK3CAK (such as allelic variants, such as those associated with one of the diseases referred to herein).

Moreover, the invention relates to a method of treating a subject suffering from a disease or condition selected from hyperproliferative diseases and cancer, such as those referred to herein.

In some embodiments, the invention provides for a method for the inhibition of both PIK3CA and beta-catenin in a cell which is expressing both PIK3CA and beta-catenin, said method comprising administering an oligomer, or a conjugate according to the invention to said cell so as to effect the inhibition of PIK3CA and beta-catenin in said cell. Suitably the oligomer which is capable of inhibiting or down-regulating both PI3CA and beta-catenin in a cell has significantly homology to, or is capable of hybridising to the reverse complement of both target nucleic acids, such as an oligomer with a sequence of nucleobases of SEQ ID 82.

Medical Indications

Hyperproliferative diseases refer to disorders which are characterised by the uncontrolled and detrimental proliferation of cells within the body, such as cancer, such as those referred to herein.

In some embodiments, said cancer is in the form of i) a solid tumor and/or a carcinoma, and/or ii) a sarcoma, and/or iii) glioma.

Said carcinoma as referred to herein may be selected from the group consisting of malignant melanoma, basal cell carcinoma, ovarian carcinoma, breast carcinoma, non-small cell lung cancer, renal cell carcinoma, bladder carcinoma, recurrent superficial bladder cancer, stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung carcinoma, cervical carcinoma, cervical dysplasia, laryngeal papillomatosis, colon carcinoma, colorectal carcinoma and carcinoid tumors. More preferably, said carcinoma is selected from the group consisting of malignant melanoma, non-small cell lung cancer, breast carcinoma, colon carcinoma and renal cell carcinoma. Preferably, said carcinoma is a malignant melanoma, preferably selected from the group consisting of superficial spreading melanoma, nodular melanoma, lentigo maligna melanoma, acral melanoma, amelanotic melanoma and desmoplastic melanoma.

Said sarcoma as referred to herein may be selected from the group consisting of osteosarcoma, Ewing's sarcoma, chondrosarcoma, malignant fibrous histiocytoma, fibrosarcoma and Kaposi's sarcoma.

In some embodiments the cancer is selected from the group consisting of solid tumours such as glioblastoma, malignant melanoma, medulloblastoma, hepatocellular carcinoma, head and neck squamous cell carcinoma, gastric, ovarian, cervix and colorectal cancers, cancers of the breast, lung and colon, large B-cell lymphoma, anaplastic astrocytoma, anaplastic oligodendroglioma, prostate cancer, endometrial cancer, pancreatic

cancer, bowel cancer, leukaemia, esophagus cancer, and thyroid cancer, or in some embodiments, liver or kidney cancer.

In some embodiments, the cancer referred to herein is selected from the group consisting of: Colorectal, glioblastoma, gastric, hepatocellular, breast, ovarian and lung
5 cancers.

In aspect the cancer as referred to herein, may be selected from the group consisting of; non-Hodgkin's lymphoma, Hodgkin's lymphoma, leukemia (e.g., acute leukemia such as acute lymphocytic leukemia, acute myelocytic leukemia, chronic myeloid leukemia, chronic lymphocytic leukemia, multiple myeloma), colon carcinoma, rectal carcinoma, pancreatic
10 cancer, breast cancer, ovarian cancer, prostate cancer, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, cervical cancer, testicular cancer, lung carcinoma, bladder carcinoma, melanoma, head and neck cancer, brain cancer, cancers of unknown primary site, neoplasms, cancers of the peripheral nervous system, cancers of the central nervous system, tumors (e.g., fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma,
15 osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma,
20 seminoma, embryonal carcinoma, Wilms' tumor, small cell lung carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma, and retinoblastoma), heavy chain disease, metastases, and any disease or disorder characterized by uncontrolled or abnormal cell growth.

25 In some embodiments the cancer referred to herein is selected from: Hodgkin's lymphoma, leukaemia such as acute lymphocytic leukaemia, colon carcinoma, rectal carcinoma, brain cancer, neural blastomas, lung cancer, pancreatic cancer, melanoma, acute myelogenous leukaemia, liver cancer, thyroid cancer, kidney cancer, urinary tract cancer and bladder cancer.

30 In some embodiments the cancer referred to herein is selected from: Hodgkin's lymphoma, leukaemia such as acute lymphocytic leukaemia, colon carcinoma, brain cancer, neural blastomas.

In some embodiments, the cancer referred to herein are selected from the group consisting of cancer diseases is a lung, breast, colon, prostate, pancreas, lung, liver, thyroid,

kidney, brain, testes, stomach, intestine, bowel, spinal cord, sinuses, bladder, urinary tract or ovaries cancer.

In some embodiments, for example for the treatment of brain cancer, it is preferred that phosphorothioate linkages are not used in the compound according to the invention.

5 Further conditions which may be associated with abnormal levels of PIK3CA kinase, and which, therefore may be treated using the compositions, conjugates and compounds according to the invention include disorders selected from the group consisting of hyperproliferative diseases, such as cancer, particularly solid tumours such as glioblastoma, malignant melanoma, medulloblastoma, hepatocellular carcinoma, head and neck
10 squamous cell carcinoma, gastric, ovarian, cervix and colorectal cancers as well as cancers of the breast, lung and colon.

In one aspect the cancers referred to herein may be selected from the group consisting of solid tumours such as glioblastoma, malignant melanoma, medulloblastoma, hepatocellular carcinoma, head and neck squamous cell carcinoma, gastric, ovarian, cervix
15 and colorectal cancers, cancers of the breast, lung and colon, large B-cell lymphoma, anaplastic astrocytoma, anaplastic oligodendroglioma, prostate cancer, endometrial cancer, pancreatic cancer, bowel cancer, leukaemia, esophagus cancer, and thyroid cancer.

In one aspect the cancers referred to herein may be kidney or liver cancer.

20 EMBODIMENTS

The following embodiments of the present invention may be used in combination with the other embodiments described herein.

- 25 1. An oligomer of between 10-50 nucleobases in length which comprises a contiguous nucleobase sequence of a total of between 10-50 nucleobases, wherein said contiguous nucleobase sequence is at least 80% homologous to a corresponding region of a nucleic acid which encodes a mammalian PIK3CA kinase.
2. The oligomer according to embodiment 1, wherein said oligomer comprises at least one LNA unit.
- 30 3. The oligomer according to embodiment 1 or 2, wherein the contiguous nucleobase sequence comprises no more than 3, such as no more than 2 mismatches to the corresponding region of a nucleic acid which encodes a mammalian PIK3CA kinase.
4. The oligomer according to embodiment 3, wherein said contiguous nucleobase sequence comprises a single mismatch to the corresponding region of a nucleic acid

which encodes a mammalian PIK3CA kinase, wherein, optionally, the single mismatch corresponds to a single nucleotide point mutation which is associated with a cancer phenotype.

- 5 5. The oligomer according to embodiment 1 or 2, wherein said contiguous nucleobase sequence comprises no mismatches, (*i.e.* is complementary to) the corresponding region of a nucleic acid which encodes a mammalian PIK3CA kinase.
6. The oligomer according to any one of embodiments 1 – 5, wherein the nucleobase sequence of the oligomer consists of the contiguous nucleobase sequence.
- 10 7. The oligomer according to any one of embodiments 1- 6, wherein the nucleic acid which encodes a mammalian PIK3CA kinase is the human PIK3CA kinase nucleotide sequence such as SEQ ID No 1, or a variant thereof, such as SEQ ID NO 1 which comprises a single point mutation at a position selected from 1781, 1790 and 3297.
- 15 8. The oligomer according to any one of embodiments 1 – 7, wherein the contiguous nucleobase sequence is complementary to a corresponding region of both the human PIK3CA kinase nucleic acid sequence and a non-human mammalian PIK3CA kinase nucleic acid sequence, such as the mouse PIK3CA kinase nucleic acid sequence..
- 20 9. The oligomer according to any one of embodiments 1 to 8, wherein the contiguous nucleobase sequence comprises a contiguous subsequence of at least 7, nucleobase residues which, when formed in a duplex with the complementary PIK3CA kinase target RNA is capable of recruiting RNaseH.
- 25 10. The oligomer according to embodiment 9, wherein the contiguous nucleobase sequence comprises of a contiguous subsequence of at least 8, at least 9 or at least 10 nucleobase residues which, when formed in a duplex with the complementary PIK3CA kinase target RNA is capable of recruiting RNaseH.
- 30 11. The oligomer according to any one of embodiments 9 or 10 wherein said contiguous subsequence is at least 9 or at least 10 nucleobases in length, such as at least 12 nucleobases or at least 14 nucleobases in length, such as 14, 15 or 16 nucleobases residues which, when formed in a duplex with the complementary PIK3CA kinase target RNA is capable of recruiting RNaseH.
12. The oligomer according to embodiment any one of embodiments 1 – 11 wherein said oligomer is conjugated with one or more non-nucleobase compounds.
13. The oligomer according to any one of embodiments 1 - 12, wherein said oligomer has a length of between 10 - 22 nucleobases.

14. The oligomer according to any one of embodiments 1 - 13, wherein said oligomer has a length of between 12 - 18 nucleobases.
15. The oligomer according to any one of embodiments 1 - 14, wherein said oligomer has a length of 14, 15 or 16 nucleobases.
- 5 16. The oligomer according to any one of embodiments 1 - 15, wherein said continuous nucleobase sequence corresponds to a contiguous nucleotide sequence present in a nucleic acid sequence selected from the group consisting of SEQ ID NO 110 - 124, or 149 - 160.
- 10 17. The oligomer according to any one of embodiments 1-16, wherein the oligomer or contiguous nucleobase sequence comprises, or is selected from a corresponding nucleobase sequence present in a nucleotide sequence selected from the group consisting of SEQ ID NO 2 - 16.
18. The oligomer according to any one of embodiments 1 - 17, wherein said contiguous nucleobase sequence comprises at least one affinity enhancing nucleotide analogue.
- 15 19. The oligomer according to embodiment 18, wherein said contiguous nucleobase sequence comprises a total of 2, 3, 4, 5, 6, 7, 8, 9 or 10 affinity enhancing nucleotide analogues, such as between 5 and 8 affinity enhancing nucleotide analogues.
- 20 20. The oligomer according to any one of embodiments 1 - 19 which comprises at least one affinity enhancing nucleotide analogue, wherein the remaining nucleobases are selected from the group consisting of DNA nucleotides and RNA nucleotides, preferably DNA nucleotides.
- 25 21. The oligomer according to any one of embodiments 1 - 20, wherein the oligomer comprises of a sequence of nucleobases of formula, in 5' to 3' direction, A-B-C, and optionally of formula A-B-C-D, wherein:
- 25 A consists or comprises of at least one nucleotide analogue, such as 1, 2, 3, 4, 5 or 6 nucleotide analogues, preferably between 2-5 nucleotide analogues, preferably 2, 3 or 4 nucleotide analogues, most preferably 2, 3 or 4 consecutive nucleotide analogues and;
- 30 B consists or comprises at least five consecutive nucleobases which are capable of recruiting RNaseH (when formed in a duplex with a complementary RNA molecule, such as the PIK3CAK mRNA target), such as DNA nucleobases, such as 5, 6, 7, 8, 9, 10, 11 or 12 consecutive nucleobases which are capable of recruiting RNaseH, or between 6-10, or between 7-9, such as 8 consecutive nucleobases which are capable of recruiting RNaseH, and;

- C consists or comprises of at least one nucleotide analogue, such as 1, 2, 3, 4, 5, or 6 nucleotide analogues, preferably between 2-5 nucleotide analogues, such as 2, 3 or 4 nucleotide analogues, most preferably 2, 3 or 4 consecutive nucleotide analogues, and;
- 5 D when present, consists or comprises, preferably consists, of one or more DNA nucleotide, such as between 1-3 or 1-2 DNA nucleotides.
22. The oligomer according to embodiment 21, wherein region A consists or comprises of 2, 3 or 4 consecutive nucleotide analogues.
23. The oligomer according to any one of embodiments 21 - 22, wherein region B consists or comprises of 7, 8, 9 or 10 consecutive DNA nucleotides or equivalent nucleobases which are capable of recruiting RNaseH when formed in a duplex with a complementary RNA, such as the PIK3CA kinase mRNA target.
- 10
24. The oligomer according to any one of embodiments 21 - 24, wherein region C consists or comprises of 2, 3 or 4 consecutive nucleotide analogues.
- 15 25. The oligomer according to any one of embodiments 21 - 24, wherein region D consists, where present, of one or two DNA nucleotides.
26. The oligomer according to any one of embodiments 21 - 25, wherein:
- A Consists or comprises of 3 contiguous nucleotide analogues;
- B Consists or comprises of 7, 8, 9 or 10 contiguous DNA nucleotides or equivalent nucleobases which are capable of recruiting RNaseH when formed in a duplex with a complementary RNA, such as the PIK3CA kinase mRNA target;
- 20
- C Consists or comprises of 3 contiguous nucleotide analogues;
- D Consists, where present, of one or two DNA nucleotides.
- 25 27. The oligomer according to embodiment 26, wherein the contiguous nucleobase sequence consists of 10, 11, 12, 13 or 14 nucleobases, and wherein;
- A Consists of 1, 2 or 3 contiguous nucleotide analogues;
- B Consists of 7, 8, or 9 consecutive DNA nucleotides or equivalent nucleobases which are capable of recruiting RNaseH when formed in a duplex with a complementary RNA, such as the PIK3CA kinase mRNA target;
- 30
- C Consists of 1, 2 or 3 contiguous nucleotide analogues;
- D Consists, where present, of one DNA nucleotide.

28. The oligomer according to anyone of embodiments 21 - 27, wherein B comprises at least one LNA nucleobase which is in the alpha-L configuration, such as alpha-L-oxy LNA.
29. The oligomer according to any one of embodiments 1 - 28, wherein the nucleotide analogue(s) are independently or collectively selected from the group consisting of:
5 Locked Nucleic Acid (LNA) units; 2'-O-alkyl-RNA units, 2'-OMe-RNA units, 2'-amino-DNA units, 2'-fluoro-DNA units, PNA units, HNA units, and INA units.
30. The oligomer according to embodiment 29 wherein all the nucleotide analogues(s) are LNA units.
- 10 31. The oligomer according to any one of embodiments 1 - 30, which comprises 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 LNA units such as between 2 and 8 nucleotide LNA units.
32. The oligomer according to any one of the embodiments 29 - 31, wherein the LNAs are independently selected from oxy-LNA, thio-LNA, and amino-LNA, in either of the beta-D and alpha-L configurations or combinations thereof.
- 15 33. The oligomer according to embodiment 32, wherein the LNAs are all beta-D-oxy-LNA.
34. The oligomer according to any one of embodiments 21 - 33, wherein the nucleotide analogues of regions A and C are beta-D-oxy-LNA.
35. The oligomer according to any one of embodiments 1 - 34, wherein at least one of the nucleobases present in the oligomer is a modified nucleobase selected from the group
20 consisting of 5-methylcytosine, isocytosine, pseudoisocytosine, 5-bromouracil, 5-propynyluracil, 6-aminopurine, 2-aminopurine, inosine, diaminopurine, and 2-chloro-6-aminopurine.
36. The oligomer according to any one of embodiments 1 - 35, wherein said oligomer hybridises with a corresponding mammalian PIK3CA kinase mRNA with a T_m of at least
25 50°C.
37. The oligomer according to any one of embodiments 1 - 36, wherein said oligomer hybridises with a corresponding mammalian PIK3CA kinase mRNA with a T_m of no greater than 80°C.
38. The oligomer according to any one of embodiments 1 - 37, wherein the internucleoside linkages are independently selected from the group consisting of: phosphodiester,
30 phosphorothioate and boranophosphate.
39. The oligomer according to embodiment 38, wherein the oligomer comprises at least one phosphorothioate internucleoside linkage.

40. The oligomer according to embodiment 39, wherein the internucleoside linkages adjacent to and/or between DNA or RNA units, or within region B are phosphorothioate linkages.
41. The oligomer according to embodiment 39 or 40, wherein the linkages between at least one pair of consecutive nucleotide analogues is a phosphodiester linkage.
42. The oligomer according to embodiment 39 or 40, wherein all the linkages between consecutive nucleotide analogues are phosphodiester linkages.
43. The oligomer according to embodiment 38 wherein all the internucleoside linkages are phosphorothioate linkages.
44. A conjugate comprising the oligomer according to any one of the embodiments 1-43 and at least one non-nucleotide or non-polynucleotide moiety covalently attached to said compound.
45. A pharmaceutical composition comprising an oligomer as defined in any of embodiments 1-43 or a conjugate as defined in embodiment 44, and a pharmaceutically acceptable diluent, carrier, salt or adjuvant.
46. A pharmaceutical composition according to 45, wherein the oligomer is constituted as a pro-drug.
47. Use of an oligomer as defined in any one of the embodiments 1-43, or a conjugate as defined in embodiment 44, for the manufacture of a medicament for the treatment of a disease or disorder selected from the group consisting of hyperproliferative diseases such as cancer.
48. A method for treating a hyperproliferative disease such as cancer, said method comprising administering an oligomer as defined in one of the embodiments 1-43, or a conjugate as defined in embodiment 44, or a pharmaceutical composition as defined in any one of the embodiments 45 - 46, to a patient in need thereof.
49. A method of reducing or inhibiting the expression of PIK3CA kinase in a cell or a tissue, the method comprising the step of contacting said cell or tissue with a compound as defined in one of the embodiments 1-43, or a conjugate as defined in embodiment 44, or a pharmaceutical composition as defined in any one of the embodiments 45 - 46, so that expression of PIK3CA kinase is reduce or inhibited.

EXAMPLES

Example 1: Monomer synthesis

The LNA monomer building blocks and derivatives were prepared following published procedures and references cited therein - see WO07/031081 and the references cited therein.

Example 2: Oligonucleotide synthesis

- 5 Oligonucleotides were synthesized according to the method described in WO07/031081. Table 1 shows examples of antisense oligonucleotide sequences of the invention. Tables 2 and 3 show examples of antisense oligonucleotides (oligos) of the invention.

Example 3: Design of the oligonucleotides

- 10 In accordance with the present invention, a series of different oligonucleotides were designed to target different regions of human PIK3CA mRNA (phosphoinositide-3-kinase, catalytic, alpha polypeptide),(GenBank accession number NM_006218, SEQ ID NO:1).

Table 1 Antisense oligonucleotide sequences of the invention

SEQ ID NOS 2-16: are oligo sequences designed to target human wild-type PIK3CA mRNA.

SEQ ID NO	Sequence (5'-3')	Length (bases)	Target site NM_006218
SEQ ID NO: 2	GAGGCATTCTAAAGTC	16	253-268
SEQ ID NO: 3	ATTCTTCCCTTTCTGC	16	386-401
SEQ ID NO: 4	TAGACATACATTGCTC	16	642-657
SEQ ID NO: 5	TACTTGCCCTGATATT	16	891-906
SEQ ID NO: 6	CACATAAGGGTTCTCC	16	1247-1262
SEQ ID NO: 7	AGCCATTCATTCCACC	16	1302-1317
SEQ ID NO: 8	CAGTAACACCAATAGG	16	1529-1544
SEQ ID NO: 9	AACTCCAACCTCTAAGC	16	1572-1587
SEQ ID NO: 10	CAGACAGAAGCAATTT	16	1856-1871
SEQ ID NO: 11	TTATTGTGCATCTCAG	16	2175-2190
SEQ ID NO: 12	GCAGAGGACATAATTC	16	2466-2481
SEQ ID NO: 13	GATGTCTGGGTTCTCC	16	2506-2521
SEQ ID NO: 14	TTCTTCTTGATCCA	16	2970-2985
SEQ ID NO: 15	AAGAAATCCTGTGTCA	16	3024-3039
SEQ ID NO: 16	TCTCCTGAAACCTCTC	16	3089-3104

SEQ ID NO	Sequence (5'-3')	Length (bases)	Target site NM_006218
SEQ ID NO: 110	CACGGAGGCATTCTAAAGTCACTA	24	249-272
SEQ ID NO: 111	AAAAATTCTTCCCTTTCTGCTTCT	24	382-405
SEQ ID NO: 112	AGGATAGACATACATTGCTCTACT	24	638-661
SEQ ID NO: 113	AATATACTTGCCCTGATATTCTAA	24	887-910
SEQ ID NO: 114	TTGTCACATAAGGGTTCTCCTCCA	24	1243-1266
SEQ ID NO: 115	ATTCAGCCATTCAATCCACCTGGG	24	1298-1321
SEQ ID NO: 116	GATCCAGTAACACCAATAGGGTTC	24	1525-1548
SEQ ID NO: 117	GTCAAACCTCCAACCTAAGCATGG	24	1568-1591
SEQ ID NO: 118	TTAACAGACAGAAGCAATTTGGGT	24	1852-1875
SEQ ID NO: 119	TGTTTTATTGTGCATCTCAGATTT	24	2171-2194
SEQ ID NO: 120	TTTTGCAGAGGACATAATTCGACA	24	2462-2485
SEQ ID NO: 121	ACATGATGTCTGGGTTCTCCCAAT	24	2502-2525
SEQ ID NO: 122	TTTTTTCTTCTTGTGATCCAAAAA	24	2966-2989
SEQ ID NO: 123	TATTAAGAAATCCTGTGTCAAAC	24	3020-3043
SEQ ID NO: 124	CACATCTCCTGAAACCTCTCAAAT	24	3085-3108

Table 2 Antisense oligonucleotide sequences of the invention

SEQ ID NOS: 17-22 are oligo sequences designed to target the three hot-spot mutations (E542K, E545K and H1047R) in human PIK3CA mRNA and SEQ ID NOS: 23-28 are their corresponding wild-type oligos. The place of the hot-spot mutation in each oligo is indicated in grey highlight. SEQ ID NO 17, 18, 125, and 126 are directed against the E542K mutation. SEQ ID NO 19, 20, 127 and 128 (SPC4168 and 4169) are directed against the E545K mutation and SEQ ID NO 21, 22, 129 and 130 (SPC4170 and 4171) are directed against the H1047R mutation.

SEQ ID NO	Sequence (5'-3')	Length (bases)	Target site NM_006218
SEQ ID NO: 17	GATTTTAGAGAGAGGA	16	1771-1786
SEQ ID NO: 18	AGTGATTTAGAGAGA	16	1774 - 1789
SEQ ID NO: 19	TCCTGCTTAGTGATTT	16	1782 - 1797

SEQ ID NO	Sequence (5'-3')	Length (bases)	Target site NM_006218
SEQ ID NO: 20	TTCTCCTGCTTAGTGA	16	1785 - 1800
SEQ ID NO: 21	GCCACCATGACGTGCA	16	3292 - 3307
SEQ ID NO: 22	ACCATGACGTGCATCA	16	3289 - 3304
SEQ ID NO: 23	GATTCAGAGAGAGGA	16	1771-1786
SEQ ID NO: 24	AGTGATTCAGAGAGA	16	1774 - 1789
SEQ ID NO: 25	TCCTGCTCAGTGATTT	16	1782 - 1797
SEQ ID NO: 26	TTCTCCTGCTCAGTGA	16	1785 - 1800
SEQ ID NO: 27	GCCACCATGATGTGCA	16	3292 - 3307
SEQ ID NO: 28	ACCATGATGTGCATCA	16	3289 - 3304
SEQ ID NO: 125	CAGTGATTTTAGAGAGAGGATCTC	24	1767 - 1790
SEQ ID NO: 126	GCTCAGTGATTTTAGAGAGAGGAT	24	1770 - 1793
SEQ ID NO: 127	TTTCTCCTGCTTAGTGATTTT CAGA	24	1778 - 1801
SEQ ID NO: 128	ATCTTTCTCCTGCTTAGTGATTTT C	24	1781 - 1804
SEQ ID NO: 129	TCCAGCCACCATGACGTGCATCAT	24	3288 - 3311
SEQ ID NO: 130	AGCCACCATGACGTGCATCATTCA	24	3285 -3308
SEQ ID NO: 131	CAGTGATTTTAGAGAGAGGATCTC	24	1767 - 1790
SEQ ID NO: 132	GCTCAGTGATTTTAGAGAGAGGAT	24	1770 - 1793
SEQ ID NO: 133	TTTCTCCTGCTCAGTGATTTT CAGA	24	1778 - 1801
SEQ ID NO: 134	ATCTTTCTCCTGCTCAGTGATTTT C	24	1781 - 1804
SEQ ID NO: 135	TCCAGCCACCATGATGTGCATCAT	24	3288 - 3311
SEQ ID NO: 136	AGCCACCATGATGTGCATCATTCA	24	3285 -3308

Table 3: Oligonucleotide designs of the invention

In SEQ ID NOs: 29 - 55, upper case letters indicates nucleotide analogue units, such as LNA, and subscript "s" represents phosphorothioate linkage. Lower case letters represent nucleotide units. Absence of "s" (if any) indicates phosphodiester linkage.

SEQ ID NO	Sequence (5'-3')
SEQ ID NO: 29	G_sA_sG_sG_sC_sa_st_st_sc_st_sa_sa_sG_sT_sC
SEQ ID NO: 30	A_sT_sT_sC_st_st_sC_sC_sC_st_st_sC_sT_sG_sC
SEQ ID NO: 31	T_sA_sG_sa_sC_sa_st_sa_sC_sa_st_sg_sC_sT_sC

SEQ ID NO	Sequence (5'-3')
SEQ ID NO: 32	T _s A _s C _s t _s t _s g _s c _s c _s c _s t _s g _s a _s t _s A _s T _s T
SEQ ID NO: 33	C _s A _s C _s a _s t _s a _s a _s g _s g _s g _s t _s t _s c _s T _s C _s C
SEQ ID NO: 34	A _s G _s C _s c _s a _s t _s t _s c _s a _s t _s t _s c _s C _s A _s C _s C
SEQ ID NO: 35	C _s A _s G _s t _s a _s a _s c _s a _s c _s c _s c _s a _s t _s A _s G _s G
SEQ ID NO: 36	A _s A _s C _s t _s c _s c _s a _s a _s c _s t _s c _s t _s a _s A _s G _s C
SEQ ID NO: 37	C _s A _s G _s a _s c _s a _s g _s a _s a _s g _s c _s a _s T _s T _s T
SEQ ID NO: 38	T _s T _s A _s t _s t _s g _s t _s g _s c _s a _s t _s c _s T _s C _s A _s G
SEQ ID NO: 39	G _s C _s A _s g _s a _s g _s g _s a _s c _s a _s t _s a _s T _s T _s C
SEQ ID NO: 40	G _s A _s T _s g _s t _s c _s t _s g _s g _s t _s t _s c _s T _s C _s C
SEQ ID NO: 41	T _s T _s C _s t _s t _s C _s t _s t _s g _s t _s g _s a _s t _s C _s C _s A
SEQ ID NO: 42	A _s A _s G _s a _s a _s a _s t _s c _s c _s t _s g _s t _s g _s T _s C _s A
SEQ ID NO: 43	T _s C _s T _s c _s c _s t _s g _s a _s a _s c _s c _s t _s C _s T _s C
SEQ ID NO: 44	G _s A _s T _s t _s t _s t _s a _s g _s a _s g _s a _s g _s A _s G _s A
SEQ ID NO: 45	A _s G _s T _s g _s a _s t _s t _s t _s t _s a _s g _s a _s g _s A _s A _s A
SEQ ID NO: 46	T _s C _s C _s t _s g _s c _s t _s t _s a _s g _s t _s g _s a _s T _s T
SEQ ID NO: 47	T _s T _s C _s t _s c _s c _s t _s g _s c _s t _s a _s g _s T _s G _s A
SEQ ID NO: 48	G _s C _s C _s a _s c _s c _s a _s t _s g _s a _s c _s g _s t _s G _s C _s A
SEQ ID NO: 49	A _s C _s C _s a _s t _s g _s a _s c _s g _s t _s g _s c _s a _s T _s C _s A
SEQ ID NO: 50	G _s A _s T _s t _s t _s t _s c _s a _s g _s a _s g _s a _s g _s A _s G _s A
SEQ ID NO: 51	A _s G _s T _s g _s a _s t _s t _s t _s c _s a _s g _s a _s g _s A _s G _s A
SEQ ID NO: 52	T _s C _s C _s t _s g _s c _s t _s c _s a _s g _s t _s g _s a _s T _s T
SEQ ID NO: 53	T _s T _s C _s t _s c _s c _s t _s g _s c _s t _s c _s a _s g _s T _s G _s A
SEQ ID NO: 54	G _s C _s C _s a _s c _s c _s a _s t _s g _s a _s t _s g _s T _s C _s A
SEQ ID NO: 55	A _s C _s C _s a _s t _s g _s a _s t _s g _s t _s g _s c _s a _s T _s C _s A

Example 4: In vitro model: Cell culture

The effect of antisense oligonucleotides on target nucleic acid expression can be tested in any of a variety of cell types provided that the target nucleic acid is present at measurable levels. The target can be expressed endogenously or by transient or stable transfection of a nucleic acid encoding said target. The expression level of target nucleic acid can be routinely determined using, for example, Northern blot analysis, Real-Time PCR, Ribonuclease protection assays. The following cell types are provided for illustrative purposes, but other cell types can be routinely used, provided that the target is expressed in the cell type chosen.

5 Cells were cultured in the appropriate medium as described below and maintained at 37°C at 95-98% humidity and 5% CO₂. Cells were routinely passaged 2-3 times weekly.

MCF7: The human breast adenocarcinoma cell line MCF7 was cultured in Egel MEM (Sigma) + 10% fetal bovine serum (FBS) + 2 mM Glutamax I + gentamicin (25µg/ml) + 1x Non Essential Amino Acid.

PC3: The human prostate adenocarcinoma cell line PC3 was cultured in DMEM (Sigma) + 10% fetal bovine serum (FBS) + 2 mM Glutamax I + gentamicin (25µg/ml).

Example 5: *In vitro* model: Treatment with antisense oligonucleotide

The cell lines listed in example 4 were treated with oligonucleotide using the cationic liposome formulation LipofectAMINE 2000 (Gibco) as transfection vehicle. Cells were seeded in 6-well cell culture plates (NUNC) and treated when 80-90% confluent. Oligo concentrations used ranged from 0.8 nM to 20 nM final concentration. Formulation of oligo-lipid complexes were carried out essentially as described by the manufacturer using serum-free OptiMEM (Gibco) and a final lipid concentration of 2.5 µg/mL (PC3) or 5 µg/mL (MCF7) LipofectAMINE 2000. Cells were incubated at 37°C for 4 hours and treatment was stopped by removal of oligo-containing culture medium. Cells were washed and serum-containing media was added. After oligo treatment cells were allowed to recover for 20 hours before they were harvested for RNA analysis.

Example 6: *In vitro* model: Extraction of RNA and cDNA synthesis

Total RNA Isolation and First strand synthesis: Total RNA was extracted from cells transfected as described above and using the Qiagen RNeasy kit (Qiagen cat. no. 74104) according to the manufacturer's instructions. First strand synthesis was performed using Reverse Transcriptase reagents from Ambion according to the manufacturer's instructions. For each sample 0.5 µg total RNA was adjusted to (10.8 µl) with RNase free H₂O and mixed with 2 µl random decamers (50 µM) and 4 µl dNTP mix (2.5 mM each dNTP) and heated to 70 °C for 3 min after which the samples were rapidly cooled on ice. After cooling the samples on ice, 2 µl 10x Buffer RT, 1 µl MMLV Reverse Transcriptase (100 U/µl) and 0.25 µl RNase inhibitor (10 U/µl) was added to each sample, followed by incubation at 42 °C for 60 min, heat inactivation of the enzyme at 95°C for 10 min and then the sample was cooled to 4 °C.

Example 7: *In vitro* model: Analysis of Oligonucleotide Inhibition of PIK3CA Expression by Real-time PCR

Antisense modulation of PIK3CA expression can be assayed in a variety of ways known in the art. For example, PIK3CA mRNA levels can be quantitated by, e.g., Northern blot analysis, competitive polymerase chain reaction (PCR), or real-time PCR. Real-time quantitative PCR is presently preferred. RNA analysis can be performed on total cellular RNA or mRNA.

Methods of RNA isolation and RNA analysis such as Northern blot analysis is routine in the art and is taught in, for example, Current Protocols in Molecular Biology, John Wiley and Sons.

Real-time quantitative (PCR) can be conveniently accomplished using the commercially available Multi-Color Real Time PCR Detection System, available from Applied Biosystem.

Real-time Quantitative PCR Analysis of PIK3CA mRNA Levels: The sample content of human PIK3CA mRNA was quantified using the human PIK3CA ABI Prism Pre-Developed TaqMan Assay Reagents (Applied Biosystems cat. no. Hs00180679_m1 according to the manufacturer's instructions.

Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA quantity was used as an endogenous control for normalizing any variance in sample preparation.

The sample content of human GAPDH mRNA was quantified using the human GAPDH ABI Prism Pre-Developed TaqMan Assay Reagent (Applied Biosystems cat. no. 4310884E) according to the manufacturer's instructions.

Real-time Quantitative PCR is a technique well known in the art and is taught in for example Heid et al. Real time quantitative PCR, Genome Research (1996), 6: 986-994.

Real time PCR: The cDNA from the first strand synthesis performed as described in example 5 was diluted 2-20 times, and analyzed by real time quantitative PCR using Taqman 7500 FAST or 7900 FAST from Applied Biosystems. The primers and probe were mixed with 2 x Taqman Fast Universal PCR master mix (2x) (Applied Biosystems Cat.# 4364103) and added to 4 μ l cDNA to a final volume of 10 μ l. Each sample was analysed in duplicate. Assaying 2 fold dilutions of a cDNA that had been prepared on material purified from a cell line expressing the RNA of interest generated standard curves for the assays.

Sterile H₂O was used instead of cDNA for the no template control. PCR program: 95° C for 30 seconds, followed by 40 cycles of 95° C, 3 seconds, 60° C, 20-30 seconds. Relative quantities of target mRNA sequence were determined from the calculated Threshold cycle using the Applied Biosystems Fast System SDS Software Version 1.3.1.21. or SDS Software Version 2.3.

Example 8: In vitro analysis: Antisense Inhibition of Human PIK3CA mRNA Expression by oligonucleotide compounds

Oligonucleotides presented in Table 3 were evaluated for their potential to knockdown of human PIK3CA mRNA at concentrations of 0.8, 4 and 20 nM in PC3 cells and MCF7 cells (see Figures 1 and 2). The most active oligonucleotides, having SEQ ID NO: 57, 60, 64, 67,

77 and 82 were further evaluated for their knockdown of human PIK3CA at the concentrations 0.04, 0.2, 0.8, 4, 10 and 20nM in PC3 and MCF7 cells (see Figures 22 and 23).

Table 4: Antisense Inhibition of Human PIK3CA mRNA expression by

5 **oligonucleotides.** The data in Table 4 are presented as percentage down-regulation relative to mock transfected cells at 20 nM. Lower case letters represent DNA units, bold upper case letters represent β -D-oxy-LNA units. All LNA C are 5'methyl C. Subscript "s" represents phosphorothioate linkage.

Test substance	Sequence (5'-3')	Percent inhibition of PIK3CA in MCF7	Percent inhibition of PIK3CA in PC3
SEQ ID NO:56	G_sA_sG_sG_sC_sa_st_st_sc_st_sa_sa_sa_sG_sT_sC	47	48
SEQ ID NO:57	A_sT_sT_sC_st_st_sC_sC_sC_st_st_sC_sT_sG_sC	94	91
SEQ ID NO:58	T_sT_sC_st_st_sC_sC_sC_st_st_sC_sT_sG	n.d.	n.d.
SEQ ID NO:59	T_sc_st_st_sC_sC_sC_st_st_sC_sT	n.d.	n.d.
SEQ ID NO:60	T_sA_sG_sa_sC_sa_st_sa_sC_sa_st_st_sG_sC_sT_sC	96	96
SEQ ID NO:61	A_sG_sa_sC_sa_st_sa_sC_sa_st_st_sG_sC_sT	n.d.	n.d.
SEQ ID NO:62	G_sa_sC_sa_st_sa_sC_sa_st_st_sG_sC	n.d.	n.d.
SEQ ID NO:63	T_sA_sC_st_st_sG_sC_sC_sC_st_sg_sa_st_sA_sT_sT	94	89
SEQ ID NO:64	C_sA_sC_sa_st_sa_sa_sg_sg_sg_st_st_sC_sT_sC_sC	97	95
SEQ ID NO:65	A_sC_sa_st_sa_sa_sg_sg_sg_st_st_sC_sT_sC	n.d.	n.d.
SEQ ID NO:66	C_sa_st_sa_sa_sg_sg_st_st_sC_sT	n.d.	n.d.
SEQ ID NO:67	A_sG_sC_sC_sa_st_st_sC_sa_st_st_sC_sC_sA_sC_sC	97	93
SEQ ID NO:68	G_sC_sC_sa_st_st_sC_sa_st_st_sC_sC_sA_sC	n.d.	n.d.
SEQ ID NO:69	C_sc_sa_st_st_sC_sa_st_st_sC_sC_sA	n.d.	n.d.
SEQ ID NO:70	C_sA_sG_st_sa_sa_sC_sa_sC_sC_sa_st_sA_sG_sG	92	94
SEQ ID NO:71	A_sG_st_sa_sa_sC_sa_sC_sC_sa_st_sA_sG	n.d.	n.d.
SEQ ID NO:72	G_st_sa_sa_sC_sa_sC_sC_sa_st_sA	n.d.	n.d.
SEQ ID NO:73	A_sA_sC_st_sC_sC_sa_sa_sC_st_sC_sa_sA_sG_sC	81	75
SEQ ID NO:74	C_sA_sG_sa_sC_sa_sg_sa_sa_sg_sC_sa_sa_sT_sT_sT	90	94
SEQ ID NO:75	A_sG_sa_sC_sa_sg_sa_sa_sg_sC_sa_sa_sT_sT	n.d.	n.d.

Test substance	Sequence (5'-3')	Percent inhibition of PIK3CA in MCF7	Percent inhibition of PIK3CA in PC3
SEQ ID NO:76	G _s a _s C _s a _s g _s a _s a _s g _s C _s a _s a _s T	n.d.	n.d.
SEQ ID NO:77	T _s T _s A _s t _s t _s g _s t _s g _s C _s a _s t _s c _s t _s C _s A _s G	91	96
SEQ ID NO:78	T _s A _s t _s t _s g _s t _s g _s C _s a _s t _s c _s t _s C _s A	n.d.	n.d.
SEQ ID NO:79	A _s t _s t _s g _s t _s g _s C _s a _s t _s C _s t _s C	n.d.	n.d.
SEQ ID NO:80	G _s C _s A _s g _s a _s g _s g _s a _s C _s a _s t _s a _s a _s T _s T _s C	76	80
SEQ ID NO:81	G _s A _s T _s g _s t _s C _s t _s g _s g _s g _s t _s t _s C _s T _s C _s C	90	81
SEQ ID NO:82	T _s T _s C _s t _s t _s C _s t _s t _s g _s t _s g _s a _s t _s C _s C _s A	92	93
SEQ ID NO:83	T _s C _s t _s t _s C _s t _s t _s g _s t _s g _s a _s t _s C _s C	n.d.	n.d.
SEQ ID NO:84	C _s t _s t _s C _s t _s t _s g _s t _s g _s a _s t _s C	n.d.	n.d.
SEQ ID NO:85	A _s A _s G _s a _s a _s a _s t _s C _s C _s t _s g _s t _s g _s T _s C _s A	87	88
SEQ ID NO:86	T _s C _s T _s C _s C _s t _s g _s a _s a _s C _s C _s t _s C _s T _s C	85	83
SEQ ID NO:87	G _s A _s T _s t _s t _s C _s a _s g _s a _s g _s a _s g _s a _s G _s G _s A	94	94
SEQ ID NO:88	A _s T _s t _s t _s C _s a _s g _s a _s g _s a _s g _s A _s G _s	n.d.	n.d.
SEQ ID NO:89	T _s t _s t _s C _s a _s g _s a _s g _s a _s g _s A _s G	n.d.	n.d.
SEQ ID NO:90	A _s G _s T _s g _s a _s t _s t _s C _s a _s g _s a _s g _s A _s G _s A	96	92
SEQ ID NO:91	G _s T _s g _s a _s t _s t _s C _s a _s g _s a _s g _s A _s G	n.d.	n.d.
SEQ ID NO:92	T _s g _s a _s t _s t _s C _s a _s g _s a _s g _s A	n.d.	n.d.
SEQ ID NO:93	T _s C _s C _s t _s g _s C _s t _s C _s a _s g _s t _s g _s A _s T _s T _s T	85	86
SEQ ID NO:94	T _s T _s C _s t _s C _s C _s t _s g _s C _s t _s C _s a _s g _s T _s G _s A	78	83
SEQ ID NO:95	G _s C _s C _s a _s C _s C _s a _s t _s g _s a _s t _s g _s T _s G _s C _s A	84	75
SEQ ID NO:96	A _s C _s C _s a _s t _s g _s a _s t _s g _s t _s g _s C _s a _s T _s C _s A	94	91
SEQ ID NO:97	C _s C _s a _s t _s g _s a _s t _s g _s t _s g _s C _s a _s T _s C	n.d.	n.d.
SEQ ID NO:98	C _s a _s t _s g _s a _s t _s g _s t _s g _s C _s a _s T	n.d.	n.d.
SEQ ID NO:99	G _s A _s T _s t _s t _s t _s a _s g _s a _s g _s a _s g _s A _s G _s A	n.d.	n.d.
SEQ ID NO: 137	A _s T _s T _s t _s t _s a _s g _s a _s g _s A _s G _s G	n.d.	n.d.
SEQ ID NO: 138	T _s T _s t _s t _s a _s g _s a _s g _s A _s G	n.d.	n.d.
SEQ ID NO:100	A _s G _s T _s g _s a _s t _s t _s t _s a _s g _s a _s g _s A _s G _s A	n.d.	n.d.

Test substance	Sequence (5'-3')	Percent inhibition of PIK3CA in MCF7	Percent inhibition of PIK3CA in PC3
SEQ ID NO: 139	G_sT_sG_sa_st_st_st_st_sa_sg_sa_sG_sA_sG	n.d.	n.d.
SEQ ID NO: 140	T_sG_sa_st_st_st_st_sa_sg_sa_sG_sA	n.d.	n.d.
SEQ ID NO:101	T_sC_sC_st_sg_sc_st_st_sa_sg_st_sg_sa_sT_sT_sT	n.d.	n.d.
SEQ ID NO: 141	C_sC_sT_sg_sC_st_st_sa_sg_st_sg_sA_sT_sT	n.d.	n.d.
SEQ ID NO: 142	C_sT_sg_sC_st_st_sa_sg_st_sg_sA_sT	n.d.	n.d.
SEQ ID NO:102	T_sT_sC_st_sC_sC_st_sg_sC_st_st_sa_sg_sT_sG_sA	n.d.	n.d.
SEQ ID NO: 143	T_sC_sT_sC_sC_st_sg_sC_st_st_sa_sG_sT_sG	n.d.	n.d.
SEQ ID NO: 144	C_sT_sC_sC_st_sg_sC_st_st_sa_sG_sT	n.d.	n.d.
SEQ ID NO:103	G_sC_sC_sa_sC_sC_sa_st_sg_sa_sC_sg_st_sG_sC_sA	n.d.	n.d.
SEQ ID NO:145	C_sC_sA_sC_sC_sa_st_sg_sa_sC_sg_sT_sG_sC	n.d.	n.d.
SEQ ID NO:146	C_sA_sC_sC_sa_st_sg_sa_sC_sg_sT_sG	n.d.	n.d.
SEQ ID NO:104	A_sC_sC_sa_st_sg_sa_sC_sg_st_sg_sC_sa_sT_sC_sA	n.d.	n.d.
SEQ ID NO:147	C_sC_sA_st_sg_sa_sC_sg_st_sg_sC_sA_sT_sC	n.d.	n.d.
SEQ ID NO:148	C_sA_st_sg_sa_sC_sg_st_sg_sC_sA_sT	n.d.	n.d.

As shown in Table 4, oligonucleotides of SEQ ID NOs: 57, 60, 64, 67, 70, 74, 77, 82, 87, 90 and 96 demonstrated about 90% or greater inhibition of PIK3CA mRNA expression at 20 nM in PC3 and MCF7 cells in these experiments and are therefore preferred.

Also preferred are oligonucleotides based on the illustrated antisense oligo sequences, for example varying the length (shorter or longer) and/or nucleobase content (e.g. the type and/or proportion of analogue units), which also provide good inhibition of PIK3CA expression.

Example 9: *In vitro* analysis: Effect of Antisense Inhibition of Human PIK3CA mRNA on cell proliferation (MTS assay).

MCF7 breast cancer, PC3 prostate cancer and HCT116 colon cancer cells were treated with oligonucleotide using the cationic liposome formulation LipofectAMINE 2000 (Invitrogen) as transfection vehicle. Cells were seeded in 6-well culture plates (NUNC) the day before transfection at a density of 2.5 x 10⁵ cells/well (MCF7 and HCT116) or 2.4 x 10⁵ cells/well (PC3). The cells were treated when 75-90% confluent with different concentrations of oligos. Formulation of oligo-lipid complexes was carried out using serum-free OptiMEM (Invitrogen)

and a final lipid concentration of 2.5 µg/ml (PC3), 5 µg/ml (MCF7) or 10 µg/ml (HCT116) LipofectAMINE 2000. Cells were incubated at 37°C for 4 hours and transfection was stopped by removal of oligo-containing culture medium. After 4 hours of treatment, media was removed and cells were trypsinized and seeded to a density of 5000 cells per well in clear 96 well plate (Scientific Orange no. 1472030100) in 100 µl media. Viable cells were measured at the times indicated by adding 10 µl the tetrazolium compound [3-(4,5-dimethyl-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulfophenyl)-2H-tetrazolium, inner salt; MTS] and an electron coupling reagent (phenazine ethosulfate; PES) (CellTiter 96® AQueous One Solution Cell Proliferation Assay, Promega). Viable cells were measured at 490 nm in a Powerwave (Biotek Instruments). The OD490 nm was plotted against time/h. (See Figures 11, 12 and 14). As shown in figure 11, oligonucleotides of SEQ ID NOs: 57, 60, 64, 67, 77 and 82 inhibited proliferation of the breast cancer cell line MCF7, while none of the oligonucleotides had any pronounced effect on proliferation of PC3 cells (Fig 12). In HCT116 cells, oligonucleotides with SEQ ID NO:s 57, 60, 67, 77 and 82 inhibited the proliferation. The cell line MCF7 has the E545K hot-spot mutation and HCT116 has the H1047R hot-spot mutation in the PIK3CA gene, which makes them more dependent on PIK3CA signalling than the PC3 cell line which has no reported hot-spot mutation in the gene. The hot-spot mutations are activating mutations.

Example 10: *In vitro analysis: Effect on Caspase-3/7 induction after antisense inhibition of PIK3CA in human cancer cell lines*

PC3 prostate cancer and HCT116 colon cancer cells were treated with oligonucleotide using the cationic liposome formulation LipofectAMINE 2000 (Invitrogen) as transfection vehicle. Cells were seeded in 6-well culture plates (NUNC) the day before transfection at a density of 2.5×10^5 cells/well (MCF7 and HCT116) or 2.4×10^5 cells/well (PC3). The cells were treated when 75-90% confluent with different concentrations of oligos. Formulation of oligo-lipid complexes was carried out using serum-free OptiMEM (Invitrogen) and a final lipid concentration of 2.5 µg/ml (PC3) or 10 µg/ml (HCT116) LipofectAMINE 2000. Cells were incubated at 37°C for 4 hours and transfection was stopped by removal of oligo-containing culture medium.

After 4 hours of treatment, media was removed and cells were trypsinized and seeded to a density of 5000 cells per well in white 96 well plate (Nunc) in 100 µl media. Caspase 3/7 activity was measured at the times indicated by adding 100 µl Caspase-Glo 3/7 assay (promega). Caspase 3/7 activity was measured using a luminometer. The the caspase 3/7

activities were measured at four different time points 24h, 32h, 48h and 72h (See Figure 13 and Figure 15). SEQ ID NO: 57, 67, 77 and 82 showed dose dependent induction in Caspase 3/7 activity in HCT116 cells, which have the H1047R hot-spot mutation (Figure 15), while the oligonucleotides had no effect on caspase 3/7 induction in PC3 cells.

5 **Example 11. In vitro analysis: Biostability of PIK3CA oligonucleotides in mouse plasma**

Mouse plasma (Lithium heparin plasma from BomTac:NMRI mice, collected 14-09-05, Taconic Europe) was defrosted and aliquoted into tubes with 45 μ l plasma/tube. Following, 5 μ l oligo (200 μ M) was added to the 45 μ l plasma to a final concentration of 20 μ M. After thorough mixing, the samples were incubated at 37°C for 0-120 hrs. At different time points
10 (0h, 24h, 48h and 120h) samples were collected and the reaction was quenched by snap freezing the samples in liquid nitrogen. For analysis, samples were added loading buffer and analysed by electrophoresis on a PAGE-sequencing gel under denaturing conditions. The PIK3CA oligonucleotides showed high plasma stability for up to 120 hrs and the results are shown in Figure 16.

15 **Example 12. In vitro analysis: T_m measurement of PIK3CA oligonucleotides against complementary RNA.**

The melting temperature of the LNAoligo/RNA duplexes was determined using a UV-spectrometry system with corresponding software (Perkin Elmer, Fremont, USA). The LNA oligo and its complementary RNA were added in final concentrations of 1.5 μ M to the T_m-
20 buffer (200 nM NaCl, 0.2 nM EDTA, 20 mM NaP, pH 7.0). Duplex formation was prepared by heating the samples to 95°C for 3 min followed by cooling at room temperature for 30 min.

Melting temperature (T_m) values were measured in a Lambda 25 UV/VIS spectrometer (Perkin Elmer) and data was collected and analysed using the TempLab software (Perkin
25 Elmer). The instrument was programmed to heat the oligo duplex sample from 20-95°C and afterwards cooling the sample to 25°C. During this process the absorbance at 260 nm was recorded. The melting curves were used to calculate T_m values.

The T_m values for SEQ ID NO: 57, 60, 64, 67, 77 and 82 are presented in Figure 17.

Example 13: In vitro analysis: Down-regulation of PIK3CA and pAkt in 15PC3 cells.

30 15PC3 cell were transfected with 30 nM of LNA or treated with LY294200 (a small molecule PI3K inhibitor) for 24 and 48 h. WB: 48 h, 15 μ g protein/lane, 8% gel. Significant reduction of PIK3CA levels was observed after transfection of 15PC3 cells with PIK3CA LNAs. (Figure 19) pAkt levels were reduced up to 80% at 24 h post transfection determined by ELISA.

(Figure 19). Transfection with the oligomer having the sequence of SEQ ID NO: 82 had less effect on downstream signals compared to the other tested LNAs.

Example 14: *In vivo* analysis: Down-regulation of mouse PIK3CA in mouse liver after i.v. administration of PIK3CA oligonucleotides.

5 Female NMRI mice received i.v. injection of oligonucleotides having the sequences of SEQ ID NO: 57, 60, 67, 77 and 82 on three consecutive days at a dosage of 25mg/kg. Animals were sacrificed 24h after last dosing. The liver was stored in RNA^{later} stabilizing solution until use. Total RNA was extracted from liver tissue and PIK3CA mRNA levels were analyzed with qPCR. Data were compared to PIK3CA expression in saline treated control animals. As shown in Figure 21, all oligonucleotides in the study showed potent down-
10 regulation of PIK3CA mRNA.

All PIK3CA oligomers used in the second screening showed potent down-regulation of PIK3CA in PC3 and MCF7 cells with IC₅₀ values below 1nM. SEQ ID NO: 82 also shows down-regulation of the control target beta-catenin gene in both MCF7 and PC3 cells (SEQ
15 ID NO: 82 has 2 mismatches when compared to the reverse complement of the best-aligned target region of beta-catenin).

Example 15: *In vivo* analysis: Effect of oligomers on lung cancer tumor size in mice

Six- to seven-week old male athymic nu/nu mice (Harlan Sprague Dawley) weighing an average of 27.3±2.4g were used in the study. Five million cells of Calu-6 (lung cancer cell
20 line) were suspended in PBS (Gibco#14190) were injected subcutaneously into each mouse. The mice were injected with two hundred µl of oligomer intravenously when the average tumor size reached 150 mm³. Oligomers were given every 3 days for a total of 5 dosings. The control vehicles were given the same dosing regimen as the oligomers. The tumor volumes for each mouse were determined by measuring two dimensions with calipers and calculated using the formula: tumor volume = (length x width²)/2). Figure 20 shows
25 down regulation of PIK3CA expression in liver by oligomers of the invention.

The following oligomers were found to have a good toxicity profile in terms of good animal survival in *in vivo* experiments at 3mg/kg dose – SEQ IDs 60, 67, 77 & 82. SEQ IDs 60,67 and 77 showed a good toxicity profile at 10mg/kg dosage.

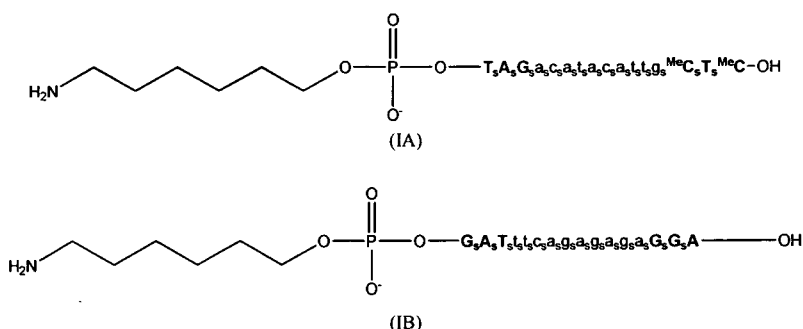
Table 6: Effect of oligomers on PIK3CA mRNA in mouse liver and tumor and on tumor size

Group	Dose (mg/kg)	Tumor KD	Liver KD	TGI on day 12 (%)
Control	----	ND		---

Table 6: Effect of oligomers on PIK3CA mRNA in mouse liver and tumor and on tumor size				
Group	Dose (mg/kg)	Tumor KD	Liver KD	TGI on day 12 (%)
Control	----	ND		---
SEQ ID 57	3	ND	20 ±23	22.9
	10	ND	62 ±16	18.0
SEQ ID 60	3	ND	27 ± 14	24.7
	10	ND	66 ±11	53.6
	30	ND	84 ± 8	49.4
	100	ND	88 ± 4.0	54.1
SEQ ID 67	3	16 ± 12	33 ± 37	50.6
	10	36 ±11	73 ±16	50.5
	30	58 ±5.2	82 ± 17	44.5
	100	65 ±12	81 ± 4.2	31.5
SEQ ID 77	3	ND	65 ±18	57.6
	10	ND	86 ± 5.6	21.2
	30	ND	91 ± 6.9	48.5
SEQ ID 82	3	ND	62 ± 26	37.5
	10	ND	72 ± 10	50.0

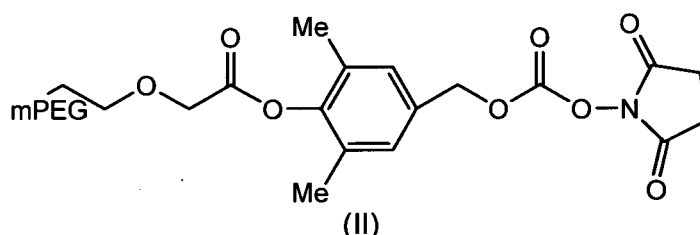
Example 16: Preparation of conjugates of oligomers with polyethylene glycol

The oligomers having sequences shown as SEQ ID NO: 60 or SEQ ID NO: 87 are functionalized on the 5' terminus by attaching an aminoalkyl group, such as hexan-1-amine blocked with a blocking group such as Fmoc to the 5' phosphate groups of the oligomers using routine phosphoramidite chemistry, oxidizing the resultant compounds, deprotecting them and purifying them to achieve the functionalized oligomers, respectively, having the formulas (IA) and (IB):

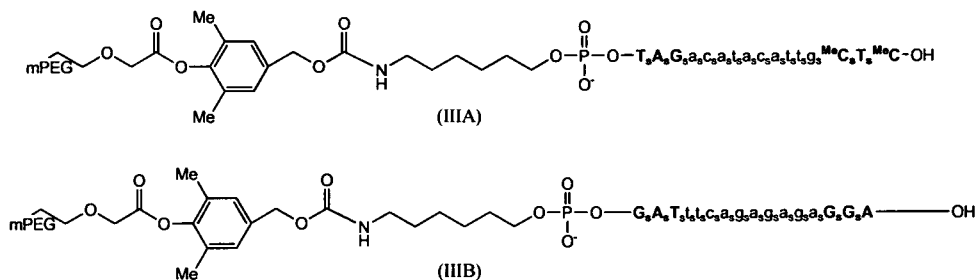


wherein the bold uppercase letters represent nucleoside analogue monomers, lowercase letters represent DNA monomers, the subscript "s" represents a phosphorothioate linkage, and ^{Me}C represents 5-methylcytosine.

5 A solution of activated PEG, such as the one shown in formula (II):

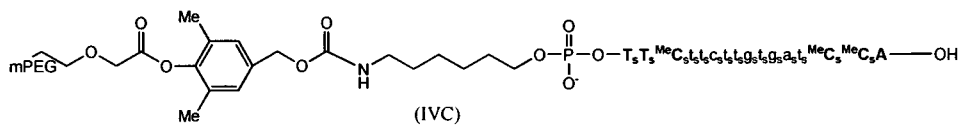
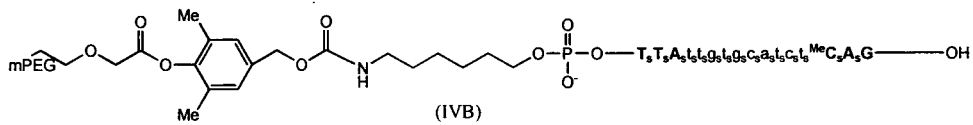
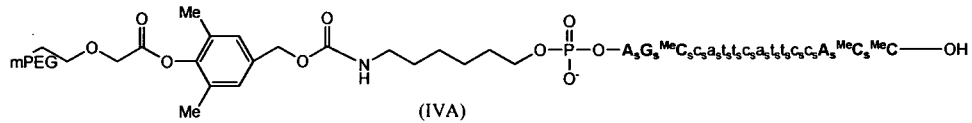


wherein the PEG moiety has an average molecular weight of 12,000, and each of the compounds of formulas (IA) and (IB) in PBS buffer are stirred in separate vessels at room temperature for 12 hours. The reaction solutions are extracted three times with methylene chloride and the combined organic layers are dried over magnesium sulphate and filtered and the solvent is evaporated under reduced pressure. The resulting residues are dissolved in double distilled water and loaded onto an anion exchange column. Unreacted PEG linker is eluted with water and the products are eluted with NH₄HCO₃ solution. Fractions containing pure products are pooled and lyophilized to yield the conjugates SEQ ID NOs: 60 and 87, respectively as show in formulas (IIIA) and (IIIB):



wherein each of the oligomers of SEQ ID NOs: 60 and 87 is attached to a PEG polymer having average molecular weight of 12,000 via a releasable linker.

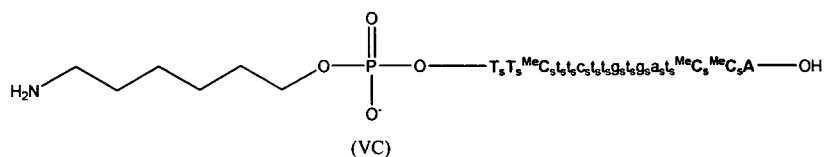
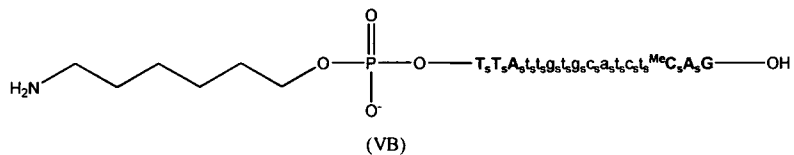
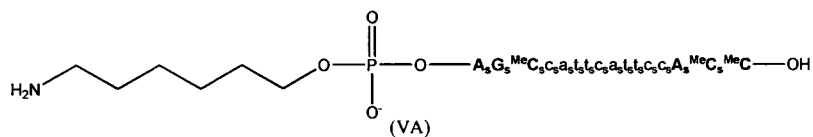
Chemical structures of PEG polymer conjugates that can be made with oligomers having sequences shown in SEQ ID NOs: 67, 77 and 82 using the process described above are respectively shown in formulas (IVA), (IVB) and (IVC):



5

wherein bold uppercase letters represent beta-D-oxy-LNA monomers, lowercase letters represent DNA monomers, the subscript "s" represents a phosphorothioate linkage and ^{Me}C represent 5-methylcytosine.

Activated oligomers that can be used in this process to respectively make the conjugates shown in formulas (IVA), (IVB) and (IVC) have the chemical structures shown in formulas (VA), (VB) and (VC):



CLAIMS

1. An oligomer of between 10 - 30 nucleotides in length which comprises a contiguous nucleotide sequence of a total of between 10 – 30 nucleotides, wherein said contiguous nucleotide sequence is at least 80% homologous to a region corresponding to a mammalian PIK3CA gene or the reverse complement of an mRNA, such as SEQ ID NO: 1 or naturally occurring variant thereof, wherein said oligomer comprises at least one LNA unit.
2. The oligomer according to claim 1, wherein the contiguous nucleotide sequence is at least 80% homologous to a region corresponding to i) SEQ ID 115 or SEQ ID NO 7 or ii) SEQ ID NO 119 or SEQ ID NO 11, or iii) a sequence selected from any of SEQ ID NOs 2 - 16 and/or 17 - 28 and/or 110 - 124 and/or 125 – 136 and/or 149 – 160.
3. The oligomer according to claim 1 or 2, wherein the contiguous nucleotide sequence comprises no mismatches or no more than one or two mismatches with the reverse complement of the corresponding region of SEQ ID NO 1.
4. The oligomer according to any one of claims 1 – 3, wherein the nucleotide sequence of the oligomer consists of the contiguous nucleotide sequence.
5. The oligomer according to any one of claims 1 – 4, wherein the contiguous nucleotide sequence is between 10 – 18 nucleotides in length.
6. The oligomer according to any one of claims 1 – 5, wherein the contiguous nucleotide sequence comprises nucleotide analogues.
7. The oligomer according to claim 6, wherein the nucleotide analogues are sugar modified nucleotides, such as sugar modified nucleotides selected from the group consisting of: Locked Nucleic Acid (LNA) units; 2'-O-alkyl-RNA units, 2'-OMe-RNA units, 2'-amino-DNA units, and 2'-fluoro-DNA units.
8. The oligomer according to claim 6, wherein the nucleotide analogues are LNA.
9. The oligomer according to any one of claims 6 – 8 which is a gapmer.
10. The oligomer according to any one of claims 1 – 9, which inhibits the expression of PIK3CA gene or mRNA in a cell which is expressing PIK3CA gene or mRNA.

11. The oligomer according to any one of claims 1 - 10, wherein the oligomer consists or comprises an contiguous nucleotide sequence selected from

5'- A_sG_s^{Me}C_sC_sa_st_st_sC_sa_st_st_sC_sC_sA_s^{Me}C_s^{Me}C -3' (SEQ ID NO: 67) and

5'- T_sT_sA_st_st_sg_st_sg_sc_sa_st_sc_st_s^{Me}C_sA_sG -3' (SEQ ID NO: 77),

5 wherein uppercase letters denote beta-D-oxy-LNA monomers and lowercase letters denote DNA monomers, the subscript "s" denotes a phosphorothioate linkage, and ^{Me}C denotes a beta-D-oxy-LNA monomer containing a 5-methylcytosine base.

12. A conjugate comprising the oligomer according to any one of claims 1 – 11, and at least one non-nucleotide or non-polynucleotide moiety covalently attached to said oligomer.

10 13. A pharmaceutical composition comprising the oligomer according to any one of claims 1 – 11, or the conjugate according to claim 12, and a pharmaceutically acceptable diluent, carrier, salt or adjuvant.

14. The oligomer according to any one of claims 1 – 11, or the conjugate according to claim 12, for use as a medicament, such as for the treatment of such as hyperproliferative
15 diseases such as cancer.

15. The use of an oligomer according to any one of the claims 1-11, or a conjugate as defined in claim 12, for the manufacture of a medicament for the treatment of such as hyperproliferative diseases such as cancer.

20 16. A method of treating such as hyperproliferative diseases such as cancer, said method comprising administering an oligomer according to any one of the claims 1-11, or a conjugate according to claim 12, or a pharmaceutical composition according to claim 13, to a patient suffering from, or likely to suffer from such as hyperproliferative diseases such as cancer.

25 17. A method for the inhibition of PIK3CA in a cell which is expressing PIK3CA, said method comprising administering an oligomer according to any one of the claims 1-11, or a conjugate according to claim 12 to said cell so as to inhibit PIK3CA in said cell.

FIGURE 2

PIK3CA m RNA expression in P63 cells 24h after transfection
Data from three independent screens

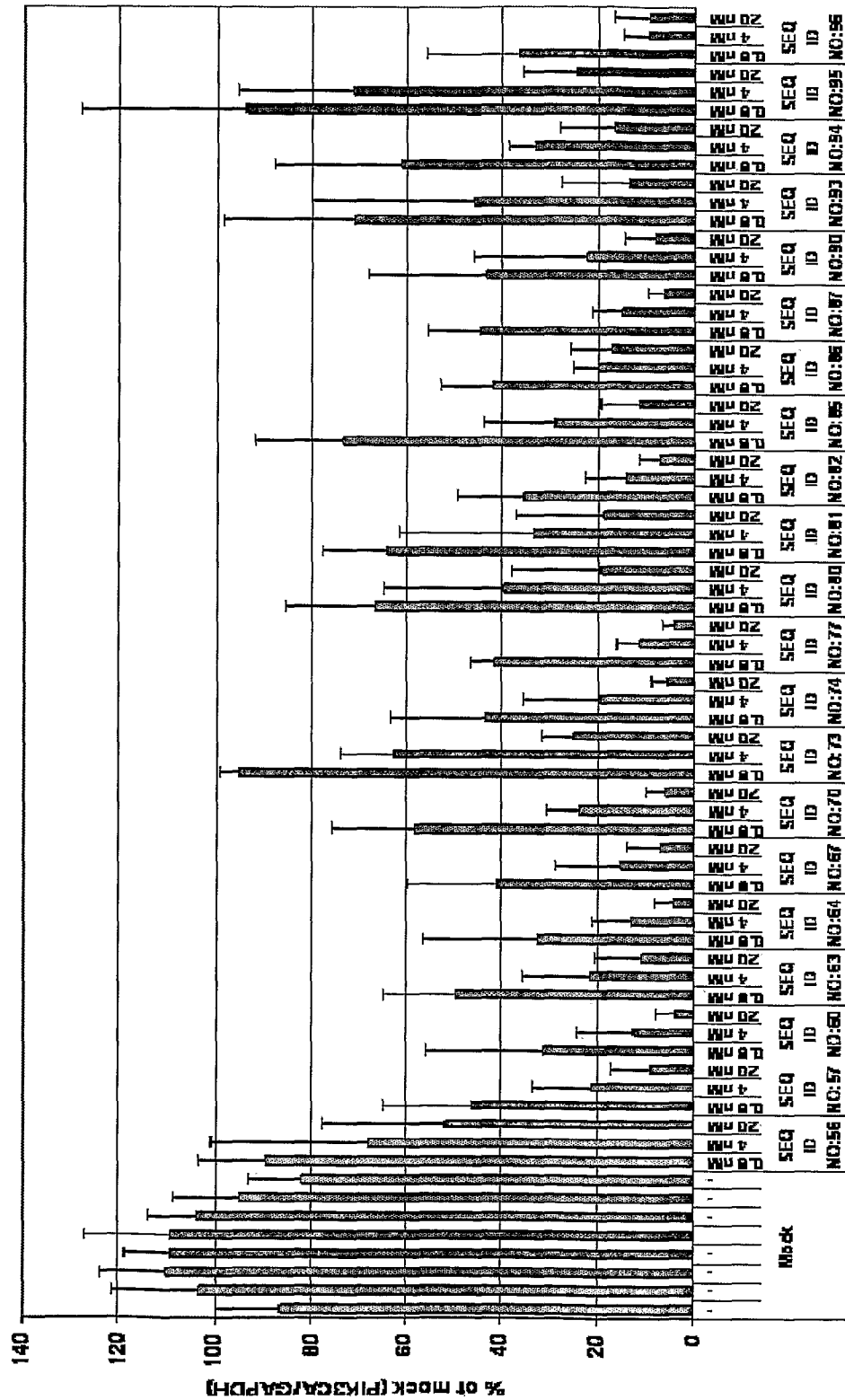


FIGURE 3

NM_006218	(1)	1	TCTCCCTCGGCGCCGCCGCCGCCGCCGCCGGGCTGGGACCCGATGCGGT	50
NM_008839	(1)		-----	
Consensus	(1)			
NM_006218	(51)	51	TAGAGCCGCGGAGCCTGGAAGAGCCCCGAGCGTTTCTGCTTGGGACAAC	100
NM_008839	(1)		-----	
Consensus	(51)			
NM_006218	(101)	101	CATACATCTAATTCCTTAAAGTAGTTTTATATGTAAAACCTTGCAAGAAT	150
NM_008839	(1)		-----	
Consensus	(101)			
NM_006218	(151)	151	CAGAACAAATGCCTCCACGACCATCATCAGGTGAACCTGPGGGCATCCACT	200
NM_008839	(1)		-----ATGCCTCCACGACCATCTTCGGGTGAACCTGPGGGCATCCACT	
Consensus	(151)		ATGCCTCCACGACCATC TC GGTGAACCTGPGGGCATCCACT	
NM_006218	(201)	201	TGATGCCCCCAAGAATCCTAGTAGAATGTTTACTACCAAAATGGAATGATA	250
NM_008839	(44)		TGATGCCCCCAAGAAATCCTAGTAGAATGTTTACTCCCAATGGAATGATA	
Consensus	(201)		TGATGCCCCCA GAATCCTAGT GAATGTTTACT CC AATGGAATGATA	
NM_006218	(251)	251	GTGACTTTAGAATGCCCTCCGTGAGGCTACATTAATAACCAATAAGCATGA	300
NM_008839	(94)		GTGACTTTAGAATGCCCTCCGTGAGGCCACACTCGTCACCAATCAAAATGATA	
Consensus	(251)		GTGACTTTAGAATGCCCTCCGTGAGGC ACA T T ACCAT AA CATGA	
NM_006218	(301)	301	ACTATTTAAGAAGCAAGAAAATACCCCTCCATCAACTTCTTCAAGATG	350
NM_008839	(144)		ACTGTTTCAAGAGGCCAGGAAATACCCCTCCATCAGCTTCTGCAAGACG	
Consensus	(301)		ACT TT A AGA GC AG AAATACCC CTCCATCA CTCT CAAGA G	
NM_006218	(351)	351	AACTCTTACATTTTCGTAAAGTGTACTCAAGAAGCAGAAAGGGAAGAA	400
NM_008839	(194)		AACTCTTACATTTTCGTAAAGTGTACCCCAAGCAGAAAGGGAAGAA	
Consensus	(351)		AA CTCTTACATTTTCGTAAAGTGT AC CAAGAAGCAGAAAGGGAAGAA	
NM_006218	(401)	401	TTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTCAACCCTT	450
NM_008839	(244)		TTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTCAACCCTT	
Consensus	(401)		TTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTCAACCCTT	
NM_006218	(451)	451	TTTAAAAGTAATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATC	500
NM_008839	(294)		TTTAAAAGTATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATC	
Consensus	(451)		TTTAAAAGT ATTGAACCAAGTAGGCAACCGTGAAGAAAAGATCCTCAATC	
NM_006218	(501)	501	GAGAAATGGTTTTGGTATCGGCATGCCAGTGTGTGAATTTGATATGGTT	550
NM_008839	(344)		GAGAAATGGTTTTGGTATCGGCATGCCAGTGTGTGAATTTGATATGGTT	
Consensus	(501)		GAGAAATGGTTTTG TAT GGCATGCCAGTGTGTGAATTTGATATGGTT	
NM_006218	(551)	551	AAAGATCCAGAAGTACAGGACTTCCGAAGAAATATTCTGAACGTTTGTAA	600
NM_008839	(394)		AAAGATCCAGAAGTCCAGACTTTCGAAGAAACATTTCTGAATGTTTGCAN	
Consensus	(551)		AAAGATCCAGAAGT CA GACTT CGAAG AA ATCTGAA GTTIG AA	
NM_006218	(601)	601	AGAAGCTGTGGATCTTAGGGACCTCAATTCACCTCATAGTAGAGCAATGT	650
NM_008839	(444)		AGAAGCTGTGGACCTGCGGGATCTCAACTCGCCTCATAGCAGAGCAATGT	
Consensus	(601)		AGAAGCTGTGGA CT GGA CTCAA TC CCTCATAG AGAGCAATGT	
NM_006218	(651)	651	ATGTCTATCCTCCAAATGTAGAATCTTACCAGAAATGCCAAAGCACATA	700
NM_008839	(494)		ATGTCTACCCTCCAAATGTGAGTCTTCCAGAAACTGCCAAAGCACATC	
Consensus	(651)		ATGTCTA CCTCCAAATGT GA TCTTC CCAGAA TGCCAAAGCACAT	
NM_006218	(701)	701	TATAATAAATTAGATAAAGGGCAAATAATAGTGGTGAATCTGGGTAATAGT	750
NM_008839	(544)		TACAACAAGTATAGATAAAGGACAAATCATAGTGGTGAATTTGGGTAATAGT	
Consensus	(701)		TA AA AA TTAGATAAAGG CAAAT ATAGTGGTGAAT TGGGTAATAGT	
NM_006218	(751)	751	TTCTCCAAATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACT	800
NM_008839	(594)		TTCTCCAAACAACGACAAGCAGAAGTACTCTGAAATCAATCATGACT	
Consensus	(751)		TTCTCCAAA AA GACAAGCAGAAGTA ACTCTGAA ATCAA CATGACT	
NM_006218	(801)	801	CTGTACCAGAACAACTAATGCTGAAGCAATCAGGAAAAAACTCGAAGT	850
NM_008839	(644)		CTGTACCAGAACAACTAATGCTGAAGCAATCAGGAAAAAACTCGGAGT	
Consensus	(801)		GTGT CCAGA CAAGT ATTGCTGAAGC ATCAGGAAAA ACTCG AG	
NM_006218	(851)	851	ATGTTGCTATCCTCTGAACAATAAACTCTGTGTTTTAGAATATCAGGG	900
NM_008839	(694)		ATGTTGTTGCTCCTCTGAGCAGCTGAAACTCTGTGTTTAGAATATCAGGG	
Consensus	(851)		ATGTTG T TCCTCTGA CA CT AAATCTGTGT TTAGAATATCAGGG	
NM_006218	(901)	901	CAAGTATATTTAAAAGTGTGTGGATGTGATGAATACTTCTAGAAAAAT	950
NM_008839	(744)		CAAGTATATTTGAAAAGTGTGTGGATGTGATGAATACTTCTAGAAAAAT	
Consensus	(901)		CAAGTATATT T AAAGTGTGTGG TGTGA GAATACTTCT GAAAA T	
NM_006218	(951)	951	ATCTCTGAGTCAGTATTAAGTATATAAGAAGCTGTATAATGCTTGGGAGG	1000
NM_008839	(794)		ACCTCTGAGTCAGTACAAGTACATAAGAAGCTGTATAATGCTTGGGAGG	
Consensus	(951)		A CCTCTGAGTCAGTA AAGTA ATAAGAAGCTGTATAATGCT GGGAGG	
NM_006218	(1001)	1001	ATGCCCAATTTGATGTTGATGGCTAAAAGAAAGCCTTTATTTCTCAACTGCC	1050
NM_008839	(844)		ATGCCCAACTTTGATGTTGATGGCCAAAAGAAAGCCTTACTTCTCAGCTGCC	

Consensus (1001) ATGCCCAA TTGATG TGATGGC AAAGAAAGCCT TA TCTCA CTGCC
1051 1100

NM_006218 (1051) AATGGACTGTTTACAAATGCCATCTTATTCAGACGCATTTCCACAGCTA
NM_008839 (894) GATTGATAGCTTCACCATGCCGTCATCTCCAGGGGCATCTCCACAGCCA
Consensus (1051) AT GA G TT AC ATGCC TC TA TCCAG CGCAT TCCACAG A
1101 1150

NM_006218 (1101) CACCATATATGAATGGAGAAACATCTACAAAATCCCTTTGGTTATAAAT
NM_008839 (944) CACCCTACATGAATGGAGAGACATCTACGAAATCCCTCTGGTTCATAAAT
Consensus (1101) CACC TA ATGAATGGAGA ACATCTAC AAATCCCT TGGGT ATAAAT
1151 1200

NM_006218 (1151) AGTGCACCTCAGAATAAAAATTCCTTTGTGCAACCTACGTGAATGTAATAT
NM_008839 (994) AGTGGCCTCAGAATAAAAATTCCTTTGTGCAACCTATGTAATGTAATAT
Consensus (1151) AGTGC CTCAGAATAAAAATTCCTTTGTGCAACCTA GT AATGTAATAT
1201 1250

NM_006218 (1201) TCGAGACATTGATAAGATCTATGTTGCAACAGGTATCTACCATGGAGGAG
NM_008839 (1044) TCGAGACATTGATAAGATCTATGTTGCAACAGGTATCTACCATGGAGGAG
Consensus (1201) TCGAGACATTGATAAGATCTATGTTGCAACAGGTATCTACCATGGAGGAG
1251 1300

NM_006218 (1251) AACCTTATGTGACAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCC
NM_008839 (1094) AACCTTATGTGACAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCC
Consensus (1251) AACCTTATGTGACAATGTGAACACTCAAAGAGTACCTTGTTCCAATCC
1301 1350

NM_006218 (1301) AGGTGGAATGAATGGCTGAATATGATATATACATTCCTGATCTTCCTCG
NM_008839 (1144) AGGTGGAATGAATGGCTGAATATGATATATACATTCCTGATCTTCCTCG
Consensus (1301) AGGTGGAATGAATGGCTGAATATGATATATACATTCCTGATCTTCCTCG
1351 1400

NM_006218 (1351) TGCTGCTCGACTTTGCCCTTTCATTTGCTCTGTTAAAGGCCGAAAGGGTG
NM_008839 (1194) TCTGGCGCGCTTTGCCCTTTCATTTGCTCTGTTAAAGGCCGAAAGGGTG
Consensus (1351) T GC CG CTTTGCCTTTC AT TGCTCTGTTAAAGGCCGAAAGGGTG
1401 1450

NM_006218 (1401) CTAAAGAGGAACACTGTCCATTGGCATGGGAAAATATAAACTTGTTTGAT
NM_008839 (1244) CTAAAGAGGAGCACTGTCCGTTGGCTGGGGAAACATAAACTTGTTTGAT
Consensus (1401) CTAAGAGGAGCACTGTCCGTTGGCTGGGGAAACATAAACTTGTTTGAT
1451 1500

NM_006218 (1451) TACACAGACACTCTAGTATCTGAAAAATGGCTTTGAATCTTTGGCCAGT
NM_008839 (1294) TATACAGACACCTAGTGTCCGGAAAAATGGCTTTGAATCTTTGGCCAGT
Consensus (1451) TA ACAGACAC CTAGT TC GG AAAATGGCTTTGAATCT TGGCC AG
1501 1550

NM_006218 (1501) ACCTCATGGATTAGAAGATTTGCTGAACCCCTATTGGTGTACTGGATCAA
NM_008839 (1344) ACCGCATGGGTTAGAAGATCTGCTGAACCCCTATTGGTGTACTGGATCAA
Consensus (1501) ACC CATGG TTAGAAGAT TGCTGAACCCCTATTGGTGTACTGG TCAA
1551 1600

NM_006218 (1551) ATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAGTTGACTGGTTGAGC
NM_008839 (1394) ATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAGTTGACTGGTTGAGC
Consensus (1551) ATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAGTTGA TGTTGAGC
1601 1650

NM_006218 (1601) AGTGTGGTAAAGTTCCAGATATGTCAGTGAATGAAGAGCATGCCAATTG
NM_008839 (1444) AGTGTGGTAAAGTTCCAGATATGTCAGTGAATGAAGAGCATGCCAATTG
Consensus (1601) AGTGTGGT AAGTT CCAGA ATGTC GTGAT GAAGA CATGCCAATTG
1651 1700

NM_006218 (1651) GTCGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTA
NM_008839 (1494) GTCGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTA
Consensus (1651) GTC GT TCCCGAGAAGC GGATT AG TA TCCCA CAGGACTGAGTA
1701 1750

NM_006218 (1701) ACAGACTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTC
NM_008839 (1544) ACAGACTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAACAGCTC
Consensus (1701) ACAGACTAGC AGAGACAATGA TTAAG GAAAATGACAA GAACAGCTC
1751 1800

NM_006218 (1751) AAAGCAATTTCTACACAGATTCCTCTCTGAAATCACTGAGCAGGAGAA
NM_008839 (1594) CGAGCACTTTGCACCCGGGACCCACTATCTGAATCACTGAACAGAGAA
Consensus (1751) AGCA TTT AC CG GA CC CT TCTGAAATCACTGA CA GAGAA
1801 1850

NM_006218 (1801) AGATTTTCTATGGAGTACACAGACACTATTGTGTAACATATCCCCGAAATTC
NM_008839 (1644) AGACTTCCTATGGAGCCACAGACACTACTGCGTAACATATPCCTGAAATTC
Consensus (1801) AGA TT CTATGGAG CACAGACACTA TG GTAACATAT CC GAAAT C
1851 1900

NM_006218 (1851) TACCCAAATTCCTTCTGTCTGTAAATGGAATTOTAGAGATGAAGTAGCC
NM_008839 (1694) TACCCAAATTCCTTCTGTCTGTAAATGGAATTCAGAGACGAAGTGGCC
Consensus (1851) TACCCAAATTCCTTCTGTCTGT AA TGGAATTC AGAGA GAAGT GCC
1901 1950

NM_006218 (1901) CAGATGTATTGCTTTGGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGC
NM_008839 (1744) CAGATGTACTGCTTAGTAAAAGATTGGCCTCCAATCAAACCTGAACAGGC
Consensus (1901) CAGATGTA TGCTT GAAAAGATTGGCCTCCAATCAAACC GA CA GC
1951 2000

NM_006218 (1951) TATGGAACCTCTGGACTGTAATFACCCAGATCCTATGGTTCGAGGTTTGT
NM_008839 (1794) CATGGAACCTCCTGGACTGTAACATCCAGATCCTATGGTTCGAGGTTTGT
Consensus (1951) ATGGAACCT CTGGACTGTAA TA CCAGATCCTATGGTTCG GTTTGT
2001 2050

NM_006218 (2001) CTGTTCCGCTTGGAAAAATATTTAACAGATGACAAAATTTCTCAGTAT
NM_008839 (1844) CTGTTCCGCTTGGAAAAATATTTAACAGATGACAAAATTTCTCAGTAT
Consensus (2001) CTGTTCCGCTT GAAAAATATTTAACAGATGACAAAATTTCTCAGTAT
2051 2100

NM_006218 (2051) TTAATTCAGCTAGTACAGGTCCTAAAATATGAACAAATTTGGATAACTT
NM_008839 (1894) CTCATTCAACTTGACAGGTCCTAAAATATGAACAAATTTGGATAACTT
Consensus (2051) T APTCA CT GTACAGGTC TAAAATATGAACA TATTTGGATAAC T

		2101	2150
NM_006218	(2101)	GCTTGTGAGATTTTACTGAAGAAAGCATTGACTAATCAAAGGATTGGCC	
NM_008839	(1944)	GCTTGTGAGATTTTACTCAAGAAAGCATTGACAAATCAAAGGATTGGCC	
Consensus	(2101)	GCTTGTGAGATTTTACT AAGAAAGCATTGAC AATCAAAGGATTGG C	2151
NM_006218	(2151)	ACTTTTCTTTTGGCATTAAAATCTGAGATGCACAATAAAACAGTTAGC	2200
NM_008839	(1994)	ATTTTCTTTTGGCATTAAAATCTGAGATGCACAATAAAGACTGTCAGT	
Consensus	(2151)	A TTTTCTTTTGGCATTAAAATCTGAGATGCACAATAA AC GT AG	2201
NM_006218	(2201)	CAGAGGTTTGGCCTGCTTTTGGAGTCTATTTGTCGTGCATGTGGGATGTA	2250
NM_008839	(2044)	CAGAGGTTTGGCCTGCTATTGGAGTCTACTGCCGTGCTGTGGGATGTA	
Consensus	(2201)	CAGAGGTTTGGCCTGCT TTGGAGTCTTA TG CGTGC TGTGGGATGTA	2251
NM_006218	(2251)	TTTGAAGCACCTGAATAGGCCAAGTCGAGGCAATGGAAAAGCTCAATAACT	2300
NM_008839	(2094)	TCTGAAGCACCTGAACAGACAAGTAGAGGCCATGGAGAAGCTCATCAACC	
Consensus	(2251)	T TGAAGCACCTGAA AG CAAGT GAGGC ATGGA AAGCTCAT AAC	2301
NM_006218	(2301)	TAACTGACATTTCTCAAACAGGAGAAGAAGGATGAAACACAAAAGGTACAG	2350
NM_008839	(2144)	TAACTGACATTTCTTAAACAGGAGAAGAAGGATGAAACACAAAAGGTACAG	
Consensus	(2301)	TAAC GACAT CT AA CAGGAGAAGAAGGATGA ACACAAAAGGTACAG	2351
NM_006218	(2351)	ATGAAGTTTTTACTTGAACAAATGAGGCGACCAGATTTTCATGGATGCTCT	2400
NM_008839	(2194)	ATGAAGTTTTTGGTTGACAGATGAGACAGCCAGACTTCATGGATGCTCT	
Consensus	(2351)	ATGAAGTTTTT GTGA CA ATGAG C CCAGA TTCATGGATGCT T	2401
NM_006218	(2401)	ACAGGGCTTTCTGCTCTCTTAAACCCTGCTCATCACTAGGAAACCTCA	2450
NM_008839	(2244)	GCAGGGTTTTCTGCTCTCTGAATCCCTGCTCACCACTAGGAAACCTCA	
Consensus	(2401)	CAGGG TTTCTGTC CCTCT AA CCTGCTCA CACTAGGAAACCTCA	2451
NM_006218	(2451)	GGCTTGAAGAGTGTGCAATTATGTCCTCTGCAAAAAGGCCACTGTGGTTG	2500
NM_008839	(2294)	GGCTTGAAGAGTGTGCAATTATGTCCTCTGCAAAAAGGCCACTGTGGTTG	
Consensus	(2451)	GGCTTGAAGAGTGTGCAATTATGTCCTCTGCAAAAAGGCCACTGTGGTTG	2501
NM_006218	(2501)	AAATGGGAGAACCCAGACATCATGTCAGAGTACTGTTTCAGAACAAATGA	2550
NM_008839	(2344)	AAATGGGAGAACCCAGACATCATGTCAGAGTACTGTTTCAGAACAAATGA	
Consensus	(2501)	AAATGGGAGAACCCAGACATCATGTCAGAG TACTGTTTCAGAACAAATGA	2551
NM_006218	(2551)	GATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAAACCTTC	2600
NM_008839	(2394)	GATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAAACCTTC	
Consensus	(2551)	GATCATCTTTAAAAATGG GA GA TTACGGCAAGATATG TAAC CTTT	2601
NM_006218	(2601)	AAATATATTCGTAATATGAAAAATATCTGGCAAAATCAAGGTTCTGATCTT	2650
NM_008839	(2444)	AGATCATCCGAATCATGGAGAACATCTGGCAAAATCAAGGTTCTGATCTT	
Consensus	(2601)	A AT AT CG AT ATGGA AA ATCTGGCAAAA CAAGG CTTGA CTT	2651
NM_006218	(2651)	CGAATGTTACCTTATGGTTGCTGTCAATCGGTGACTGTGTGGGACTTAT	2700
NM_008839	(2494)	CGATGCTACCTTATGGTTGCTGTCAATCGGTGACTGTGTGGGACTTAT	
Consensus	(2651)	CG ATG TACCTTATGG TGTCT TC AT GG GACTGTGTGGG CT AT	2701
NM_006218	(2701)	TGAGGTGGTGCAGAAATCTCACACTATTATGCAAAATTCAGTGCAAAAGCC	2750
NM_008839	(2544)	CGAGGTGGTGCAGAAATCTCACACTATTATGCAAAATTCAGTGCAAAAGCC	
Consensus	(2701)	GAGGTGGTG GAAA TCTCACAC AT ATGCAAAAT CAGTGCAAAAG G	2751
NM_006218	(2751)	GOTTGAAGGTGCACTGCAGTTCAACAGCCACACACTACATCAGTGGCTC	2800
NM_008839	(2594)	GCCTGAAGGGGGCGCTGCAGTTCAACAGCCACACACTGCATCAATGGCTC	
Consensus	(2751)	GC TGAA GG GC CTGCAGTTCAACAGCCACACACT CATCA TGGCTC	2801
NM_006218	(2801)	AAAGACAAGAACAAGGAGAAATATATGATGCAGCCATTGACCTGTTTAC	2850
NM_008839	(2644)	AAAGACAAGAACAAGGCGAGATATATGATGCAGCCATTGACCTGTTTAC	
Consensus	(2801)	AA GACAAGAACA G G GA ATATATGATGCAGCCATTGACCTGTT AC	2851
NM_006218	(2851)	ACGTTTATGCTGGATCTGTGAGCTACCTTCAATTTGGGAATTGGAG	2900
NM_008839	(2694)	TCGGTCTGCTGGTGGTACTGCGTGGCAACCTTATCTTGGGAATTGGAG	
Consensus	(2851)	CG TC TG GCTGG TACTG GT GC ACCTT AT TTGGGAATTGGAG	2901
NM_006218	(2901)	ATCGTCAACAATAGTAACATCATGGTGAAGACGATGGACAACCTGTTCA	3000
NM_008839	(2744)	ACCGGCACAAACAGCAACATCATGGTGAAGATGACGGACAGCTGTTTCAT	
Consensus	(2901)	A CG CACAA AG AACATCATGGTGAAGA GA GGACA CTGTTTCAT	2951
NM_006218	(2951)	ATAGATTTTGGACACTTTTGGATCACAAGAAGAAAAATTTGGTTATAA	3050
NM_008839	(2794)	ATAGATTTTGGGCACTTTTGGATCACAAGAAGAAAAATTTGGTTATAA	
Consensus	(2951)	ATAGATTTTGG CACTTTTGGATCACAAGAAGAAAAATTTGG TATAA	3001
NM_006218	(3001)	ACGAGAACGTGTGCCATTTGTTTGGACACAGGATTTCTTAATAGTGATTA	3100
NM_008839	(2844)	CCGGGAACGTGTGCCATTTGTTTGGACACAGGATTTCTTAATAGTGATTA	
Consensus	(3001)	CG GAACGTGTGCCATTTGT TTGACACAGGATTTCTT AT GTGATTA	3051
NM_006218	(3051)	GTAAAGGAGCCCAAGAAATGCACAAGACAAGAAATTTGAGAGTTTCAG	3150
NM_008839	(2894)	GTAAAGGAGCCCAAGAAATGCACAAGACAAGAAATTTGAGAGTTTCAG	
Consensus	(3051)	GTAA GGAGC CAAGA T CAC AAGAC AGAGA TTTGAGAGTTTCAG	3101
NM_006218	(3101)	GAGATGTTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAATCTCTT	3200
NM_008839	(2944)	GAGATGTTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAATCTCTT	
Consensus	(3101)	GAGATGTTTACAAGGCTTA CTAGC ATTCG CAGCATGCCAATCTCTT	3151

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NM_006218 (3151) CATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAAT
NM_008839 (2994) CATCAACCTTTTTCATGATGCTTGGCTCTGGAATGCCAGAACTACAAT
Consensus (3151) CAT AA CTTTT TCAATGATGCTTGGCTCTGGAATGCCAGAACTACAAT
                                     3250
NM_006218 (3201) CTTTTGATGACATTGCATATCGAAAGACCTAGCCTTAGATAAAACT
NM_008839 (3044) CTTTTGATGACATTGCATATATCCGAAAGACTCTAGCCTTGGACAAAAC
Consensus (3201) CTTTTGATGACATTGCATA AT CGAAAGAC CTAGCCTT GA AAAACT
                                     3251
NM_006218 (3251) GAGCAAGAGGCTTTGGAGTATTCATGAAACAAATGAATGATGCACATCA
NM_008839 (3094) GAGCAAGAGGCTTTGGATATTTCAAAAAGCAAATGAATGATGCACATCA
Consensus (3251) GAGCAAGA GCTTTGGA TATTCA AA CAAATGAATGATGCACATCA
                                     3300
NM_006218 (3301) TGGTGGCTGGACAACAAAATGGATTGGATCTCCACACAATTAACAGC
NM_008839 (3144) TGGTGGATGGACGACAAAATGGATTGGATCTCCACACCAATCAAGCAGC
Consensus (3301) TGGTGG TGGAC ACAAATGGATTGGATCTCCACAC AT AA CAGC
                                     3351
NM_006218 (3351) ATGCATTGAACTGAAAAGATAAAGTGAAGAAATGAAAGCTCACTCTGGATT
NM_008839 (3194) ATGCTTTGAACTGA-----
Consensus (3351) ATGC TTGAACTGA
                                     3400
NM_006218 (3401) CCACACTGCACTGTTAATAACTCTCAGCAGGCAAAGACCGATTGCATAGG
NM_008839 (3208) -----
Consensus (3401) -----
                                     3451
NM_006218 (3451) AATTCACCAATCCATGAACAGCATTAGAATTTACAGCAAGAACAGAAATA
NM_008839 (3208) -----
Consensus (3451) -----
                                     3500
NM_006218 (3501) AAATACTATATAATTTAATAAATGTAACGCAACAGGGTTTGATAGCAC
NM_008839 (3208) -----
Consensus (3501) -----
                                     3550
NM_006218 (3551) TTAAACTAGTTCATTTCAAATTAAGCTTTAGAATAATCCGCAATTCAT
NM_008839 (3208) -----
Consensus (3551) -----
                                     3600
NM_006218 (3601) GTTATGCCTTAAGTCCAAAAAGGTAACTTTGAAGATTGTTGTATCTTT
NM_008839 (3208) -----
Consensus (3601) -----
                                     3650
NM_006218 (3651) TTTTAAAAAACAAAACAAAACAAAATCCCCAAAATATATAGAAATGATG
NM_008839 (3208) -----
Consensus (3651) -----
                                     3700
NM_006218 (3701) GAGAAGGAAAAAAAAAAAAAAAAAAAA
NM_008839 (3208) -----
                                     3724

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FIGURE 4

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1      TCTCC CTCGG CGCCG CCGCC GCCGC CCGCG GGGCT GGGAC CCGAT GCGGT
51     TAGAG CCGCG GAGCC TGGAA GAGCC CCGAG CGTTT CTGCT TTGGG ACAAC
101    CATAc ATCTA ATTCC TTAAA GTAGT TTTAT ATGTA AAAct TGCAA AGAAc
151    CAGAA CAATG CCTCC ACGAC CATCA TCAGG TGAAC TGTGG GGCAT CCAcT
201    TGATG CCCCc AAGAA TCCTA GTAGA ATGTT TACTA CCAAA TGGAA TGATA
251    GTGAC TTTAG AATGC CTCCG TGAGG CTACA TTAAT AACCA TAAAG CATGA
      ~~~~~
      SEQ ID NO: 2
301    ACTAT TTAAA GAAGC AAGAA AATAC CCCCT CCATC AACTT CTTCA AGATG
351    AATCT TCTTA CATTt TCGTA AGTGT TACTC AAGAA GCAGA AAGGG AAGAA
      ~~~~~
      SEQ ID NO: 3
401    TTTTT TGATG AAACA AGACG ACTTT GTGAC CTTCG GCTTT TTCAA CCCTT
      ~
451    TTAA  AAGTA ATTGA ACCAG TAGGC AACCG TGAAG AAAAG ATCCT CAATC
501    GAGAA ATFGG TTTTG CTATC GGCAT GCCAG TGTGT GAATT TGATA TGGTt
551    AAAGA TCCAG AAGTA CAGGA CTTCC GAAGA AATAT TCTGA ACGTT TGTAa
601    AGAAG CTGTG GATCT TAGGG ACCTC AATTC ACCTC ATAGT AGAGC AATGT
      ~~~~~
      SEQ ID NO: 4
651    ATGTC TATCC TCCAA ATGTA GAATC TTCAC CAGAA TTGCC AAAGC ACATA
      ~~~~~
701    TATA  TAAAT TAGAT AAAGG GCAAA TAATA GTGGT GATCT GGGTA ATAGT
751    TTCTC CAATt AATGA CAAGC AGAAG TATAC TCTGA AAATC AACCA TGACT
801    GTGTA CCAGA ACAAG TAATt GCTGA AGCAA TCAGG AAAAA AACTC GAAGT
851    ATGTT GCTAT CCTCT GAACA ACTAA AACTC TGTGT TTTAG AATAT CAGGG
      ~~~~~
      SEQ ID NO: 5
901    CAAGT ATATT TTAAA AGTGT GTGGA TGTGA TGAAT ACTTC CTAGA AAAAT
      ~~~~~
951    ATCCT CTGAG TCAGT ATAAG TATAT AAGAA GCTGT ATAAT GCTTG GGAGG
1001   ATGCC CAATt TGATG TTGAT GGCTA AAGAA AGCCT TTATT CTCAA CTGCC
1051   AATGG ACTGT TTTAC AATGC CATCT TATTC CAGAC GCATT TCCAC AGCTA
1101   CACCA TATAT GAATG GAGAA ACATC TACAA AATCC CTTTG GGTTA TAAAT
1151   AGTGC ACTCA GAATA AAAAT TCTTT GTGCA ACCTA CGTGA ATGTA AATAT
1201   TCGAG ACATt GATAA GATCT ATGTT CGAAC AGGTA TCTAC CATGG AGGAG
      ~~~~~
1251   AACCC TTATG TGACA ATGTG AACAC TCAA  GAGTA CCTTG TTCCA ATCCC
      ~~~~~
      SEQ ID NO: 6
1301   AGGTG GAATG AATGG CTGAA TTATG ATATA TACAT TCCTG ATCCT CCTCG
      ~~~~~
      SEQ ID NO: 7
1351   TGCTG CTCGA CTTTG CCTTT CCATt TGCTC TGTTA AAGGC CGAAA GGGTG
1401   CTAAA GAGGA ACAct GTCCA TTGGC ATGGG GAAAT ATAAA CTTGT TTGAT
1451   TACAC AGACA CTCTA GTATC TGGAA AAATG GCTTT GAATC TTTGG CCAGT
1501   ACCTC ATGGA TTAGA AGATt TGCTG AACCC TATTG GTGTT ACTGG ATCAA
      ~~~~~
      SEQ ID NO: 8
1551   ATCCA AATAA AGAAA CTCCA TGCTT AGAGT TGGAG TTTGA CTGGT TCAGC
      ~~~~~
      SEQ ID NO: 9
1601   AGTGT GGTAA AGTTC CCAGA TATGT CAGTG ATTGA AGAGC ATGCC AATGT
1651   GTCTG TATCC CGAGA AGCAG GATTT AGCTA TTCCC ACGCA GGAAct GAGTA
1701   ACAGA CTAGC TAGAG ACAAT GAATt AAGGG AAAAT GACAA AGAAC AGCTC
1751   AAAGC AATTT CTACA CGAGA TCCTC TCTCT GAAAT CACTG AGCAG GAGAA
      ~~~~~
      SEQ ID NO: 17
      ~~~~~
      SEQ ID NO: 18
      ~~~~~
      SEQ ID NO: 23
      ~~~~~
      SEQ ID NO: 24
      ~~~~~
      SEQ ID NO: 19
      ~~~~~
      SEQ ID NO: 20
      ~~~~~
      SEQ ID NO: 25

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SEQ ID NO: 26

1801 AGATT TTCTA TGGAG TCACA GACAC TATTG TGTAA CTATC CCCGA AATTC  
1851 TACCC AAATT GCTTC TGTCT GTTAA ATGGA ATTCT AGAGA TGAAG TAGCC  
~~~~~

SEQ ID NO: 10

1901 CAGAT GTATT GCTTG GTAAA AGATT GGCCT CCAAT CAAAC CTGAA CAGGC
1951 TATGG AACTT CTGGA CTGTA ATTAC CCAGA TCCTA TGGTT CGAGG TTTTG
2001 CTGTT CGGTG CTTGG AAAAA TATTT AACAG ATGAC AAAPT TTCTC AGTAT
2051 TTAAT TCAGC TAGTA CAGGT CCTAA AATAT GAACA ATATT TGGAT AACTT
2101 GCTTG TGAGA TTTT ACTGA AGAAA GCATT GACTA ATCAA AGGAT TGGGC
2151 ACTTT TTCTT TTGGC ATTTA AAATC TGAGA TGCAC AATAA AACAG TTAGC
~~~~~

SEQ ID NO: 11

2201 CAGAG GTTTG GCCTG CTTTT GGAGT CCTAT TGTTC TGCAT GTGGG ATGTA  
2251 TTTGA AGCAC CTGAA TAGGC AAGTC GAGGC AATGG AAAAG CTCAT TAACT  
2301 TAACT GACAT TCTCA AACAG GAGAA GAAGG ATGAA ACACA AAAGG TACAG  
2351 ATGAA GTTTT TAGTT GAGCA AATGA GCGCA CCAGA TTTCA TGGAT GCTCT  
2401 ACAGG GCTTT CTGTC TCCTC TAAAC CCTGC TCATC AACTA GGAAA CCTC  
2451 GGCTT GAAGA GTGTC GAATT ATGTC CTCTG CAAAA AGGCC ACTGT GGTTC  
~~~~~

SEQ ID NO: 12

2501 AATG GGAGA ACCCA GACAT CATGT CAGAG TTAAT GTTTC AGAAC AATGA
~~~~~

SEQ ID NO: 13

2551 GATCA TCTTT AAAAA TGGGG ATGAT TTACG GCAAG ATATG CTAAC ACTTC  
2601 AAAT ATTCG TATTA TGGAA AATAT CTGGC AAAAT CAAGG TCTTG ATCTT  
2651 CGAAT GTTAC CTTAT GGTG TCTGT CAATC GGTGA CTGTG TGGGA CTTAT  
2701 TGAGG TGGTG CGAAA TTCTC ACACT ATTAT GCAAA TTCAG TGCAA AGGCG  
2751 GCTTG AAAGG TGCAC TGCAG TTCAA CAGCC ACACA CTACA TCAGT GGCTC  
2801 AAAGA CAAGA AAAAA GGAGA AATAT ATGAT GCAGC CATTG ACCTG TTTAC  
2851 ACGTT CATGT GCTGG ATACT GTGTA GCTAC CTCA TTTTG GGAAT TGGAG  
2901 ATCGT CACAA TAGTA ACATC ATGGT GAAAG ACGAT GGACA ACTGT TTCAT  
2951 ATAGA TTTTG GACAC TTTT GGATC ACAAG AAGAA AAAAT TTGGT TATAA  
~~~~~

SEQ ID NO: 14

3001 ACGAG AACGT GTGCC ATTTG TTTTG ACACA GGATT TCTTA ATAGT GATTA
~~~~~

SEQ ID NO: 15

3051 GTAAA GGAGC CCAAG AATGC AAAAA GACAA GAGAA TTTGA GAGGT TTCAG  
~~~~~

SEQ ID NO: 16

3101 GAGAT GTGTT ACAAG GCTTA TCTAG CTATT CGACA GCATG CCAAT CTCTT
~~~~~

3151 CATAA ATCTT TTCTC AATGA TGCTT GGCTC TGAAA TGCCA GAACT ACAAT  
3201 CTTT GATGA CATTG CATAA ATTCG AAAGA CCTA GCCTT AGATA AAAPT  
3251 GAGCA AGAGG CTTTG GAGTA TTTCA TGAAA CAAAT GAATG ATGCA CATCA  
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SEQ ID NO: 21

~~~~~  
SEQ ID NO: 22

~~~~~  
SEQ ID NO: 27

~~~~~  
SEQ ID NO: 28

3301 TGGTG GCTGG ACAAC AAAAA TGGAT TGGAT CTTC ACACA ATTAA ACAGC  
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3351 ATGCA TTGAA CTGA A AAGAT AACTG AGAAA ATGAA AGCTC ACTCT GGATT  
3401 CCACA CTGCA CTGTT AATAA CTCTC AGCAG GCAAA GACCG ATTGC ATAGG  
3451 AATTG CACAA TCCAT GAACA GCATT AGAAT TTACA GCAAG AACAG AATA  
3501 AAATA CTATA TAATT TAAAT AATGT AAACG CAAAC AGGGT TTGAT AGCAC  
3551 TTAAA CTAGT TCATT TCAAA ATTAA GCTTT AGAAT AATGC GCAAT TTCAT  
3601 GTTAT GCCTT AAGTC CAAAA AGGTA AACTT TGAAG ATTGT TTGTA TCTTT  
3651 TTTTA AAAAA CAAAA CAAAA ATCCC CAAAA TATAT AGAAA TGATG  
3701 GAGAA GGAAA AAAAA AAAAA AAAAA

FIGURE 5

SEQ ID NO: 1 Homo sapiens phosphoinositide-3-kinase, catalytic, alpha polypeptide (PIK3CA)mRNA, Accession number NM\_006218, 3724 bp

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1 tctccctcgg cgccgccgcc gccgccgcg gggctgggac ccgatgcggt tagagccgcg
61 gagcctggaa gagccccgag cgtttctgct ttgggacaac catacatcta attccttaaa
121 gtagttttat atgtaaaact tgcaaagaat cagaacaatg cctccacgac catcatcagg
181 tgaactgtgg ggcattccact tgatgcccc aagaatccta gtagaatggt tactaccaa
241 ttggaatgata gtgacttttag aatgcctccg tgaggctaca ttaataacca taaagcatga
301 actattttaa gaagcaagaa aatccccct ccatcaactt cttcaagatg aatcttcta
361 cattttcgta agtgttactc aagaagcaga aagggaaagaa ttttttgatg aaacaagacg
421 actttgtgac cttcggcttt ttcaaccctt tttaaaagta attgaaccag taggcaaccg
481 tgaagaaaag atcctcaatc gagaaattgg ttttgctatc ggcattgccag tegtgtgaat
541 tgaatgggtt aaagatccag aagtacagga cttccgaaga aatattctga acgtttgtaa
601 agaagctgtg gatcttaggg acctcaattc acctcatagt agagcaatgt atgtctatcc
661 tccaaatgta gaattctcac cagaattgcc aaagcacata tataataaat tagataaagg
721 gcaaaataata gtggtgatct gggtaatagt ttctccaaat aatgacaagc agaagtatac
781 tctgaaaact aacctgactc gtgtaccaga acaagtaatt gctgaagcaa tcaggaaaaa
841 aactcgaagt atgttgctat cctctgaaca actaaaactc tgtgttttag aatctcaggg
901 caagtataat ttaaaagtgt gtggatgtga tgaatacttc ctagaaaaat atcctctgag
961 tcagtataag tatataagaa gctgtataat gcttgggagg atgcccgaat tgatgttgat
1021 ggctaaagaa agcctttatt ctcaactgcc aatggactgt tttacaatgc catcttattc
1081 cagacgcatt tccacagcta cccatataat gaatggagaa acatctacaa aatccctttg
1141 ggttataaat agtgcactca gaataaaaaa tctttgtgca acctacgtga atgtaaatat
1201 tcgagacatt gataagatct atgttcgaac aggtatctac catggaggag aacctttatg
1261 tgacaatgtg aacctcaaa gagtaccttg ttccaatccc aggtggaatg aatgggtgaa
1321 ttatgatata tacattcctg atcttcctcg tgcgtcctga ctttgccttt ccatctgctc
1381 tgttaaaggg cgaaggggtg ctaaagagga acaactgtcca ttggcatggg gaaatataaa
1441 cttgtttgat tacacagaca ctctagtatc tggaaaaatg gctttgaatc tttggccagt
1501 acctcatgga ttagaagatt tgctgaaccc tattgtgtgt actggatcaa atccaaataa
1561 agaaaactcca tgcattagat tggagtttga ctggttcagc agtgtggtaa agttcccaga
1621 tatgtcagtg attgaagagc atgccaattg gtctgtatcc cgagaagcag gatttagcta
1681 ttcccacgca ggactgagta acagactagc tagagacaat gaattaaggg aaaaatgaca
1741 agaacagctc aaagcaattt ctacacgaga tcctctctct gaaatcactg agcaggagaa
1801 agattttcta tggagtcaca gacactattg tgtaactatc cccgaatatt taccaaat
1861 gcttctgtct gttaaatgga attctagaga tgaagtagcc cagatgtatt gcttggtaaa
1921 agattggcct ccaatcaaac ctgaacagcc tatggaactt ctggactgta attaccaga
1981 tccatgggtt cgaggttttg ctgttcgggt cttggaaaaa tatttaacag atgacaact
2041 ttctcagtat ttaattcagc tagtacaggt cctaaaatat gaacaatatt tggataactt
2101 gcttgtgaga tttttactga agaaagcatt gactaatcaa aggattgggc actttttctt
2161 ttggcattta aaatctgaga tgcacaataa aacagttagc cagaggtttg gcctgctttt
2221 ggagtcctat tgcctgcatc gtgggatgta ttggaagcac ctgaataggg aagtcgaggg
2281 aatggaaaag ctcattaact taactgacat tctcaaacag gagaagaagg atgaaacaca
2341 aaaggtacag atgaagtttt tagttgagca aatgaggcga ccagatttca tggatgctct
2401 acagggcctt ctgtctctc taaccctgct tcatcaacta ggaaacctca ggcttgaaga
2461 gtgtcgaatt atgtcctctg caaaaaggcc actgtgtgtt aattgggaga acccagacat
2521 catgtcagag ttactgtttc agaacaatga gatcatcttt aaaaatgggg atgatttacg
2581 gcaagatatg ctaaaccttc aaattattcg tattatggaa aatatctggc aaaaatcaagg
2641 tcttgatctt cgaatgttac ctatgtgttg tctgtcaatc ggtgactgtg tgggacttat
2701 tgaggtgggt cgaattctc acactattat gcaattcag tgcaaggcgg gcttgaaagg
2761 tgcactgcag ttcaacagcc acacactaca tcagttggctc aaagacaaga acaaggaga
2821 aatatatgat gcagccattg acctgtttac acgttcatgt gctggatact gtgtagctac
2881 cttcattttg ggaattggag atcgtcaca tagtaacatc atggtgaaag acgatggaca
2941 actgtttcat atagattttg gacacttttt ggatcacaag aagaaaaaat ttggttataa
3001 acgagaacgt gtgccatttg ttttgacaca ggatttctta atagtgatta gtaaggagg
3061 ccaagaatgc acaagacaa gagaatttga gaggtttcag gagatgtggt acaaggctta
3121 tctagctatt cgacagcatg ccaatctctt cataaatctt ttctcaatga tgcctggctc
3181 tggaaatgca gaactacaat cttttgatga cattgcatac attcgaaga ccctagcctt
3241 agataaaaact gagcaagagg cttttgagta tttcatgaaa caaatgaatg atgcacatca
3301 tgggtggctg acaacaaaaa tggattggat cttccacaca attaaacagc atgcattgaa
3361 ctgaaaagat aactgagaaa atgaaaagctc actctggatt ccacactgca ctgttaataa
3421 ctctcagcag gcaaaagacc attgcatagg aattgcacaa tccatgaaca gcattagaat
3481 ttacagcaag aacagaataa aaatactata taatttaaat aatgtaaacg caaacagggt
3541 ttgatagcac ttaaactagt tcatttcaaa attaagcttt agaataatgc gcaatttcat
3601 gttatgcctt aagtccaaaa aggtaaacct tgaagattgt ttgtatcttt ttttaaaaaa
3661 caaaacaaa caaaaatccc caaaatata agaaatgatg gagaaggaaa aaaaaaaaaa
3721 aaaa
    
```

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## FIGURE 6

SEQ ID NO: 105  
 LOCUS NP\_006209 1068 aa  
 DEFINITION phosphoinositide-3-kinase, catalytic, alpha polypeptide [Homo sapiens].  
 ACCESSION NP\_006209  
 VERSION NP\_006209.2 GI:54792082  
 SOURCE Homo sapiens (human)

## ORIGIN

```

1 mpprpssgel wgihlmpri lvecllpngm ivtleclrea tlitikhelf kearkyplhq
61 llqdessyif vsvtqeaere effdetrrlc dlrlfqpfk viepvgnree kilnreigfa
121 igmpvcefdm vkdpevqdf rnilnvckea vdlrdlnsph sramyvypn vesspelpkh
181 iynklkdgqi ivviwvivsp nndkqkytlk inhdcvpeqv iaeairkktr smlsseqlk
241 lcvleyqgky ilkvcgcdey flekypksq kyirscimlg rmpnlmlmak eslysqlpmd
301 cftmpsysrr istatpymng etstkslwvi nsalrikilc atyvvnvird idkiyvrtgi
361 yhggeplcdn vntqrvpcsn prnewlnyd iyipdlpraa rlclsicsvk grkgakeehc
421 plawgninlf dytdtlvsgk malnlwvpvh gledlnpig vtgsnpnket pclelefdwf
481 svvkfpdms vieehanwsv sreagfsysh aglsnrlard nelrendkeq lkaistrdpl
541 seiteqekdf lwshrhycvt ipeilpklll svkwnsrdev aqmyclvkdw ppikpeqame
601 llcnydpdm vrgfavrcle kyltddklsq yliqlvqvlk yeqyldnllv rfilkkaltn
661 qrihfffwh lksemhktv sqrfglles ycracgmylk hlnrqveame klinltdiik
721 qekkdqtkv qmkflveqmr rpdfmdalqg flsplnpahq lgnlrleecr imssakrplw
781 lnwenpdims ellfqneei fknngddlrqd mltlqirrim eniwqngld lmlpygcls
841 igdcvgliev vrnshtimqi qckgglkgal qfnshthqw lkdknkgeiy daaidlftsr
901 cagyvatfi lgigdrhnsn imvkddgqlf hidfghfldh kkkkfykre rvpfvltqdf
961 liviskgagc ctktreferf qemcykayla irghanlfin lfsmmlgsgm pelqsfdia
1021 yirktlaldk teqealeyfm kqmdahhgg wttkmdwifh tikqhaln

```

FIGURE 7

SEQ ID NO: 106  
 LOCUS NM\_008839 3207 bp mRNA  
 DEFINITION Mus musculus phosphatidylinositol 3-kinase, catalytic, alpha polypeptide (Pik3ca), mRNA.  
 ACCESSION NM\_008839  
 VERSION NM\_008839.1 GI:6679316  
 SOURCE Mus musculus (house mouse)

ORIGIN

```

1 atgcctccac gaccatcttc gggggaactg tggggcatcc acttgatgcc cccacgaatc
61 ctagtggaat gtttactccc caatggaatg atagtgactt tagaatgcct ccgtgaggcc
121 aactcgtca ccatcaaaac tgaactgttc agagaggcca gaaataacc tctccatcag
181 cttctgcaag acgaaacttc ttacattttc gtaagtgtca ccaagaagc agaaagggaa
241 gaattttttg atgaaacaag acgactttgt gaccttcggc tttttcaacc ctttttaaaa
301 gttattgaac cagtaggcaa ccgtgaagaa aagatcctca atcgagaaat tggttttggt
361 attggcatgc cagtgtgtga atttgatatg gttaaagatc cagaagtcca agactttcga
421 aggaacattc tgaatgtttg caaagaagct gtggacctgc gggatctcaa ctgcctcat
481 agcagagcaa tgtatgtcta ccctccaaat gtccgagtct cccagaact gccaaagcac
541 atctacaaca agttagataa aggacaaatc atagtgggtga tttgggtaat agtctctcca
601 aacaacgaca agcagaagta cactctgaag atcaatcatg actgtgtgcc agagcaagtc
661 attgtggaag ccatcaggaa aaagactcgg agcatgttgt tgtcctctga gcagctgaaa
721 ctctgtgtct tagaataatc gggcaagtat attctgaaag tgtgtggctg tgacgaatac
781 ttcctggaaa agtaccctct gagtcagtac aagtacataa gaagctgtat aatgctgggg
841 aggatgcccc acttgatgct gatggccaaa gaaagcctat actctcagct gccgattgat
901 agcttaccac tgccgtcata ctccaggcgc atctccacag ccacacccta catgaatgga
961 gagacatcta cgaatccct ctgggtcata aatagtgcgc tcagaataaa aattcctttgt
1021 gcaacctatg taaatgtaaa tattcgagac attgataaga tctatgttcg aacaggatc
1081 taccatggag gagaaccctt atgtgacaat gtgaacactc aaagagtacc ttgttccaat
1141 cctaggtgga atgaatggct gaattatgat atatacattc ctgatcttcc tcgtctggcg
1201 cgcctttgcc tttcaatctg ctctgttaaa ggcgaaagg gtgctaagga ggagcactgt
1261 ccgttgccct ggggaaacat aaacttggtt gattatacag acaccctagt gtcgggaaa
1321 atggctttga atctctggcc tgtaccgcac ggggtagaag atctgctgaa ccctattggt
1381 gttactgggt caaatccaa taaagaaact ccatgcttag agttggagtt tgattggttc
1441 agcagtgtgg tgaagtttcc agacatgtct gtgatcgaag aacatgcaa ttggtcogtg
1501 tcccgagaag ctggattcag ttactcccat acaggactga gtaacagact agccagagac
1561 aatgagttaa gagaaaatga caaggaacag ctccgagcac tttgacccg ggaccacta
1621 tctgaaatca ctgaacaaga gaaagacttc ctatggagcc acagacacta ctgcgtaact
1681 attcctgaaa tcctacccaa attgcttctg tctgtcaagt ggaattccag agacgaagtg
1741 gccagatgt actgcttagt aaaagattgg cctccaatca aaccagagca agccatggaa
1801 ctctggact gtaactatcc agatcctatg gttcggagtt ttgctgttcg gtgcttagaa
1861 aatatattaa cagatgacaa actttctcag tacctcattc aactgtaca ggtcttaaaa
1921 tatgaacagt atttggataa cctgcttggt agatttttac tcaagaaagc attgacaaat
1981 caaaggattg gccatTTTTT cttttggcat ttaaaatctg agatgcacaa taagactgtc
2041 agtcagaggt ttggcctgct attggagtoc tactgccgtg cctgtgggat gtatctgaag
2101 cacctgaaca gacaagtaga ggccatggag aagctcatca acctaacgga catccttaag
2161 cagggaaga aggatgagac acaaaaagga cagatgaagt ttttggttga acagatgaga
2221 cagccagact tcatggatgc tttgcagggt tttctgtccc ctctgaaacc tgctcaccia
2281 ctaggaaacc tcaggcttga agagtgtcga attatgtcct ctgcaaaaag gccactgtgg
2341 ttgaattggg agaaccaga catcatgtca gagctactgt ttcagaacaa tgagatcatc
2401 tttaaaaatg gcgacgactt acggcaagat atgttaaccc ttcagatcat ccgaatcatg
2461 gagaacatct ggcaaaaacca aggccttgac cttcgcatgc taccttatgg ctgtctatcc
2521 attggggact gtgtgggtct catcgaggtg gtgagaaact ctcacacct catgcaaatc
2581 cagtgcгааг gagcctgaa gggggcgctg cagttcaaca gccacacact gcatcaatgg
2641 ctcaaggaca agaacaaggg cgagatataat gatgcagcca ttgacctgtt cactcggttc
2701 tgcgctgggt actgctggc aacctttatc ttgggaattg gagaccggca caacagcaac
2761 atcatggtga aagatgacgg acagctgttt catatagatt ttgggcaact tttggatcac
2821 aagaagaaa aatttggcta taagcgggaa cgtgtgccat ttgtgttgac acagatttc
2881 ttgattgtga ttagtaaggg agcacaagag tacaccaaga ccagagagtt tgagagttt
2941 caggagatgt gttacaaggc ttacctagca attcggcagc atgccaatct cttcatcaac
3001 cttttttcaa tgatgcttgg ctctggaatg ccagaactac aatcttttga tgacattgca
3061 tatatccgaa agactctagc cttggacaaa actgagcaag aagctttgga atatttcaca
3121 aagcaaatga atgatgcaca tcatggtgga tggacgacaa aatggattg gatcttccac
3181 accatcaagc agcatgcttt gaactga
    
```

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## FIGURE 8

SEQ ID NO: 107  
 LOCUS NP\_032865 1068 aa  
 DEFINITION phosphatidylinositol 3-kinase, catalytic, alpha polypeptide [Mus musculus].  
 ACCESSION NP\_032865  
 VERSION NP\_032865.1 GI:6679317  
 SOURCE Mus musculus (house mouse)

## ORIGIN

```

1 mpprpssgel wgihlmppri lvecllpngm ivtleclrea tlvtikhelf rearkyplhq
61 llqdetsyif vsvtqeaere effdetrrelc dlrlfqpflk viepvgnree kilnreigfv
121 igmpvcefdm vkdpevqdfv rnlnvckea vdlrdlnsph sramyvypn vesspelpkh
181 iynkldkgqi ivviwvivsp nndkqkytlk inhdcvpeqv iaeairkktr smlsseqlk
241 lcvleyggky ilkvvcgdey flekypksqy kyirscimlg rmpnlmlmak eslysqlipd
301 sftmpsysrr istatpymng etstkslwvi nsalrikilc atyvvnvird idkiyvrtgi
361 yhggeplcdn vntqrvpcsn prwnewlnyd iyipdlprla rlclsicsvk grkgakeehc
421 plawgninlf dytdtlvsgk malnlwpvph gledllnpig vtgsnnpket pclelefdwf
481 ssvvkfpdms vieehanwsv sreagfsysh tglsnrlard nelrendkeq lralctrdpl
541 seiteqekdf lwshrhycvt ipeilpklll svkwnsrdev aqmyclvkdw ppikpegame
601 lldcnypdpm vrsfavrcle kyltddklsq yliqlvqvlk yeqyldnllv rflkkaltn
661 qrighffwh lksemhnktv sqrfglles ycracgmylk hlnrqveame klinltdilk
721 qekkdetsqkv qmkflveqmr qpdfmdalqg flsplnpahq lgnlrleecr imssakrplv
781 lnwenpdims ellfqneii fkngddlrqd mltlqiirim eniwqngld lrmlpygcls
841 igdcvgliev vrnshtimqi qckggkgal qfnshtlhqw lkdknkgeiy daaidlftrs
901 cagycvatfi lgigdrhnsn imvkddgqlf hidfghfldh kkkkfgykre rvpfvltqdf
961 liviskgagv ytktreferf qemcykayla irqhanlfin lfsmmlgsgm pelqsfdia
1021 yirktlaldk teqealeyft kqmdahhgg wttkmdwifh tikghaln

```

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FIGURE 9

SEQ ID NO: 108  
 LOCUS XM\_001109162 4326 bp mRNA  
 DEFINITION PREDICTED: Macaca mulatta similar to phosphoinositide-3-kinase, catalytic, alpha polypeptide (LOC709959), mRNA.  
 ACCESSION XM\_001109162  
 VERSION XM\_001109162.1 GI:109043556  
 SOURCE Macaca mulatta (rhesus monkey)

ORIGIN

```

1 tctccctcgg cgccgccgc gccgccgcg gggctgggac ccgatgcggt tagagccgcg
61 gagcctggaa gagccccgag cgtttctgct ttgggacaac catacgtcta attcctttaa
121 gtagttttat atgtaaaacc tgcaaaaat cagaacaatg cctccacgac catcatcagg
181 tgaactgtgg ggcatccact tgatgcccc aagaatccta gtagaatggt tactaccaa
241 tggaatgata gtgactttag aatgcctcgg tgaggctaca ttaataacca taaagcatga
301 actattttaa gaagcaagaa aatccccct ccatcaactt cttcaagatg aatccttcta
361 cattttcgta agtgttacc aagaagcaga aagggagaa ttttttgatg aaacaagacg
421 actttgtgac cttcggcttt ttcaaccctt tttaaaagta attgaaccag taggcaaccg
481 tgaagaaaag atcctcaatc gagaaattgg ttttgctatt ggcatgccag tgtgtgaatt
541 tgatatggtt aaagatccag aagtacagga cttccgaaga aatattctga atgtttgtaa
601 agaagctgtg gatcttaggg atctcaattc acctcatagt agagcaatgt atgtctatcc
661 tccaaatgta gaatcttcgc cagaattgcc aaagcacata tataataaat tagataaagg
721 gcaaataata gtggtgattt ggtaatagt ttctocaaat aatgacaagc agaagtatac
781 tctgaaaatc aaccatgact gtgtaccaga acaagtaatt gctgaagcaa tcaggaaaaa
841 aactcgaagt atgttgctat cctctgaaca gctaaaactc tgtgttttag aatatcaggg
901 caagtatatt ttaaaagtgt gtggatgtga tgaatacttc ctagaaaaat atcctctgag
961 tcagtataag tatataagaa gctgtataat gcttgggagg atgcccatt tgatgttgat
1021 ggctaaagaa agcctttatt ctcaactgcc aatggactgt tttacaatgc catcttattc
1081 cagacgcatt tccacagcta caccatatat gaatggagaa acatctaca aatcccttgg
1141 ggtataaaat agtgcactca gaataaaaat tctttgtgca acctacgtga atgtaaatat
1201 tcgagacatt gataagatct atgttcgaac aggtatctac catggaggag aacccttatg
1261 tgacaatgtg aacactcaaa gagtaccttg ttccaatccc aggtggaatg aatggctgaa
1321 ttatgatata tacattcctg acctcctcgg tgctgctcga ctttgccctc ccatgtctc
1381 tgttaaaggc cgaaaggggt ctaaagagga acaactgtcca ttggcatggg gaaataaaa
1441 cttgtttgat tacacagaca ctctagtatc tggaaaaatg gctttgaatc tttggccagt
1501 acctcatgga ttagaagatt tgctgaacct tattgggtgt actggatcaa atccaaataa
1561 agaaactcca tgcttagagt tggagtttga ctggttcagc agtgtggtaa agttcccaga
1621 tatgtcagtg attgaagagc atgccaattg gtctgtgtcc cgagaagcag gatttagcta
1681 tccccacgca ggactgagta acaggctagc tagagacaat gaattaaggg aaaatgacaa
1741 agaacagctc aaagcaatth ctacacgaga tcctctctct gaaatcactg agcaggagaa
1801 agatthctg tggagccaca gacactattg tgtaactatc cccgaaatc tacccaaat
1861 gcttctgtct gttaaatgga attctagaga tgaagtagcc cagatgtatt gcttggtaaa
1921 agactggcct ccaatcaaac ctgaacagcc tatggaactt ctggactgta attaccaga
1981 tcctatgggt cgaggthttg ctgttcgggt cttggaaaaa tatttaacag atgacaact
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2101 gcttgtgaga tttttactga agaaagcatt gactaatcaa aggattggg actthttctt
2161 ttggcattta aaatctgaga tgcacaataa aacagttagc cagaggthtt gcctgctttt
2221 ggagtcctat tgtcgtgcat gtgggatgta tttgaagcac ctgaataggc aagtcgaggc
2281 aatggaaaag ctcattaact taactgacat tctcaaacag gagaaaaagg atgaaacaca
2341 aaaggtacag atgaagthtt tagttgagca aatgaggcga ccagatttca tggatgctct
2401 gcagggctth ctatctctc taaaccctgc tcatcaacta ggaaatctca ggcttgaaga
2461 gtgtcgaatt atgtcctctg caaaaaggcc actgtggttg aattgggaga acccagacat
2521 catgtcagag ttactgthttc agaacaatga gatcatcttt aaaaatgggg atgatttacg
2581 gcaagatag ctaacacttc aaattattcg tattatggaa aatattctggc aaaatcaagg
2641 tcttgatctt cgaatgttac cttatgthtt tctgtcaatc ggtgactgtg tgggacttat
2701 tgaggthgtg cgaaatctc acactattat gcaaatcag tgcaaaaggc gcttgaagg
2761 tgcactgcag ttcaacagcc acactctaca tcagtggctc aaagacaaga acaaggaga
2821 aatatatgat gcagccattg acctgtttac acgttcatgt gctggatatt gtgtcgctac
2881 cttcattctg ggaattggag atcgtcaca tagtaacatc atggtgaaag acgatggaca
2941 actgthttcat atagatthtt gacactthtt ggatcacaag aagaaaaat tggctataa
3001 acgagaacgt gtgccatttg ttttgacaca ggatttctta atagtgatta gtaaaggagc
3061 ccaagaatgc acaagacaa gagaatthtt gaggtthcag gagatgtgtt acaaggctta
3121 tctagctatt cgacagcatg ccaatctctt cataaatctt ttctcaatga tgcctggctc
3181 tggaaatgcca gaactacaat cthttgatga cattgcatac attcgaaga ccctagcctt
    
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3241 agataaaact gagcaagagg ctttgggaata tttcatgaaa caaatgaatg atgcacatca
3301 tgggtggctgg acaacaaaaa tggattggat cttccacaca attaaacagc atgcattgaa
3361 ctgaaaagat aactgagaaa atgaaagctc actctctgga ttccacactg cactgttaat
3421 aactatcagc aggcaaagac cgattgcata ggaattgcac aatccatgaa cagcattaga
3481 atttacagca agaacagaaa taaaatacta tataatntaa tgtaaacgca aacagggttt
3541 gatagcactt aaactagttc atttcacaat taagcttttag aataatgctc aatttcatgt
3601 tatgccttaa gtccaaaaag gtaaactttg aagattgttt gtatcttttt ttaaaaaaca
3661 aaacaaaaaca aaaatcccca aaatatatag aaatgatgga gaaggaaaaa tgatgttttt
3721 ttttgtcttg caaatgttct atgttttgaa atgtggacac acaaaaagct gttattgttt
3781 taggtgtaag taaactggag tttatgntaa attacattaa gattggaaaa gaatgaaaat
3841 ttcttatttt tccattgctg ttcaatttat agtttgagtg ggtttttgag tccttgttta
3901 atgaagaaaa atgcttgggg tggaaagggac tcttgagatt tcaccagaga ctttttcttt
3961 ttaataaatc aaactttttg atgatttgag gtcttatctg cagtttttga agcagtcaca
4021 aatgagacct gttataaggt ggtatttttt ttttttttct ggacagtatt taaaggattt
4081 tatttcccag ggaattctg ggctcccaca gagtttaaaa aaaaaaaaaa aaaaaaatca
4141 tagaaaaaga atgaacagga atagttctta ttccaaaatt gtacagtatt caccttaagt
4201 tgattttttt ctccttttgc agttgaactg aatacatttt tcatgcatgt tttccaaaaa
4261 atagaagtat taatgttatt aaaaagatta ttttttttat taaaggctat ttatattata
4321 gaaact

```

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FIGURE 10

```

SEQ ID NO: 109
LOCUS      XP_001109162                1068 aa
DEFINITION PREDICTED: similar to phosphoinositide-3-kinase, catalytic,
alpha polypeptide [Macaca mulatta].
ACCESSION  XP_001109162
VERSION    XP_001109162.1  GI:109043557
SOURCE     Macaca mulatta (rhesus monkey)

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ORIGIN

```

1  mpprpssgel wgihlmppri lvecllpngm ivtleclrea tlitikhelf kearkyplhq
61  llqdessyif vsvtqeaere effdetrllc dlrlfqpflk viepvgntree kilnreigfa
121 igmpvcefdm vkdpevqdfv rnlnvckeaa vdldrlnsph sramyvppn vesspelpkh
181 iynklldkgqi ivviwvivsp nndkqkytlk inhdcvpeqv iaeairkktr smlsseqlk
241 lcvleyqgky ilkvcgdey flekyplsqy kyirscimlg rmpnlmlmak eslyslpmd
301 cftmpsysrr istatpymng etstkslwvi nsalrikilc atyvvnird idkiyvtgi
361 yhggeplcdn vntqrvpcsn prwnewlnyd iyipdlpraarlclsicsvk grkgakeehc
421 plawgnlnlf dytdtlvsgk malnlwpvph gledlnpig vtgsnpnket pclelefdwf
481 ssvvkfpdms vieehanvsv sreagfsysh aglsnrlard nelrendkeq lkaistrdpl
541 seitegekdf lwshrhyctv ipeilpklll svkwnsrdev aqmyclvkdw ppikpegame
601 lldcnypdpm vrgfavrcl kylvtdklsq yliqlvqvkl yeqyldnllv rflikkaltn
661 qrighfffwl lksemhktv sqrfglles ycracgmylk hlnrqveame klinltdilk
721 qekkdetqkv qmkflveqmr rpdfmdalgg flsplnpahq lgnlrleecr imssakrplw
781 lnwenpdims ellfqneii fkngddlrqd mltlqiirim eniwqnggld lrmlpygcls
841 igdcvgliev vrnshtimqi qckggkqgal qfnshthlqw lkdknkgeiy daaidlftsr
901 cagycvatfi lgigdrhnsn imvkddgqlf hidfghfldh kkkkfykre rvpfvltqdf
961 liviskgagc ctktreferf qemcykayla irqhanlfin lfsmmlgsgm pelqsfddia
1021 yirktlaldk teqealeyfm kqmdahhgg wttkmdwifh tikqhaln

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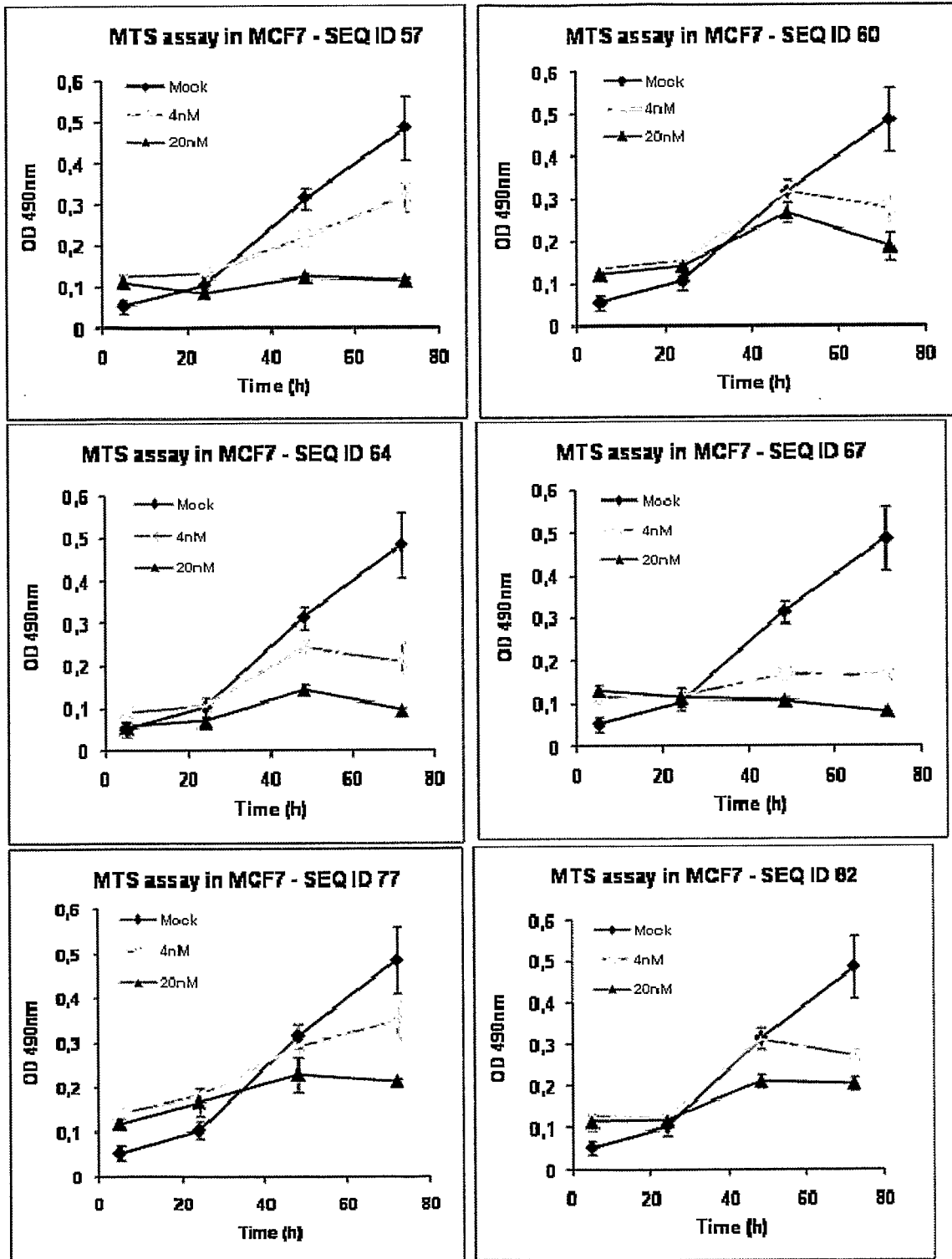


FIGURE 11

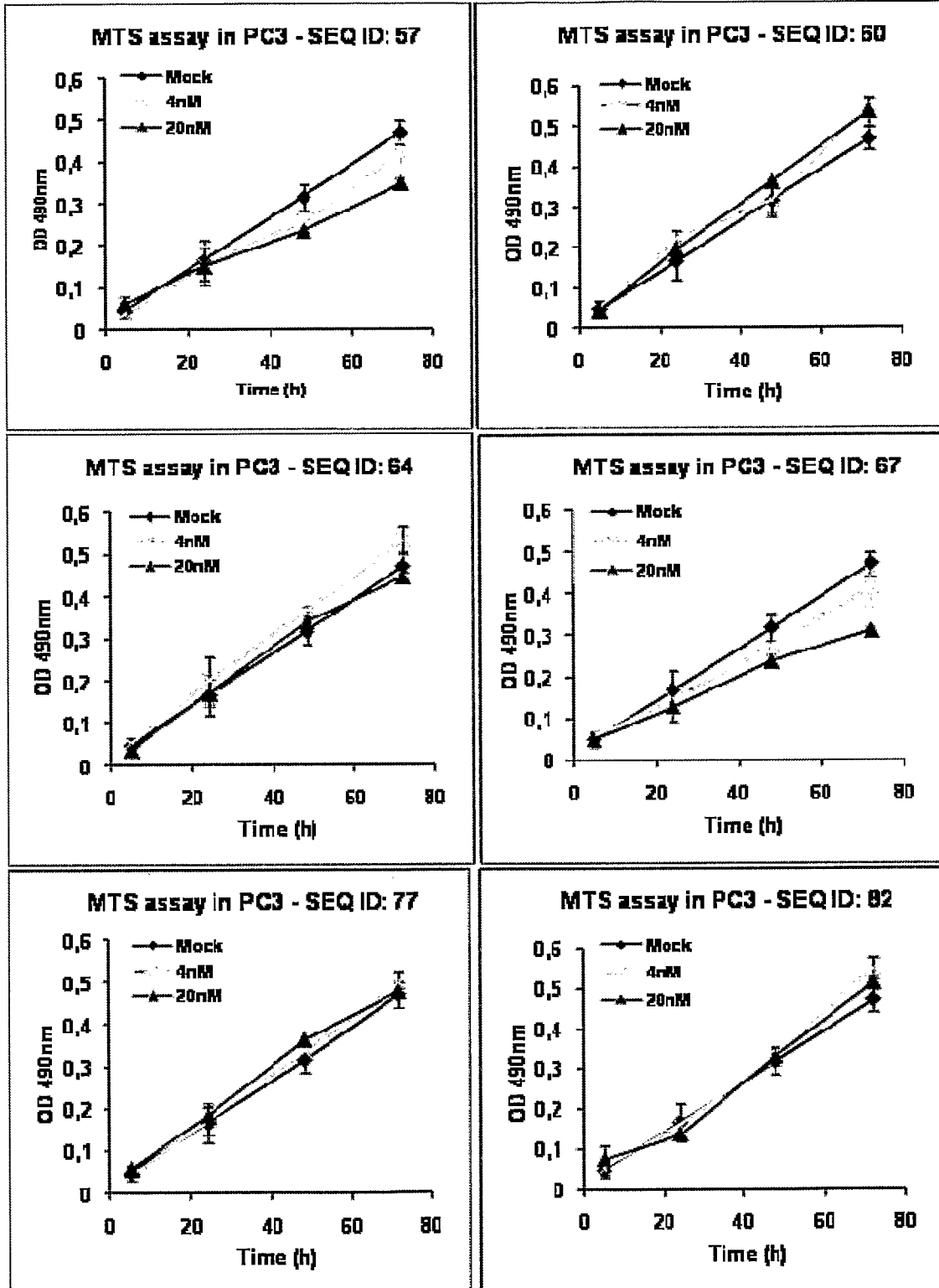


FIGURE 12

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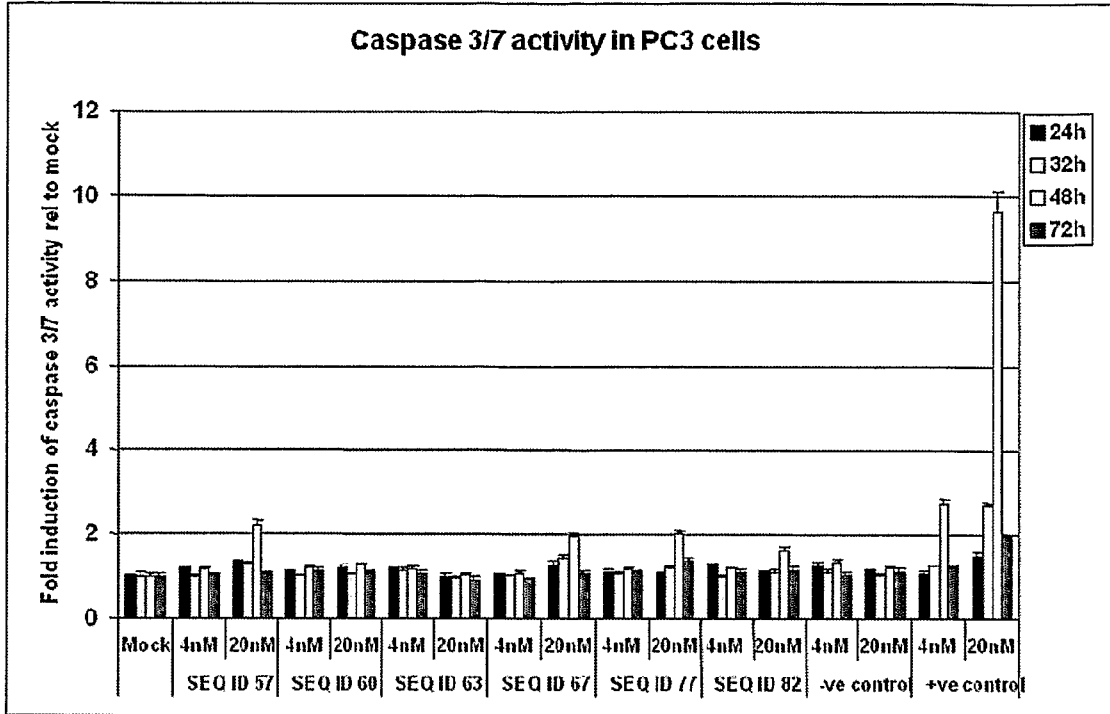


FIGURE 13

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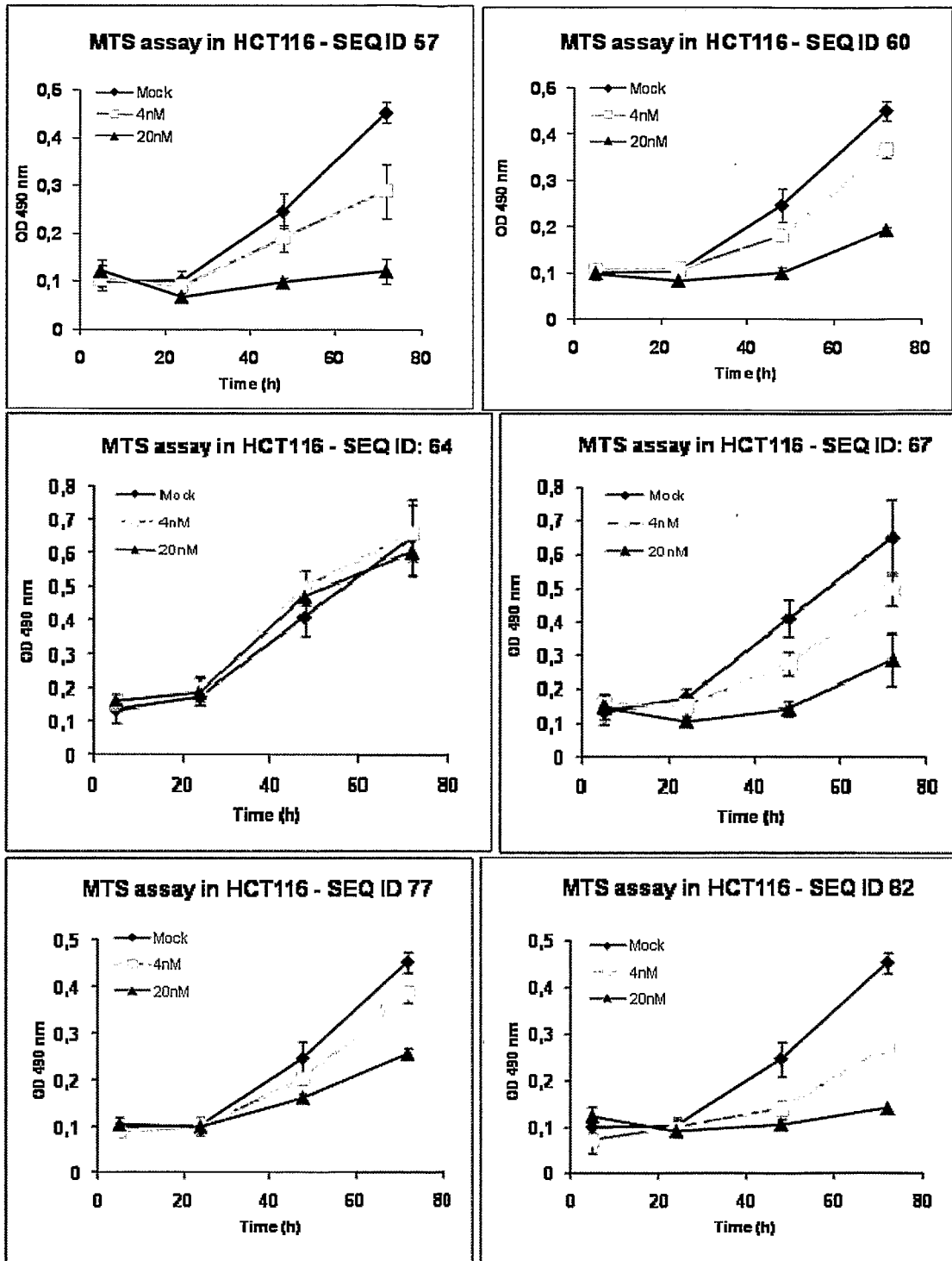


FIGURE 14

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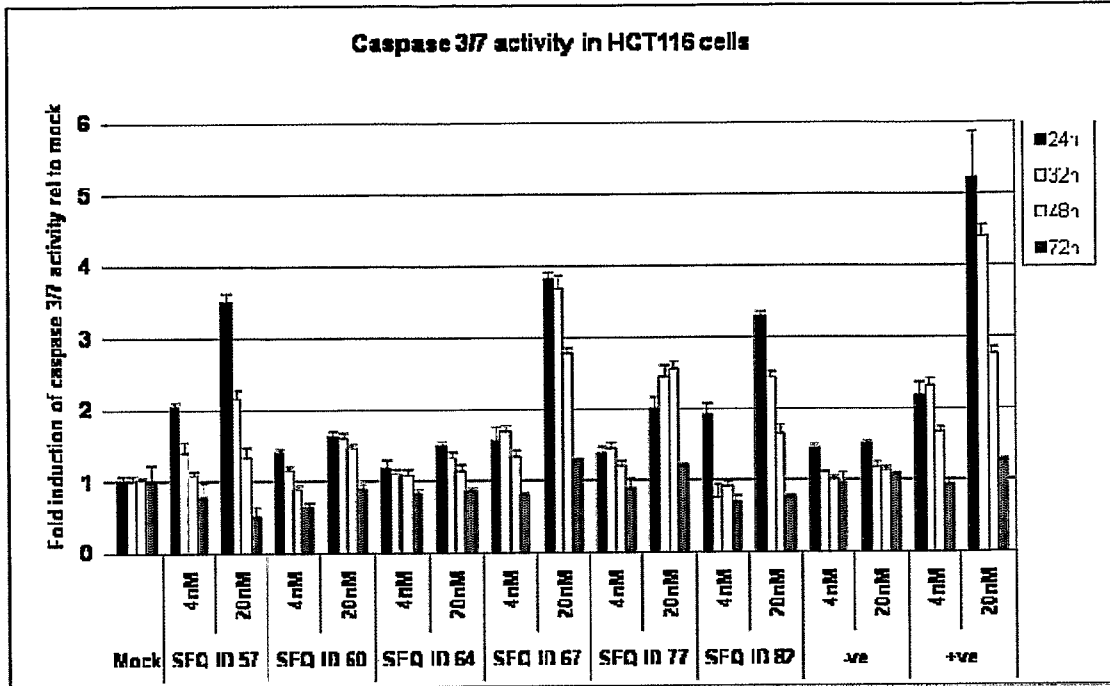


FIGURE 15

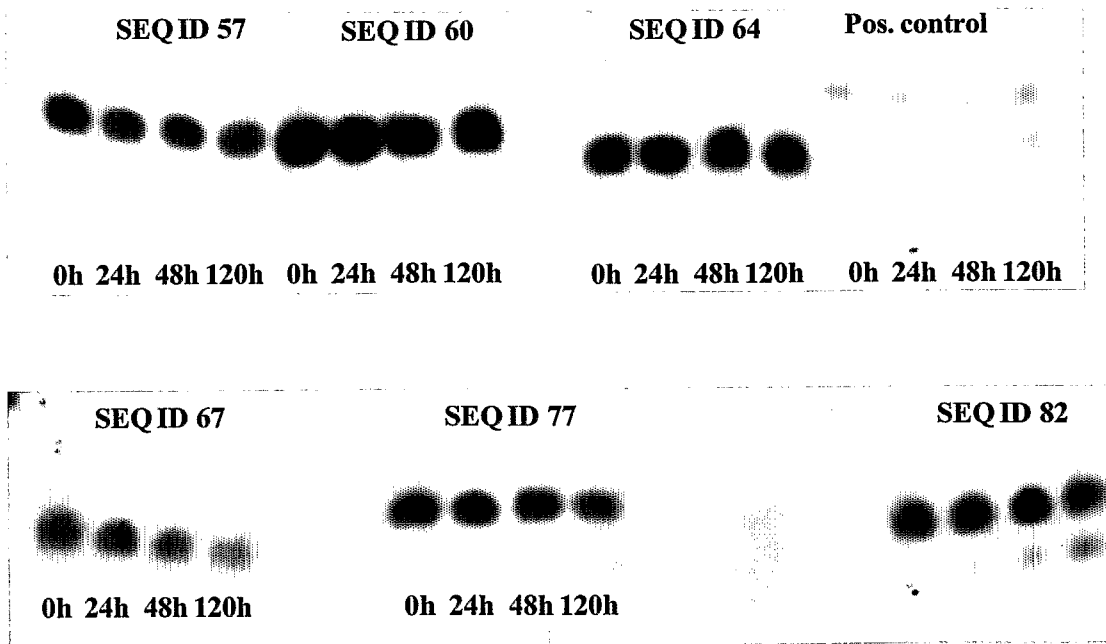


FIGURE 16

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| Oligo  | Sequence                                                                                                                                                                                                                                                                                                                                  | T <sub>m</sub> |
|--------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------|
| SEQ.57 | 5'- A <sub>S</sub> <sup>o</sup> T <sub>S</sub> <sup>o</sup> T <sub>S</sub> <sup>o</sup> c <sub>S</sub> t <sub>S</sub> t <sub>S</sub> c <sub>S</sub> c <sub>S</sub> c <sub>S</sub> t <sub>S</sub> t <sub>S</sub> t <sub>S</sub> c <sub>S</sub> T <sub>S</sub> <sup>o</sup> G <sub>S</sub> <sup>o</sup> mC <sub>S</sub> <sup>o</sup> -3'    | 66.5°C         |
| SEQ.60 | 5'- T <sub>S</sub> <sup>o</sup> A <sub>S</sub> <sup>o</sup> G <sub>S</sub> <sup>o</sup> a <sub>S</sub> c <sub>S</sub> a <sub>S</sub> t <sub>S</sub> a <sub>S</sub> c <sub>S</sub> a <sub>S</sub> t <sub>S</sub> t <sub>S</sub> g <sub>S</sub> mC <sub>S</sub> <sup>o</sup> T <sub>S</sub> <sup>o</sup> mC <sub>S</sub> <sup>o</sup> -3'   | 58.7°C         |
| SEQ.64 | 5'- mC <sub>S</sub> <sup>o</sup> A <sub>S</sub> <sup>o</sup> mC <sub>S</sub> <sup>o</sup> a <sub>S</sub> t <sub>S</sub> a <sub>S</sub> a <sub>S</sub> g <sub>S</sub> g <sub>S</sub> g <sub>S</sub> t <sub>S</sub> t <sub>S</sub> c <sub>S</sub> T <sub>S</sub> <sup>o</sup> mC <sub>S</sub> <sup>o</sup> mC <sub>S</sub> <sup>o</sup> -3' | 62.1°C         |
| SEQ.67 | 5'- A <sub>S</sub> <sup>o</sup> G <sub>S</sub> <sup>o</sup> mC <sub>S</sub> <sup>o</sup> c <sub>S</sub> a <sub>S</sub> t <sub>S</sub> t <sub>S</sub> c <sub>S</sub> a <sub>S</sub> t <sub>S</sub> t <sub>S</sub> c <sub>S</sub> c <sub>S</sub> A <sub>S</sub> <sup>o</sup> mC <sub>S</sub> <sup>o</sup> mC <sub>S</sub> <sup>o</sup> -3'  | 66.5°C         |
| SEQ.77 | 5'- T <sub>S</sub> <sup>o</sup> T <sub>S</sub> <sup>o</sup> A <sub>S</sub> <sup>o</sup> t <sub>S</sub> t <sub>S</sub> g <sub>S</sub> t <sub>S</sub> g <sub>S</sub> c <sub>S</sub> a <sub>S</sub> t <sub>S</sub> c <sub>S</sub> t <sub>S</sub> mC <sub>S</sub> <sup>o</sup> A <sub>S</sub> <sup>o</sup> G <sub>S</sub> <sup>o</sup> -3'    | 58.7°C         |
| SEQ.82 | 5'- T <sub>S</sub> <sup>o</sup> T <sub>S</sub> <sup>o</sup> mC <sub>S</sub> <sup>o</sup> t <sub>S</sub> t <sub>S</sub> c <sub>S</sub> t <sub>S</sub> t <sub>S</sub> g <sub>S</sub> t <sub>S</sub> g <sub>S</sub> a <sub>S</sub> t <sub>S</sub> mC <sub>S</sub> <sup>o</sup> mC <sub>S</sub> <sup>o</sup> A <sub>S</sub> <sup>o</sup> -3'  | 64.3°C         |

FIGURE 17

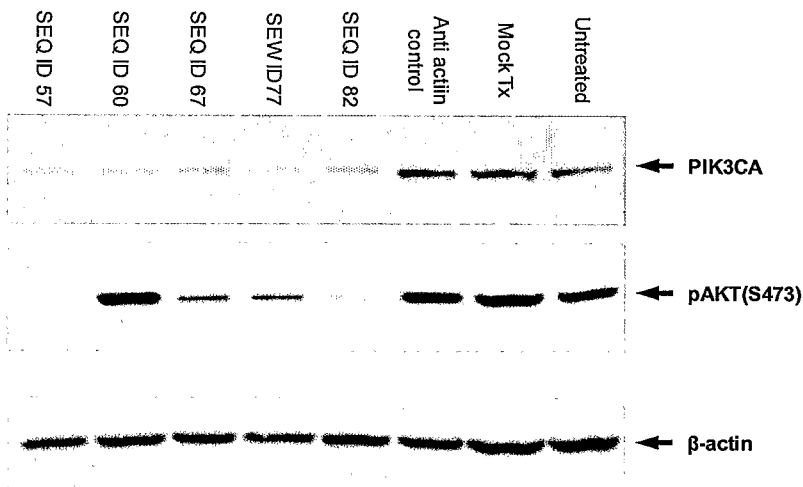


FIGURE 18

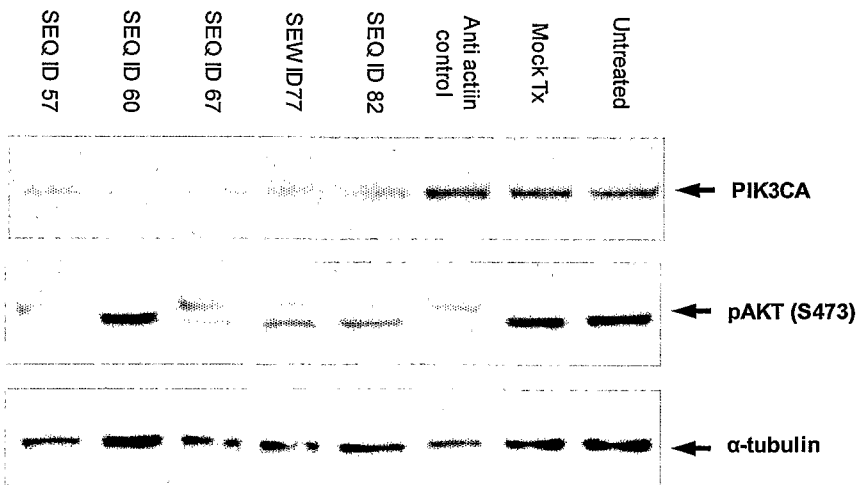
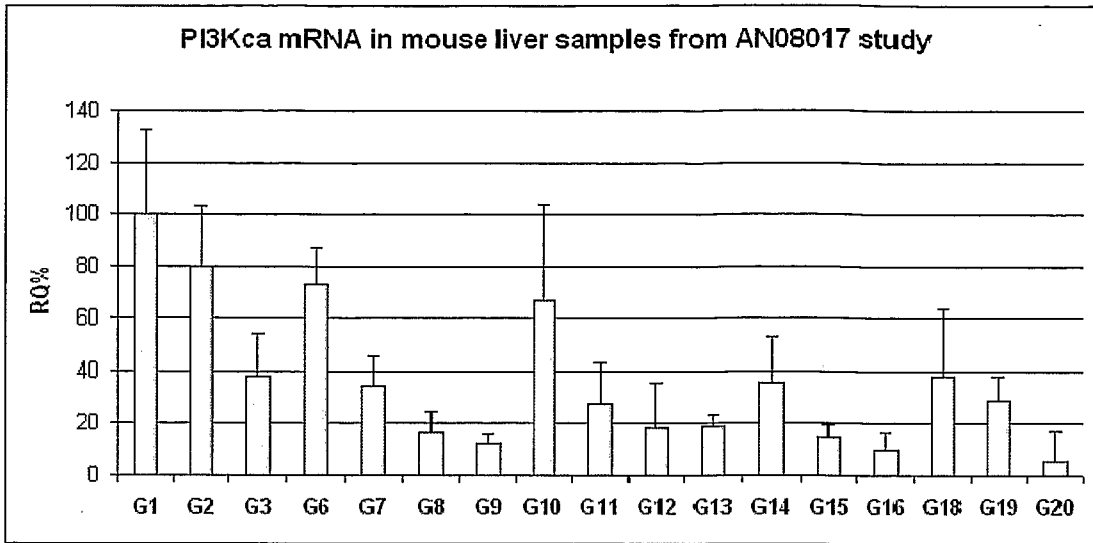


FIGURE 19

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G1: saline (KD 0 ± 32.6%)  
 G2: SEQ ID 57, 3mg/kg (KD 20.0 ± 23.3%)  
 G3: SEQ ID 57, 10mg/kg (KD 61.8 ± 16.2%)  
 G6: SEQ ID 60, 3mg/kg (KD 26.6 ± 13.9%)  
 G7: SEQ ID 60, 10mg/kg (KD 65.7 ± 11.1%)  
 G8: SEQ ID 60, 30mg/kg (KD 83.5 ± 8.1%)  
 G9: SEQ ID 60, 100mg/kg (KD 88.1 ± 3.7%)  
 G10: SEQ ID 67, 3mg/kg (KD 32.8 ± 36.9%)  
 G11: SEQ ID 67, 10mg/kg (KD 72.5 ± 15.5%)  
 G12: SEQ ID 67, 30mg/kg (KD 81.8 ± 17.3%)  
 G13: SEQ ID 67, 100mg/kg (KD 80.7 ± 4.2%)  
 G14: SEQ ID 77, 3mg/kg (KD 64.8 ± 18.1%)  
 G15: SEQ ID 77, 10mg/kg (KD 85.7 ± 5.6%)  
 G16: SEQ ID 77, 30mg/kg (KD 90.6 ± 6.9%)  
 G18: SEQ ID 82, 3mg/kg (KD 62.2 ± 26.4%)  
 G19: SEQ ID 82, 10mg/kg (KD 71.7 ± 9.7%)  
 G20: SEQ ID 82, 30mg/kg (KD 94.5 ± 11.7%)

FIGURE 20

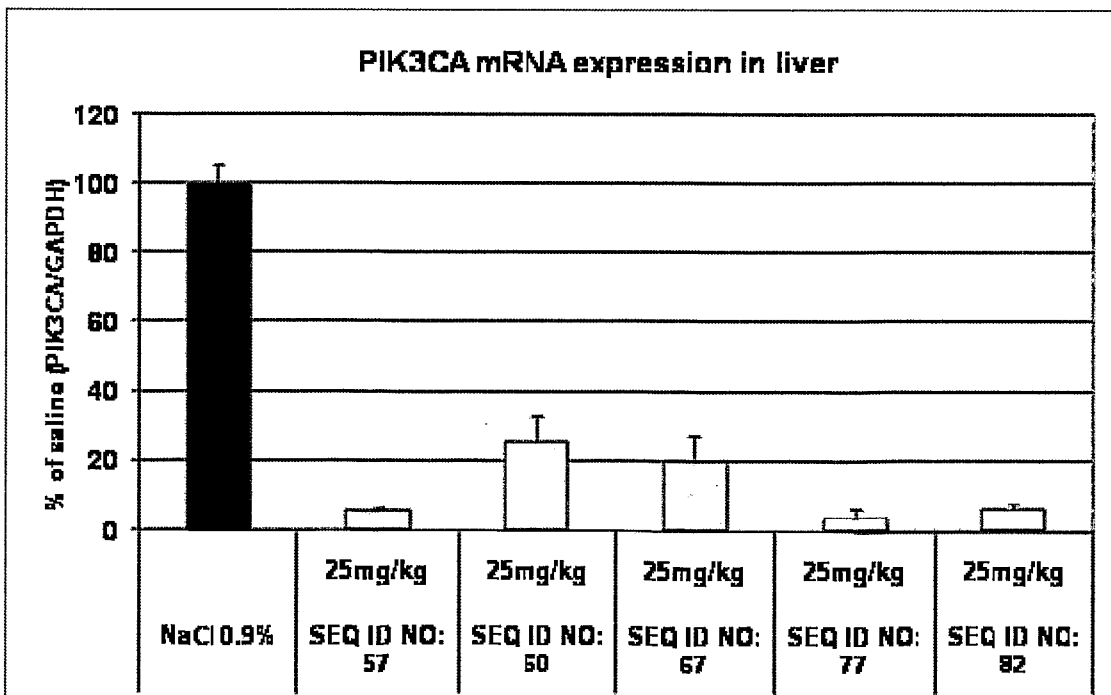


FIGURE 21



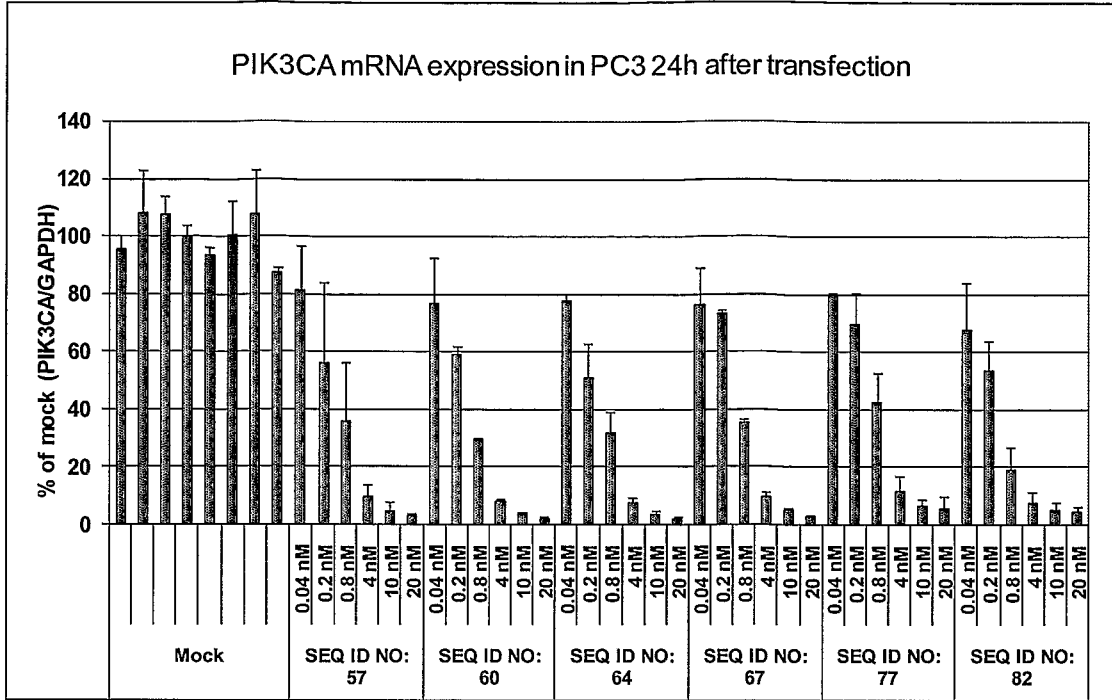


FIGURE 22

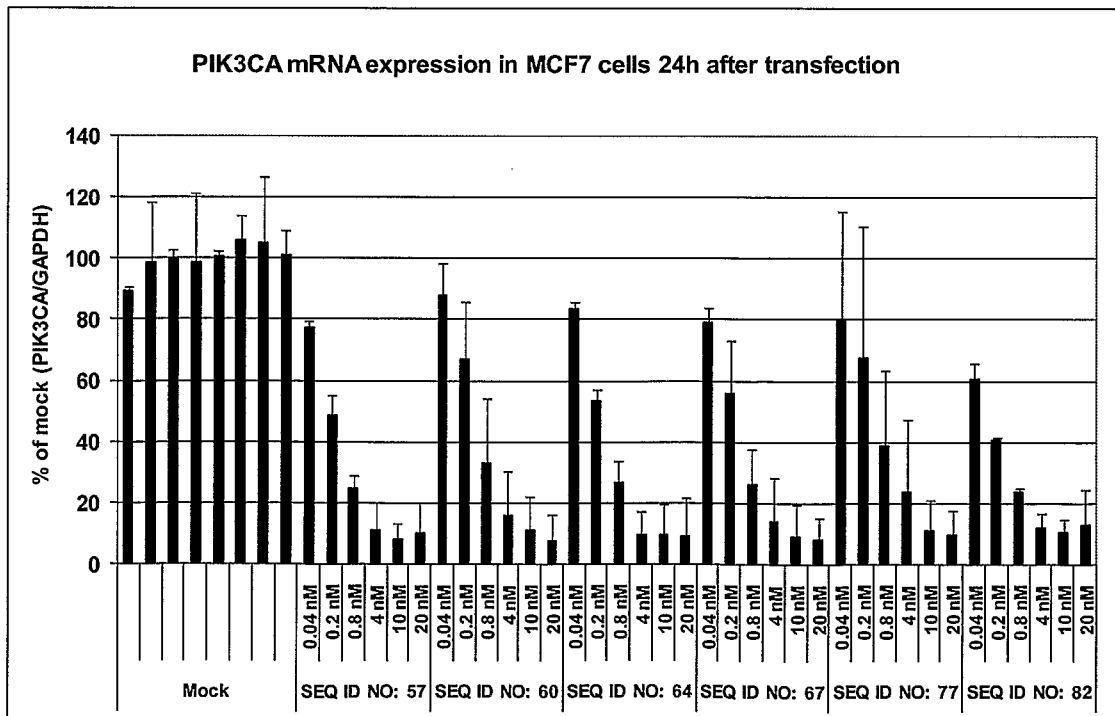


FIGURE 23.