(19) Europäisches Patentamt
European Patent Office
Office européen des brevets

(11) EP 4 220 360 B1

(12) EUROPEAN PATENT SPECIFICATION

(45) Date of publication and mention of the grant of the patent:
26.06.2024 Bulletin 2024/26

(21) Application number: **23152543.7**

(22) Date of filing: **11.11.2016**

(51) International Patent Classification (IPC):
C12N 15/113 $^{(2010.01)}$

(52) Cooperative Patent Classification (CPC):
G01N 33/5014; A61P 25/00; A61P 25/08; A61P 25/14; A61P 25/20; A61P 25/28; C12N 5/0619; C12N 5/0623; C12N 15/113; G01N 33/5058; C12N 2310/11; C12N 2310/20; C12N 2310/315; C12N 2310/3231; C12N 2310/3341; (Cont.)

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(54) OLIGONUCLEOTIDES FOR INDUCING PATERNAL UBE3A EXPRESSION

OLIGONUKLEOTIDE ZUR INDUKTION DER PATERNALEN UBE3A-EXPRESSION

OLIGONUCLÉOTIDES POUR INDUIRE L'EXPRESSION DE PATERNAL UBE3A

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(84) Designated Contracting States:
AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IS IT LI LT LU LV MC MK MT NL NO PL PT RO RS SE SI SK SM TR
Designated Validation States:
MA

(30) Priority: **12.11.2015 EP 15194367**
19.09.2016 EP 16189502

(43) Date of publication of application:
02.08.2023 Bulletin 2023/31

(62) Document number(s) of the earlier application(s) in accordance with Art. 76 EPC:
20204481.4 / 3 798 307
16798440.0 / 3 374 509

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WO-A2-03/000707
WO-A2-2004/028458
WO-A2-2014/004572
US-A1- 2005 124 572

Remarks:
The complete document including Reference Table(s) and the Sequence Listing(s) can be downloaded from the EPO website

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Processed by Luminess, 75001 PARIS (FR)

(Cont. next page)

(52) Cooperative Patent Classification (CPC): (Cont.)
C12N 2310/341; C12N 2310/346; C12N 2320/34;
C12N 2500/38; C12N 2500/44; C12N 2501/01;
C12N 2501/11; C12N 2501/115; C12N 2501/119;
C12N 2501/13; C12N 2501/41; C12N 2501/60;
C12N 2501/727; C12N 2501/999; C12N 2503/02;
C12N 2506/45; C12N 2533/52

Description

FIELD OF INVENTION

[0001] The present invention relates to oligonucleotides (oligomers) that are complementary to and hybridize to SNHG14 downstream of SNORD109B, leading to induction of paternal expression of Ubiquitin-protein ligase E3A (UBE3A) in an animal or human. The present invention further relates to pharmaceutical compositions and methods for treatment of Angelman syndrome.

BACKGROUND

[0002] Angelman syndrome is neuro-genetic disorder caused by deletion or inactivation of the UBE3A genes on the maternally inherited chromosome 15q11.2. The paternal copy of the UBE3A gene is subject to genomic imprinting and silencing in neurons by an endogenous antisense transcript of UBE3A, termed SNHG14 (also known as UBE3A-ATS) (Meng et al. 2012 Hum Mol Genet. Vol. 21 pp. 3001-12). Other cell types than neurons seem to express the UBE3A gene from both the maternal and paternal allele.

[0003] Angelman syndrome is characterized by severe intellectual and developmental disability, sleep disturbance, seizures, jerky movements, EEG abnormalities, frequent laughter or smiling, and profound language impairments.

[0004] WO 2012/064806 discloses a method of inducing UBE3A expression in a cell by using a topoisomerase inhibitor. The method can be used to treat Angelman syndrome. There is no disclosure of antisense oligonucleotides.

[0005] WO 2014/004572 discloses oligonucleotides with 2'-O-methoxyethyl-RNA (MOE) modifications targeting mouse UBE3A-ATS. The oligonucleotides are only tested in mice related assays. In the region downstream of MBII-52 snoRNA (also known as SNORD115) and upstream of the UBE3A pre-mRNA there is no conservation between mouse and human.Oligonucleotides targeting mouse UBE3A-ATS can therefore not be translated into oligonucleotides that will function in a human. There is no disclosure of oligonucleotides targeting human UBE3A-ATS.

OBJECTIVE OF THE INVENTION

[0006] The present invention identifies novel oligonucleotides which induce human paternal UBE3A expression in neuronal without affection expression of the paternal SNORD115, SNORD116 and SNRPN transcripts significantly.

SUMMARY OF INVENTION

[0007] The present invention relates to oligonucleotides targeting a nucleic acid capable of supressing the expression of UBE3A and to treat or prevent diseases related to decreased activity of UBE3A, in particular in neuronal cells.

[0008] Accordingly, in a first aspect the invention provides antisense oligonucleotides which comprise a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 98% complementarity to the part of human SNHG14 long non-coding RNA corresponding to position 25278410 to 25419462 on human chromosome 15 version GRCh38.p2 for use in the treatment or prevention of Angelman syndrome in a subject. This region is also resembled by SEQ ID NO: 1. The oligonucleotide is an antisense oligonucleotide, preferably with a gapmer design. The oligonucleotide is capable of inducing the expression of UBE3A, in particular paternal UBE3A expression in a neuron, by degradation, reduction or removal of the UBE3A suppressor, in particular by reduction of the SNHG14 long non-coding RNA transcript downstream of SNORD109B. The UBE3A re-expression is achieved, without significantly affecting the expression of SNORD115. The degradation of the target nucleic acid is preferably achieved via nuclease recruitment.

[0009] In a further aspect, the invention provides an antisense oligonucleotide capable of inducing human paternal UBE3A expression for use in the treatment or prevention of Angelman syndrome in a subject, wherein said antisense oligonucleotide comprises a contiguous nucleotide sequence that is 100% complementary to a region of the target nucleic acid of position 1 to 55318 of SEQ ID NO: 1, wherein the oligonucleotide is either 15 to 20 nucleotides in length or 17 to 22 nucleotides in length, wherein the oligonucleotide comprises one or more modified nucleosides, wherein the one or more modified nucleosides is a 2' sugar modified nucleoside, wherein the one or more 2' sugar modified nucleoside is independently selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA, 2'-amino-DNA, 2'-fluoro-DNA, arabino nucleic acid (ANA), 2'-fluoro-ANA and LNA nucleosides, wherein the oligonucleotide comprises at least one modified internucleoside linkage, wherein said modified internucleoside linkage is a phosphorothioate linkage, wherein the oligonucleotide is a gapmer of the formula F-G-F' wherein each of regions F and F' independently consists of 2, 3, 4 or 5 modified nucleoside units and region G consists of 9, 10, 11, 12, 13, 14 or 15 nucleoside units. In a further aspect, the invention provides a conjugate for use in the treatment or prevention of Angelman syndrome in a subject, the conjugate comprising an antisense oligonucleotide of the invention and at least one conjugate moiety covalently attached to the oligonucleotide.

[0010] In a further aspect, the invention provides pharmaceutical compositions comprising the oligonucleotides or conjugates of the invention and pharmaceutically acceptable diluents, carriers, salts and/or adjuvants.

[0011] In a further aspect, the invention provides methods for *in vitro* induction of UBE3A expression in a target cell where expression of paternal UBE3A is suppressed, by administering an oligonucleotide, conjugate or composition of the invention in an effective amount to said cell.

BRIEF DESCRIPTION OF FIGURES

[0012]

Figure 1: The upper strand illustrates the region of the SNHG14 transcript downstream of SNORD109B (UBE3A-ATS) where the black boxes indicate the location of the tested mouse oligonucleotides. The lower strand illustrates the UBE3A coding region, where the black boxes indicate exons. Exon 1 is located around 160kb. The oligonucleotides are placed in the antisense region of Exon 9 (positioned at ~97kb), Exon 10 (positioned at ~92kb), Exon 13 (positioned at ~77kb) and the 5' end of Exon 16 (positioned at ~60kb).

Figure 2: Representation of the ability of the oligonucleotides, tested in Example 2, to induce re-expression of UBE3A in human neuronal cell cultures. Oligonucleotides complementary to the region of human SNHG14 long non-coding RNA between SNORD109B and the region upstream of the UBE3A coding region (position 1 to 55318 of SEQ ID NO: 1) are indicated with • nonoverlap.

Oligonucleotides complementary to the region of human SNHG14 long non-coding RNA which is antisense to the UBE3A pre-mRNA (position 55319 to 141053 of SEQ ID NO: 1) are indicated with ▲overlap. Oligonucleotides from Table 3 with conservation to human and rhesus monkey are indicated at the bottom of each plot as ▨. Conservation between human:rhesus:mouse is indicated by ■. The oligonucleotide concentrations were 0.2, 1 and 5 microM as indicated in the right hand side each plot.

DEFINITIONS

Oligonucleotide

[0013] The term "oligonucleotide" as used herein is defined as it is generally understood by the skilled person as a molecule comprising two or more covalently linked nucleosides. Such covalently bound nucleosides may also be referred to as nucleic acid molecules or oligomers. Oligonucleotides are commonly made in the laboratory by solid-phase chemical synthesis followed by purification. When referring to a sequence of the oligonucleotide, reference is made to the sequence or order of nucleobase moieties, or modifications thereof, of the covalently linked nucleotides or nucleosides. The oligonucleotide of the invention is man-made, and is chemically synthesized, and is typically purified or isolated. The oligonucleotide of the invention may comprise one or more modified nucleosides or nucleotides.

Antisense oligonucleotides

[0014] The term "Antisense oligonucleotide" as used herein is defined as oligonucleotides capable of modulating expression of a target gene by hybridizing to a target nucleic acid, in particular to a contiguous sequence on a target nucleic acid. The antisense oligonucleotides are not essentially double stranded and are therefore not siRNAs. Preferably, the antisense oligonucleotides of the present invention are single stranded.

Contiguous Nucleotide Sequence

[0015] The term "contiguous nucleotide sequence" refers to the region of the oligonucleotide which is complementary to the target nucleic acid. The term is used interchangeably herein with the term "contiguous nucleobase sequence" and the term "oligonucleotide motif sequence". In some embodiments all the nucleotides of the oligonucleotide are present in the contiguous nucleotide sequence. In some embodiments the oligonucleotide comprises the contiguous nucleotide sequence and may, optionally comprise further nucleotide(s), for example a nucleotide linker region which may be used to attach a functional group to the contiguous nucleotide sequence. The nucleotide linker region may or may not be complementary to the target nucleic acid.

Nucleotides

[0016] Nucleotides are the building blocks of oligonucleotides and polynucleotides, and for the purposes of the present invention include both naturally occurring and non-naturally occurring nucleotides. In nature, nucleotides, such as DNA and RNA nucleotides comprise a ribose sugar moiety, a nucleobase moiety and one or more phosphate groups (which is absent in nucleosides). Nucleosides and nucleotides may also interchangeably be referred to as "units" or "monomers".

Modified nucleoside

[0017] The term "modified nucleoside" or "nucleoside modification" as used herein refers to nucleosides modified as compared to the equivalent DNA or RNA nucleoside by the introduction of one or more modifications of the sugar moiety or the (nucleo)base moiety. In a preferred embodiment the modified nucleoside comprises a modified sugar moiety. The term modified nucleoside may also be used herein interchangeably with the term "nucleoside analogue" or modified "units" or modified "monomers".

Modified internucleoside linkage

[0018] The term "modified internucleoside linkage" is defined as generally understood by the skilled person as linkages other than phosphodiester (PO) linkages, that covalently couples two nucleosides together. Nucleotides with modified internucleoside linkage are also termed "modified nucleotides". In some embodiments, the modified internucleoside linkage increases the nuclease resistance of the oligonucleotide compared to a phosphodiester linkage. For naturally occurring oligonucleotides, the internucleoside linkage includes phosphate groups creating a phosphodiester bond between adjacent nucleosides. Modified internucleoside linkages are particularly useful in stabilizing oligonucleotides for in vivo use, and may serve to protect against nuclease cleavage at regions of DNA or RNA nucleosides in the oligonucleotide of the invention, for example within the gap region of a gapmer oligonucleotide, as well as in regions of modified nucleosides.

[0019] In an embodiment, the oligonucleotide comprises one or more internucleoside linkages modified from the natural phosphodiester to a linkage that is for example more resistant to nuclease attack. Nuclease resistance may be determined by incubating the oligonucleotide in blood serum or by using a nuclease resistance assay (e.g. snake venom phosphodiesterase (SVPD)), both are well known in the art. Internucleoside linkages which are capable of enhancing the nuclease resistance of an oligonucleotide are referred to as nuclease resistant internucleoside linkages. In preferred embodiments at least 50% of the internucleoside linkages in the oligonucleotide, or contiguous nucleotide sequence thereof, are modified, such as at least 60%, such as at least 70%, such as at least 80 or such as at least 90% of the internucleoside linkages in the oligonucleotide, or contiguous nucleotide sequence thereof, are modified. In some embodiments all of the internucleoside linkages of the oligonucleotide, or contiguous nucleotide sequence thereof, are modified. It will be recognized that, in some embodiments the nucleosides which link the oligonucleotide of the invention to a non-nucleotide functional group, such as a conjugate, may be phosphodiester. In some embodiments all of the internucleoside linkages of the oligonucleotide, or contiguous nucleotide sequence thereof, are nuclease resistant internucleoside linkages.

[0020] Modified internucleoside linkages may be selected from the group comprising phosphorothioate, diphosphorothioate and boranophosphate. In preferred embodiments, the modified internucleoside linkages are compatible with the RNaseH recruitment of the oligonucleotide of the invention, for example phosphorothioate, diphosphorothioate or boranophosphate.

[0021] In some embodiments the internucleoside linkage comprises sulphur (S), such as a phosphorothioate internucleoside linkage.

[0022] A phosphorothioate internucleoside linkage is particularly useful due to nuclease resistance, beneficial pharmakokinetics and ease of manufacture. In preferred embodiments at least 50% of the internucleoside linkages in the oligonucleotide, or contiguous nucleotide sequence thereof, are phosphorothioate, such as at least 60%, such as at least 70%, such as at least 80 or such as at least 90% of the internucleoside linkages in the oligonucleotide, or contiguous nucleotide sequence thereof, are phosphorothioate. In some embodiments all of the internucleoside linkages of the oligonucleotide, or contiguous nucleotide sequence thereof, are phosphorothioate.

[0023] In some embodiments, the oligonucleotide comprises one or more neutral internucleoside linkage, particularly a internucleoside linkage selected from phosphotriester, methylphosphonate, MMI, amide-3, formacetal or thioformacetal.

[0024] Further internucleoside linkages are disclosed in WO2009/124238. In an embodiment the internucleoside linkage is selected from linkers disclosed in WO2007/031091. Particularly, the internucleoside linkage may be selected from $-O-P(O)_2-O-$, -O-P(O,S)-O-, -O-P(S)z-O-, -S-P(O)z-O-, -S-P(O,S)-O-, -S-P(S)z-O-, $-O-P(O)_2-S-$, -O-P(O,S)-S-, $-S-P(O)_2-S-$, $-O-PO(R^H)-O-$, $0-PO(OCH_3)-O-$, $-O-PO(NR^H)-O-$, $-O-PO(OCH_2CH_2S-R)-O-$, $-O-PO(BH_3)-O-$, $-O-PO(NHR^H)-O-$, $-OP(O)_2-NR^H-$, $-NR^H-P(O)_2-O-$, $-NR^H-CO-O-$, $-NR^H-CO-NR^H-$, and/or the internucleoside linker may be selected form the group consisting of: -O-CO-O-, $-O-CO-NR^H-$, $-NR^H-CO-CH_2-$, $-O-CHz-CO-NR^H-$, $-O-CH_2-CH_2-NR^H-$, $-CO-NR^H-CH_2-$, $-CH_2-NR^HCO-$, $-O-CH_2-CH_2-S-$, $-S-CH_2-CH_2-O-$, $-S-CH_2-CH_2-S-$, $-CH_2-SO_2-CH_2-$, $-CH_2-CO-NR^H-$, $-O-CH_2-CH_2-NR''-CO$ -, $-CH_2-NCH_3-O-CH_2-$, where R^H is selected from hydrogen and C1 -4-alkyl.

[0025] Nuclease resistant linkages, such as phosphothioate linkages, are particularly useful in oligonucleotide regions capable of recruiting nuclease when forming a duplex with the target nucleic acid, such as region G for gapmers, or the non-modified nucleoside region of headmers and tailmers. Phosphorothioate linkages may, however, also be useful in non-nuclease recruiting regions and/or affinity enhancing regions such as regions F and F' for gapmers, or the modified nucleoside region of headmers and tailmers.

[0026] Each of the design regions may however comprise internucleoside linkages other than phosphorothioate, such as phosphodiester linkages, in particularly in regions where modified nucleosides, such as LNA, protect the linkage against nuclease degradation. Inclusion of phosphodiester linkages, such as one or two linkages, particularly between or adjacent to modified nucleoside units (typically in the non-nuclease recruiting regions) can modify the bioavailability and/or bio-distribution of an oligonucleotide - see WO2008/113832.

[0027] In an embodiment all the internucleoside linkages in the oligonucleotide are phosphorothioate and/or boranophosphate linkages. Preferably, all the internucleoside linkages in the oligonucleotide are phosphorothioate linkages.

Nucleobase

[0028] The term nucleobase includes the purine (e.g. adenine and guanine) and pyrimidine (e.g. uracil, thymine and cytosine) moiety present in nucleosides and nucleotides which form hydrogen bonds in nucleic acid hybridization. In the context of the present invention the term nucleobase also encompasses modified nucleobases which may differ from naturally occurring nucleobases, but are functional during nucleic acid hybridization. In this context "nucleobase" refers to both naturally occurring nucleobases such as adenine, guanine, cytosine, thymidine, uracil, xanthine and hypoxanthine, as well as non-naturally occurring variants. Such variants are for example described in Hirao et al (2012) Accounts of Chemical Research vol 45 page 2055 and Bergstrom (2009) Current Protocols in Nucleic Acid Chemistry Suppl. 37 1.4.1.

[0029] In a some embodiments the nucleobase moiety is modified by changing the purine or pyrimidine into a modified purine or pyrimidine, such as substituted purine or substituted pyrimidine, such as a nucleobased selected from isocytosine, pseudoisocytosine, 5-methyl cytosine, 5-thiozolo-cytosine, 5-propynyl-cytosine, 5-propynyl-uracil, 5-bromouracil 5-thiazolo-uracil, 2-thio-uracil, 2'thio-thymine, inosine, diaminopurine, 6-aminopurine, 2-aminopurine, 2,6-diaminopurine and 2-chloro-6-aminopurine.

[0030] The nucleobase moieties may be indicated by the letter code for each corresponding nucleobase, e.g. A, T, G, C or U, wherein each letter may optionally include modified nucleobases of equivalent function. For example, in the exemplified oligonucleotides, the nucleobase moieties are selected from A, T, G, C, and 5-methyl cytosine. Optionally, for LNA gapmers, 5-methyl cytosine LNA nucleosides may be used.

Modified oligonucleotide

[0031] The term modified oligonucleotide describes an oligonucleotide comprising one or more sugar-modified nucleosides and/or modified internucleoside linkages. The term chimeric" oligonucleotide is a term that has been used in the literature to describe oligonucleotides with modified nucleosides.

Complementarity

[0032] The term complementarity describes the capacity for Watson-Crick base-pairing of nucleosides/nucleotides. Watson-Crick base pairs are guanine (G)-cytosine (C) and adenine (A) - thymine (T)/uracil (U). It will be understood that oligonucleotides may comprise nucleosides with modified nucleobases, for example 5-methyl cytosine is often used in place of cytosine, and as such the term complementarity encompasses Watson Crick base-paring between non-modified and modified nucleobases (see for example Hirao et al (2012) Accounts of Chemical Research vol 45 page 2055 and Bergstrom (2009) Current Protocols in Nucleic Acid Chemistry Suppl. 37 1.4.1).

[0033] The term "% complementary" as used herein, refers to the number of nucleotides in percent of a contiguous nucleotide sequence in a nucleic acid molecule (e.g. oligonucleotide) which, at a given position, are complementary to (i.e. form Watson Crick base pairs with) a contiguous nucleotide sequence, at a given position of a separate nucleic acid molecule (e.g. the target nucleic acid). The percentage is calculated by counting the number of aligned bases that form pairs between the two sequences, dividing by the total number of nucleotides in the oligonucleotide and multiplying by 100. In such a comparison a nucleobase/nucleotide which does not align (form a base pair) is termed a mismatch.

[0034] The term "fully complementary", refers to 100% complementarity.

Hybridization

[0035] The term "hybridizing" or "hybridizes" as used herein is to be understood as two nucleic acid strands (e.g. an oligonucleotide and a target nucleic acid) forming hydrogen bonds between base pairs on opposite strands thereby forming a duplex. The affinity of the binding between two nucleic acid strands is the strength of the hybridization. It is often described in terms of the melting temperature (T_m) defined as the temperature at which half of the oligonucleotides are duplexed with the target nucleic acid. At physiological conditions T_m is not strictly proportional to the affinity (Mergny and Lacroix, 2003,Oligonucleotides 13:515-537). The standard state Gibbs free energy $\Delta G°$ is a more accurate representation of binding affinity and is related to the dissociation constant (K_d) of the reaction by $\Delta G° = -RTln(K_d)$, where R is the gas constant and T is the absolute temperature. Therefore, a very low $\Delta G°$ of the reaction between an oligonucleotide and the target nucleic acid reflects a strong hybridization between the oligonucleotide and target nucleic acid. $\Delta G°$ is the energy associated with a reaction where aqueous concentrations are 1M, the pH is 7, and the temperature is 37°C. The hybridization of oligonucleotides to a target nucleic acid is a spontaneous reaction and for spontaneous reactions $\Delta G°$ is less than zero. $\Delta G°$ can be measured experimentally, for example, by use of the isothermal titration calorimetry (ITC) method as described in Hansen et al., 1965, Chem. Comm. 36-38 and Holdgate et al., 2005, Drug Discov Today. The skilled person will know that commercial equipment is available for $\Delta G°$ measurements. $\Delta G°$ can also be estimated numerically by using the nearest neighbor model as described by SantaLucia, 1998, Proc Natl Acad Sci USA. 95: 1460-1465 using appropriately derived thermodynamic parameters described by Sugimoto et al., 1995, Biochemistry 34:11211-11216 and McTigue et al., 2004, Biochemistry 43:5388-5405. In order to have the possibility of modulating its intended nucleic acid target by hybridization, oligonucleotides of the present invention hybridize to a target nucleic acid with estimated $\Delta G°$ values below -10 kcal for oligonucleotides that are 10-30 nucleotides in length. In some embodiments the degree or strength of hybridization is measured by the standard state Gibbs free energy $\Delta G°$. The oligonucleotides may hybridize to a target nucleic acid with estimated $\Delta G°$ values below the range of -10 kcal, such as below -15 kcal, such as below -20 kcal and such as below -25 kcal for oligonucleotides that are 8-30 nucleotides in length. In some embodiments the oligonucleotides hybridize to a target nucleic acid with an estimated $\Delta G°$ value of -10 to -60 kcal, such as -12 to -40, such as from -15 to -30 kcal or-16 to -27 kcal such as -18 to -25 kcal.

The target

[0036] The target refers to the protein which it is desired to modulate.

Target nucleic acid

[0037] A target nucleic acid is the intended target which the oligonucleotide of the invention hybridizes to, and may for example be a gene, a RNA, a non-coding RNA, a long non-coding RNA, a mRNA, and pre-mRNA, a mature mRNA or a cDNA sequence. In some embodiments the target nucleic acid is a non-coding RNA or a long non-coding RNA, or a subsequence thereof. For *in vivo* or *in vitro* application, the oligonucleotide of the invention is capable of decreasing the level of the SNHG14 transcript downstream of SNORD109B of and thereby relieving the suppression of the paternal UBE3A transcript in the intended target cell. The contiguous sequence of nucleobases of the oligonucleotide of the invention is complementary to the target nucleic acid, as measured across the length of the oligonucleotide, optionally with the exception of one or two mismatches, and optionally excluding nucleotide based linker regions which may link the oligonucleotide to an optional functional group such as a conjugate.

Target Sequence

[0038] The oligonucleotide comprises a contiguous nucleotide sequence which is complementary to or hybridizes to a sub-sequence of the target nucleic acid molecule. The term "target sequence" as used herein refers to a sequence of nucleotides present in the target nucleic acid which comprises the nucleobase sequence which is complementary to the oligonucleotide of the invention. In some embodiments, the target sequence consists of a region on the target nucleic acid which is complementary to the contiguous nucleotide sequence of the oligonucleotide of the invention. In some embodiments the target sequence is longer than the complementary sequence of a single oligonucleotide, and may, for example represent a preferred region of the target nucleic acid which may be targeted by several oligonucleotides of the invention.

[0039] The oligonucleotide of the invention comprises a contiguous nucleotide sequence which is complementary to the target nucleic acid, such as a target sequence.

[0040] The oligonucleotide comprises a contiguous nucleotide sequence of at least 8 nucleotides which is complementary to or hybridizes to a target sequence present in the target nucleic acid molecule. The contiguous nucleotide sequence (and therefore the target sequence) comprises of at least 8 contiguous nucleotides, such as 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 contiguous nucleotides, such as from 12-25, such as from 14-18 contiguous nucleotides.

Target Cell

[0041] The term a target cell as used herein refers to a cell which is expressing the target nucleic acid. In some embodiments the target cell may be *in vivo* or *in vitro.* In some embodiments the target cell is a mammalian cell such as a rodent cell, such as a mouse cell or a rat cell, or a primate cell such as a monkey cell or a human cell. In preferred embodiments the target cell is a neuronal cell.

Naturally occurring variant

[0042] The term "naturally occurring variant" refers to variants of SNHG14 transcript downstream of SNORD109B gene or transcripts which originate from the same genetic loci as the target nucleic acid, but may differ for example, by virtue of degeneracy of the genetic code causing a multiplicity of codons in the long non-coding RNA. The oligonucleotide of the invention may therefore be designed to target the target nucleic acid and naturally occurring variants thereof.

Modulation of expression

[0043] The term "modulation of expression" as used herein is to be understood as an overall term for an oligonucleotide's ability to alter the amount of UBE3A protein when compared to the amount of UBE3A before administration of the oligonucleotide. Alternatively modulation of expression may be determined by reference to a control experiment where the oligonucleotide of the invention is not administered. The modulation effected by the oligonucleotide is related to it's ability to reduce, remove, prevent, lessen, lower or terminate the suppression of the paternal UBE3A transcript, e.g. by degradation or removal of the non-coding SNHG14 transcript downstream of SNORD109B or by blockage or prevention of polymerase activity associated with the SNHG14 transcript downstream of SNORD109B. The modulation can also be viewed as the oligonucleotide's ability to restore, increase or enhance expression of paternal UBE3A, e.g. by removal or blockage of inhibitory mechanisms affected by the non-coding SNHG14 transcript downstream of SNORD109B.

High affinity modified nucleosides

[0044] A high affinity modified nucleoside is a modified nucleotide which, when incorporated into the oligonucleotide enhances the affinity of the oligonucleotide for its complementary target, for example as measured by the melting temperature (T^m). A high affinity modified nucleoside of the present invention preferably result in an increase in melting temperature between +0.5 to +12°C, more preferably between +1.5 to +10°C and most preferably between+3 to +8°C per modified nucleoside. Numerous high affinity modified nucleosides are known in the art and include for example, many 2' substituted nucleosides as well as locked nucleic acids (LNA) (see e.g. Freier & Altmann; Nucl. Acid Res., 1997, 25, 4429-4443 and Uhlmann; Curr. Opinion in Drug Development, 2000, 3(2), 293-213).

Sugar modifications

[0045] The oligomer of the invention may comprise one or more nucleosides which have a modified sugar moiety, *i.e.* a modification of the sugar moiety when compared to the ribose sugar moiety found in DNA and RNA.

[0046] Numerous nucleosides with modification of the ribose sugar moiety have been made, primarily with the aim of improving certain properties of oligonucleotides, such as affinity and/or nuclease resistance.

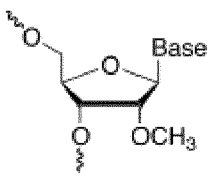
[0047] Such modifications include those where the ribose ring structure is modified, e.g. by replacement with a hexose ring (HNA), or a bicyclic ring, which typically have a biradicle bridge between the C2 and C4 carbons on the ribose ring (LNA), or an unlinked ribose ring which typically lacks a bond between the C2 and C3 carbons (e.g. UNA). Other sugar modified nucleosides include, for example, bicyclohexose nucleic acids (WO2011/017521) or tricyclic nucleic acids (WO2013/154798). Modified nucleosides also include nucleosides where the sugar moiety is replaced with a non-sugar moiety, for example in the case of peptide nucleic acids (PNA), or morpholino nucleic acids.

[0048] Sugar modifications also include modifications made via altering the substituent groups on the ribose ring to groups other than hydrogen, or the 2'-OH group naturally found in DNA and RNA nucleosides. Substituents may, for example be introduced at the 2', 3', 4' or 5' positions. Nucleosides with modified sugar moieties also include 2' modified nucleosides, such as 2' substituted nucleosides. Indeed, much focus has been spent on developing 2' substituted nucleosides, and numerous 2' substituted nucleosides have been found to have beneficial properties when incorporated into oligonucleotides, such as enhanced nucleoside resistance and enhanced affinity.

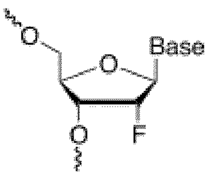
2' modified nucleosides.

[0049] A 2' sugar modified nucleoside is a nucleoside which has a substituent other than H or -OH at the 2' position

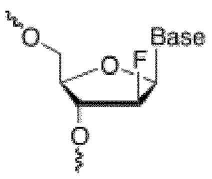
(2' substituted nucleoside) or comprises a 2' linked biradicle, and includes 2' substituted nucleosides and LNA (2' - 4' biradicle bridged) nucleosides. For example, the 2' modified sugar may provide enhanced binding affinity and/or increased nuclease resistance to the oligonucleotide. Examples of 2' substituted modified nucleosides are 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA (MOE), 2'-amino-DNA, 2'-Fluoro-RNA, and 2'-fluoro-ANA (F-ANA). For further examples, please see e.g. Freier & Altmann; Nucl. Acid Res., 1997, 25, 4429-4443 and Uhlmann; Curr. Opinion in Drug Development, 2000, 3(2), 293-213; and Deleavey and Damha, Chemistry and Biology 2012, 19, 937. Below are illustrations of some 2' substituted modified nucleosides.



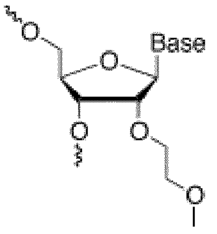
2'-*O*-Me



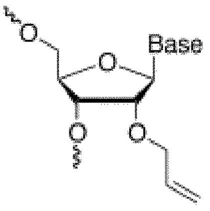
2'F-RNA



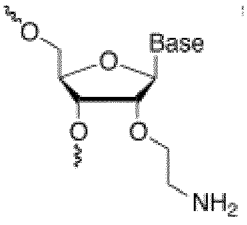
2'F-ANA



2'-*O*-MOE



2'-*O*-Allyl

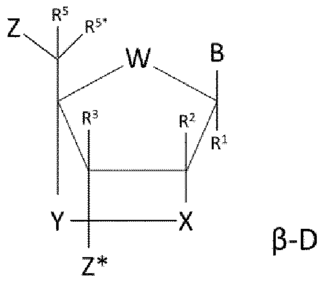


2'-*O*-Ethylamine

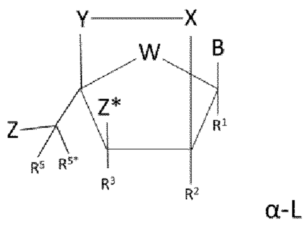
Locked Nucleic Acid Nucleosides (LNA).

[0050] LNA nucleosides are modified nucleosides which comprise a linker group (referred to as a biradicle or a bridge) between C2' and C4' of the ribose sugar ring of a nucleotide. These nucleosides are also termed bridged nucleic acid or bicyclic nucleic acid (BNA) in the literature.

[0051] In some embodiments, the modified nucleoside or the LNA nucleosides of the oligomer of the invention has a general structure of the formula I or II:



or



Formula I

Formula II

wherein W is selected from -O-, -S-, -N(R^a)-, -C(R^aR^b)-, such as, in some embodiments -O-;
B designates a nucleobase or modified nucleobase moiety;
Z designates an internucleoside linkage to an adjacent nucleoside, or a 5'-terminal group;
Z* designates an internucleoside linkage to an adjacent nucleoside, or a 3'-terminal group;
X designates a group selected from the list consisting of -C(R^aR^b)-, -C(R^a)=C(R^b)-, - C(R^a)=N-, -O-, -Si(R^a)$_2$-, -S-, -SO$_2$-, -N(R^a)-, and >C=Z

[0052] In some embodiments, X is selected from the group consisting of: -O-, -S-, NH-, NR^aR^b, -CH$_2$-, CR^aR^b, -C(=CH$_2$)-, and -C(=CR^aR^b)-

[0053] In some embodiments, X is -O-

[0054] Y designates a group selected from the group consisting of -C(R^aR^b)-, -C(R^a)=C(R^b)-, - C(R^a)=N-, -O-, -Si(R^a)$_2$-, -S-, -SO_2-, -N(R^a)-, and >C=Z

[0055] In some embodiments, Y is selected from the group consisting of: -CH_2-, -C(R^aR^b)-, - CH_2CH_2-, -C(R^aR^b)-C(R^aR^b)-, -$CH_2CH_2CH_2$-, -C(R^aR^b)C(R^aR^b)C(R^aR^b)-, -C(R^a)=C(R^b)-, and -C(R^a)=N-

[0056] In some embodiments, Y is selected from the group consisting of: -CH_2-, -CHR^a-, - $CHCH_3$-, CR^aR^b- or -X-Y- together designate a bivalent linker group (also referred to as a radicle) together designate a bivalent linker group consisting of 1, 2, 3 or 4 groups/atoms selected from the group consisting of -C(R^aR^b)-, -C(R^a)=C(R^b)-, -C(R^a)=N-, -O-, -Si(R^a)$_2$-, -S-, -SO_2-, -N(R^a)-, and >C=Z,

[0057] In some embodiments, -X-Y- designates a biradicle selected from the groups consisting of: -X-CH_2-, -X-CR^aR^b-, -X-$CHR^{a,}$, -X-C(HCH_3)$^-$, -O-Y-, -O-CH_2-, -S-CH_2-, -NH-CH_2-, -O-$CHCH_3$-, -CH_2-O-CH_2, -O-CH(CH_3CH_3)-, -O-CH_2-CH_2-, OCH_2-CH_2-CH_2-,-O-CH_2OCH_2-,-O-NCH_2-, -C(=CH_2)-CH_2-, -NR^a-CH_2-, N-O-CH_2, -S-CR^aR^b- and -S-CHR^a-.

[0058] In some embodiments -X-Y- designates -O-CH_2- or -O-CH(CH_3)-.

wherein Z is selected from -O-, -S-, and -N(R^a)-,

and R^a and, when present R^b, each is independently selected from hydrogen, optionally substituted C_{1-6}-alkyl, optionally substituted C_{2-6}-alkenyl, optionally substituted C_{2-6}-alkynyl, hydroxy, optionally substituted C_{1-6}-alkoxy, C_{2-6}-alkoxyalkyl, C_{2-6}-alkenyloxy, carboxy, C_{1-6}-alkoxycarbonyl, C_{1-6}-alkylcarbonyl, formyl, aryl, aryloxy-carbonyl, aryloxy, arylcarbonyl, heteroaryl, heteroaryloxy-carbonyl, heteroaryloxy, heteroarylcarbonyl, amino, mono- and di(C_{1-6}-alkyl)amino, carbamoyl, mono- and di(C_{1-6}-alkyl)-amino-carbonyl, amino-C_{1-6}-alkylaminocarbonyl, mono- and di(C_{1-6}-alkyl)amino-C_{1-6}-alkyl-aminocarbonyl, C_{1-6}-alkylcarbonylamino, carbamido, C_{1-6}-alkanoyloxy, sulphono, C_{1-6}-alkylsulphonyloxy, nitro, azido, sulphanyl, C_{1-6}-alkylthio, halogen, 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), wherein for all chiral centers, asymmetric groups may be found in either R or *S* orientation.

wherein R^1, R^2, R^3, R^5 and R^{5*} are independently selected from the group consisting of: hydrogen, optionally substituted C_{1-6}-alkyl, optionally substituted C_{2-6}-alkenyl, optionally substituted C_{2-6}-alkynyl, hydroxy, C_{1-6}-alkoxy, C_{2-6}-alkoxyalkyl, C_{2-6}-alkenyloxy, carboxy, C_{1-6}-alkoxycarbonyl, C_{1-6}-alkylcarbonyl, formyl, aryl, aryloxy-carbonyl, aryloxy, arylcarbonyl, heteroaryl, heteroaryloxy-carbonyl, heteroaryloxy, heteroarylcarbonyl, amino, mono- and di(C_{1-6}-alkyl)amino, carbamoyl, mono- and di(C_{1-6}-alkyl)-amino-carbonyl, amino-C_{1-6}-alkylaminocarbonyl, mono- and di(C_{1-6}-alkyl)amino-C_{1-6}-alkyl-aminocarbonyl, C_{1-6}-alkylcarbonylamino, carbamido, C_{1-6}-alkanoyloxy, sulphono, C_{1-6}-alkylsulphonyloxy, nitro, azido, sulphanyl, C_{1-6}-alkylthio, halogen, where aryl and heteroaryl may be optionally substituted, and where two geminal substituents together may designate oxo, thioxo, imino, or optionally substituted methylene.

[0059] In some embodiments R^1, R^2, R^3, R^5 and R^{5*} are independently selected from C_{1-6} alkyl, such as methyl, and hydrogen.

[0060] In some embodiments R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen.

[0061] In some embodiments R^1, R^2, R^3, are all hydrogen, and either R^5 and R^{5*} is also hydrogen and the other of R^5 and $R^{5*}$is other than hydrogen, such as C_{1-6} alkyl such as methyl.

[0062] In some embodiments, R^a is either hydrogen or methyl. In some embodiments, when present, R^b is either hydrogen or methyl.

[0063] In some embodiments, one or both of R^a and R^b is hydrogen

[0064] In some embodiments, one of R^a and R^b is hydrogen and the other is other than hydrogen

[0065] In some embodiments, one of R^a and R^b is methyl and the other is hydrogen

[0066] In some embodiments, both of R^a and R^b are methyl.

[0067] In some embodiments, the biradicle -X-Y- is -O-CH_2-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such LNA nucleosides are disclosed in WO99/014226, WO00/66604, WO98/039352 and WO2004/046160, and include what are commonly known as beta-D-oxy LNA and alpha-L-oxy LNA nucleosides.

[0068] In some embodiments, the biradicle -X-Y- is -S-CH_2-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such thio LNA nucleosides are disclosed in WO99/014226 and WO2004/046160.

[0069] In some embodiments, the biradicle -X-Y- is -NH-CH_2-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such amino LNA nucleosides are disclosed in WO99/014226 and WO2004/046160.

[0070] In some embodiments, the biradicle -X-Y- is -O-CH_2-CH_2- or -O-CH_2-CH_2- CH_2-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such LNA nucleosides are disclosed in WO00/047599 and Morita et al, Bioorganic & Med.Chem. Lett. 12 73-76, and include what are commonly known as 2'-O-4'C-ethylene bridged nucleic acids (ENA).

[0071] In some embodiments, the biradicle -X-Y- is -O-CH_2-, W is O, and all of R^1, R^2, R^3, and one of R^5 and R^{5*} are hydrogen, and the other of R^5 and R^{5*} is other than hydrogen such as C_{1-6} alkyl, such as methyl. Such 5' substituted LNA nucleosides are disclosed in WO2007/134181.

[0072] In some embodiments, the biradicle -X-Y- is -O-CR^aR^b-, wherein one or both of R^a and R^b are other than hydrogen, such as methyl, W is O, and all of R^1, R^2, R^3, and one of R^5 and R^{5*} are hydrogen, and the other of R^5 and R^{5*} is other than hydrogen such as C_{1-6} alkyl, such as methyl. Such bis modified LNA nucleosides are disclosed in WO2010/077578.

[0073] In some embodiments, the biradicle -X-Y- designate the bivalent linker group -O-$CH(CH_2OCH_3)$- (2' O-methoxyethyl bicyclic nucleic acid - Seth at al., 2010, J. Org. Chem. Vol 75(5) pp. 1569-81). In some embodiments, the biradicle -X-Y- designate the bivalent linker group -O-$CH(CH_2CH_3)$- (2'O-ethyl bicyclic nucleic acid - Seth at al., 2010, J. Org. Chem. Vol 75(5) pp. 1569-81). In some embodiments, the biradicle -X-Y- is -O-CHR^a-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such 6' substituted LNA nucleosides are disclosed in WO10036698 and WO07090071.

[0074] In some embodiments, the biradicle -X-Y- is -O-$CH(CH_2OCH_3)$-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such LNA nucleosides are also known as cyclic MOEs in the art (cMOE) and are disclosed in WO07090071.

[0075] In some embodiments, the biradicle -X-Y- designate the bivalent linker group -O-$CH(CH_3)$-. - in either the R- or S- configuration. In some embodiments, the biradicle -X-Y- together designate the bivalent linker group -O-CH_2-O-CH_2- (Seth at al., 2010, J. Org. Chem). In some embodiments, the biradicle -X-Y- is -O-$CH(CH_3)$-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such 6' methyl LNA nucleosides are also known as cET nucleosides in the art, and may be either (S)cET or (R)cET stereoisomers, as disclosed in WO07090071 (beta-D) and WO2010/036698 (alpha-L).

[0076] In some embodiments, the biradicle -X-Y- is -O-CR^aR^b-, wherein in neither R^a or R^b is hydrogen, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. In some embodiments, R^a and R^b are both methyl. Such 6' di-substituted LNA nucleosides are disclosed in WO 2009006478.

[0077] In some embodiments, the biradicle -X-Y- is -S-CHR^a-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such 6' substituted thio LNA nucleosides are disclosed in WO11156202. In some 6' substituted thio LNA embodiments R^a is methyl.

[0078] In some embodiments, the biradicle -X-Y- is -C(=CH2)-C(R^aR^b)-, such as -C(=CH_2)-CH_2- , or -C(=CH_2)-$CH(CH_3)$-W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such vinyl carbo LNA nucleosides are disclosed in WO08154401 and WO09067647.

[0079] In some embodiments the biradicle -X-Y- is -N(-OR^a)-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. In some embodiments R^a is C_{1-6}alkyl such as methyl. Such LNA nucleosides are also known as N substituted LNAs and are disclosed in WO2008/150729. In some embodiments, the biradicle -X-Y- together designate the bivalent linker group -O-NR^a-CH_3-(Seth at al., 2010, J. Org. Chem). In some embodiments the biradicle -X-Y- is -N(R^a)-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. In some embodiments R^a is C_{1-6} alkyl such as methyl.

[0080] In some embodiments, one or both of R^5 and R^{5*} is hydrogen and, when substituted the other of R^5 and R^{5*} is C_{1-6} alkyl such as methyl. In such an embodiment, R^1, R^2, R^3, may all be hydrogen, and the biradicle -X-Y- may be selected from -O-CH2- or -O-C(HCR^a)-, such as -O-C(HCH3)-.

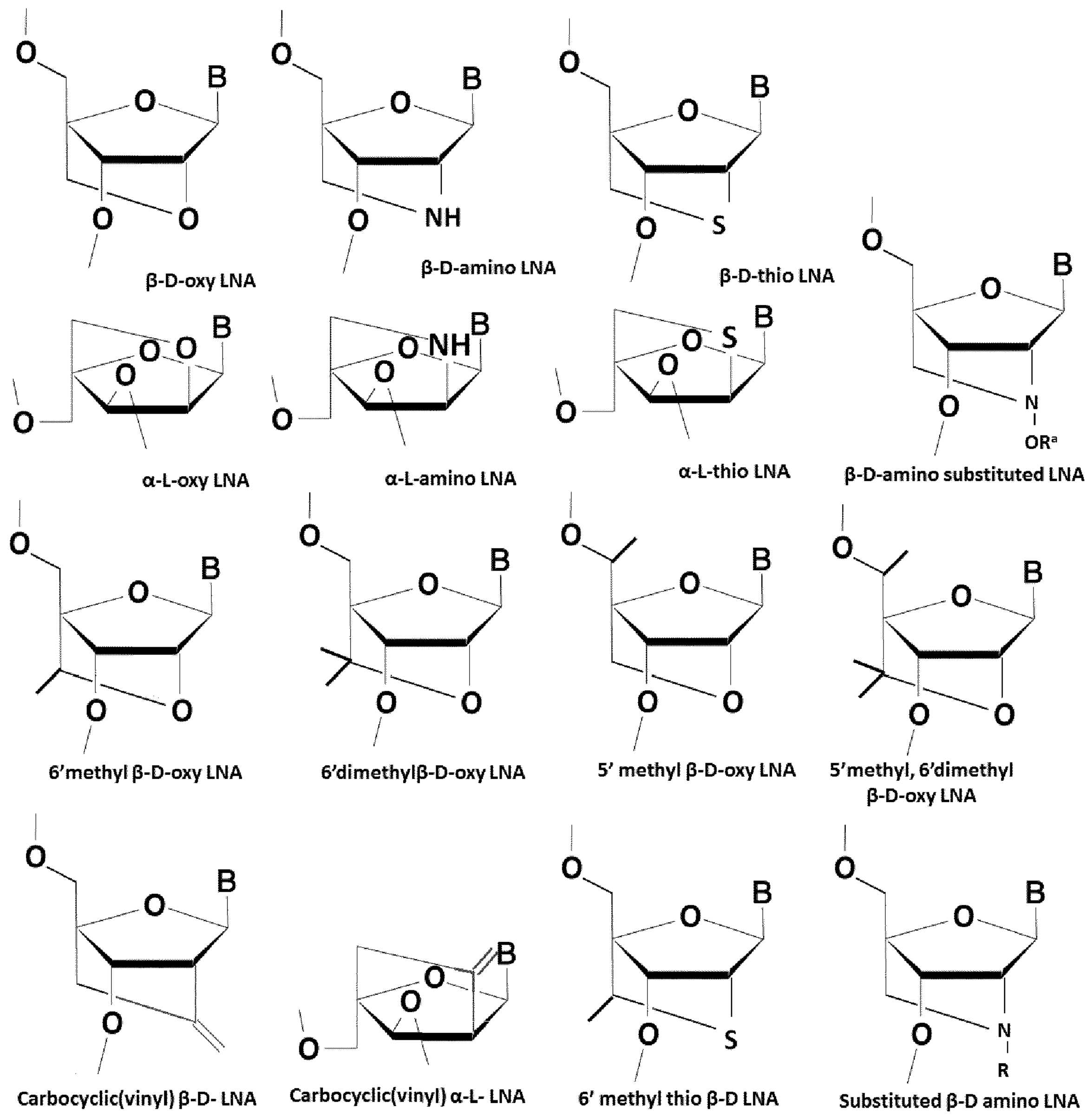
[0081] In some embodiments, the biradicle is -CR^aR^b-O-CR^aR^b-, such as CH_2-O-CH_2-, W is O and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. In some embodiments R^a is C_{1-6} alkyl such as methyl. Such LNA nucleosides are also known as conformationally restricted nucleotides (CRNs) and are disclosed in WO2013036868.

[0082] In some embodiments, the biradicle is -O-CR^aR^b-O-CR^aR^b-, such as O-CH_2-O-CH_2-, W is O and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. In some embodiments R^a is C_{1-6} alkyl such as methyl. Such LNA nucleosides are also known as COC nucleotides and are disclosed in Mitsuoka et al., Nucleic Acids Research 2009 37(4), 1225-1238.

[0083] It will be recognized than, unless specified, the LNA nucleosides may be in the beta-D or alpha-L stereoisoform.

[0084] Certain examples of LNA nucleosides are presented in Scheme 1.

Scheme 1



[0085] As illustrated in the examples, in preferred embodiments of the invention the LNA nucleosides in the oligonucleotides are beta-D-oxy-LNA nucleosides.

Nuclease mediated degradation

[0086] Nuclease mediated degradation refers to an oligonucleotide capable of mediating degradation of a complementary nucleotide sequence when forming a duplex with such a sequence.

[0087] In some embodiments, the oligonucleotide may function via nuclease mediated degradation of the target nucleic acid, where the oligonucleotides of the invention are capable of recruiting a nuclease, particularly and endonuclease, preferably endoribonuclease (RNase), such as RNase H. Examples of oligonucleotide designs which operate via nuclease mediated mechanisms are oligonucleotides which typically comprise a region of at least 5 or 6 DNA nucleosides and are flanked on one side or both sides by affinity enhancing nucleosides, for example gapmers, headmers and tailmers.

RNase H Activity and Recruitment

[0088] The RNase H activity of an antisense oligonucleotide refers to its ability to recruit RNase H when in a duplex with a complementary RNA molecule. WO01/23613 provides *in vitro* methods for determining RNaseH activity, which may be used to determine the ability to recruit RNaseH. Typically an oligonucleotide is deemed capable of recruiting RNase H if it, when provided with a complementary target nucleic acid sequence, has an initial rate, as measured in pmol/l/min, of at least 10% or more than 20% of the of the initial rate determined when using a oligonucleotide having the same base sequence as the modified oligonucleotide being tested, but containing only DNA monomers, with phosphorothioate linkages between all monomers in the oligonucleotide, and using the methodology provided by Example 91 - 95 of WO01/23613.

Gapmer

[0089] The term gapmer as used herein refers to an antisense oligonucleotide which comprises a region of RNase H recruiting oligonucleotides (gap) which is flanked 5' and 3' by one or more affinity enhancing modified nucleosides (flanks). Various gapmer designs are described herein. Headmers and tailmers are oligonucleotides capable of recruiting RNase H where one of the flanks is missing, i.e. only one of the ends of the oligonucleotide comprises affinity enhancing modified nucleosides. For headmers the 3' flank is missing (i.e. the 5' flanc comprise affinity enhancing modified nucleosides) and for tailmers the 5' flank is missing (i.e. the 3' flank comprises affinity enhancing modified nucleosides).

LNA Gapmer

[0090] The term LNA gapmer is a gapmer oligonucleotide wherein at least one of the affinity enhancing modified nucleosides is an LNA nucleoside.

Mixed Wing Gapmer

[0091] The term mixed wing gapmer refers to a LNA gapmer wherein the flank regions comprise at least one LNA nucleoside and at least one non-LNA modified nucleoside, such as at least one 2' substituted modified nucleoside, such as, for example, 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA (MOE), 2'-amino-DNA, 2'-Fluoro-RNA, and 2'-F-ANA nucleoside(s). In some embodiments the mixed wing gapmer has one flank which comprises LNA nucleosides (e.g. 5' or 3') and the other flank (3' or 5' respectfully) comprises 2' substituted modified nucleoside(s).

Conjugate

[0092] The term conjugate as used herein refers to an oligonucleotide which is covalently linked to a non-nucleotide moiety (conjugate moiety or region C or third region).

[0093] Conjugation of the oligonucleotide of the invention to one or more non-nucleotide moieties may improve the pharmacology of the oligonucleotide, e.g. by affecting the activity, cellular distribution, cellular uptake or stability of the oligonucleotide. In some embodiments the conjugate moiety modify or enhance the pharmacokinetic properties of the oligonucleotide by improving cellular distribution, bioavailability, metabolism, excretion, permeability, and/or cellular uptake of the oligonucleotide. In particular the conjugate may target the oligonucleotide to a specific organ, tissue or cell type and thereby enhance the effectiveness of the oligonucleotide in that organ, tissue or cell type. A the same time the conjugate may serve to reduce activity of the oligonucleotide in non-target cell types, tissues or organs, e.g. off target activity or activity in non-target cell types, tissues or organs. WO 93/07883 and WO 2013/033230 provides suitable conjugate moieties. WO 2012/143379 provides a method of delivering a drug across the blood-brain-barrier by conjugation to an antibody fragment with affinity to the transferrin receptor.

[0094] Oligonucleotide conjugates and their synthesis has also been reported in comprehensive reviews by Manoharan in Antisense Drug Technology, Principles, Strategies, and Applications, S.T. Crooke, ed., Ch. 16, Marcel Dekker, Inc., 2001 and Manoharan, Antisense and Nucleic Acid Drug Development, 2002, 12, 103.

[0095] In an embodiment, the non-nucleotide moiety (conjugate moiety) is selected from the group consisting of carbohydrates, cell surface receptor ligands, drug substances, hormones, lipophilic substances, polymers, proteins, peptides, toxins (e.g. bacterial toxins), vitamins, viral proteins (e.g. capsids) or combinations thereof. In some embodiments the non-nucleotide moiety an antibody or antibody fragment, such as an antibody or antibody fragment that facilitates delivery across the blood-brain-barrier, in particular an antibody or antibody fragment targeting the transferrin receptor.

Linkers

[0096] A linkage or linker is a connection between two atoms that links one chemical group or segment of interest to another chemical group or segment of interest via one or more covalent bonds. Conjugate moieties can be attached to the oligonucleotide directly or through a linking moiety (e.g. linker or tether). Linkers serve to covalently connect a third region, e.g. a conjugate moiety (Region C), to a first region, e.g. an oligonucleotide (region A).

[0097] In some embodiments of the invention the conjugate or oligonucleotide conjugate of the invention may optionally, comprise a linker region (second region or region B and/or region Y) which is positioned between the oligonucleotide (region A or first region) and the conjugate moiety (region C or third region).

[0098] Region B refers to biocleavable linkers comprising or consisting of a physiologically labile bond that is cleavable under conditions normally encountered or analogous to those encountered within a mammalian body. Conditions under which physiologically labile linkers undergo chemical transformation (e.g., cleavage) include chemical conditions such as pH, temperature, oxidative or reductive conditions or agents, and salt concentration found in or analogous to those encountered in mammalian cells. Mammalian intracellular conditions also include the presence of enzymatic activity normally present in a mammalian cell such as from proteolytic enzymes or hydrolytic enzymes or nucleases. In one embodiment the biocleavable linker is susceptible to S1 nuclease cleavage. In a preferred embodiment the nuclease susceptible linker comprises between 1 and 10 nucleosides, such as 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 nucleosides, more preferably between 2 and 6 nucleosides and most preferably between 2 and 4 linked nucleosides comprising at least two consecutive phosphodiester linkages, such as at least 3 or 4 or 5 consecutive phosphodiester linkages. Preferably the nucleosides are DNA or RNA. Phosphodiester containing biocleavable linkers are described in more detail in WO 2014/076195.

[0099] Region Y refers to linkers that are not necessarily biocleavable but primarily serve to covalently connect a conjugate moiety (region C or third region), to an oligonucleotide (region A or first region). The region Y linkers may comprise a chain structure or an oligomer of repeating units such as ethylene glycol, amino acid units or amino alkyl groups The oligonucleotide conjugates of the present invention can be constructed of the following regional elements A-C, A-B-C, A-BY-C, A-Y-B-C or A-Y-C. In some embodiments the linker (region Y) is an amino alkyl, such as a C2 - C36 amino alkyl group, including, for example C6 to C12 amino alkyl groups. In a preferred embodiment the linker (region Y) is a C6 amino alkyl group.

Control

[0100] By the term "control" when used in relation to measurements of the effect of an oligonucleotide it is generally understood that the control is an untreated individual or target cell or a individual or target cell treated with a non-targeting oligonucleotide (mock). It may however also be an individual treated with the standard of care.

Treatment

[0101] 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 recognized that treatment as referred to herein may, in some embodiments, be prophylactic.

DETAILED DESCRIPTION OF THE INVENTION

The Target

[0102] An aspect of the invention is to modulate the level of pig, primate or human UBE3A protein expression, in particular to increase the expression of paternal UBE3A expression in neuronal cells, in particular in human neuronal cells. The human UBE3A protein exists in several isoforms which are listed under Uniprot nr. Q05086. Several mutations in the maternal UBE3A gene can results in Angelman syndrome.

[0103] The target nucleic acid for the oligonucleotides of the invention is RNA, in particular a long non-coding RNA. The long non-coding RNA which is targeted by the oligonucleotides of the present invention is human SNHG14 (also known as UBE3A-ATS with Ensembl entry number ENSG00000224078, version GRCh38.p2). In particular the target nucleic acid is the region downstream of SNORD109B corresponding to position 25278410 to 25419462 on chromosome 15 (SEQ ID NO: 1). In Rhesus monkey (Macaca mulatta) the UBE3A supressor is defined as region downstream of SNORD109A corresponding to position 4222848 to 4373084 (forward strand) on chromosome 7 using the Ensembl assembly MMUL 1.0 (SEQ ID NO: 2).

[0104] In some embodiments, the target nucleic acid is SEQ ID NO: 1, or naturally occurring variants thereof.

[0105] In certain embodiments the target nucleic acid correspond to regions which are conserved between human (SEQ ID NO: 1) and Rhesus monkey (SEQ ID NO: 2). In certain embodiments target nucleic acid correspond to regions which are conserved between human (SEQ ID NO:1), Rhesus monkey (SEQ ID NO: 2) and mouse (SEQ ID NO: 3).

[0106] In certain embodiments the target nucleic acid is the region that is antisense to the UBE3A pre-mRNA, this region corresponds to position 55319 to 141053 of SEQ ID NO: 1.

[0107] In certain embodiments the target nucleic acid is the region that is downstream of SNORD109B and upstream of the region that is antisense to the UBE3A pre-mRNA, this region corresponds to position 1 to 55319 of SEQ ID NO: 1.

[0108] In some embodiments, the target nucleic acid is present in a cell, such as a mammalian cell in particular a human cell *in vitro* or *in vivo* (the target cell). In certain embodiments the target cell is a neuron, preferably a human neuronal cell.

[0109] The target sequence may be a sub-sequence of the target nucleic acid. In some embodiments the oligonucleotide targets sub-sequence selected from the group consisting of the antisense region of exon 9, exon10, exon13, exon14, intron 14, exon 15, intron15 and exon 16 of UBE3A. In some embodiments the oligonucleotide or contiguous nucleotide sequence hybridize or is complementary to a single stranded nucleic acid molecule selected from the group consisting of positions: 55319-76274, 77483-77573, 92157-93403 and 97056-97354 of SEQ ID NO: 1. In some embodiments the oligonucleotide or contiguous nucleotide sequence hybridize or is complementary to a single stranded nucleic acid molecule selected from the group consisting of positions: 60821-60849, 77567-77583, 92323-92339 and 97156-97172 of SEQ ID NO: 1.

[0110] In some embodiments the target nucleic acid is a region corresponding to positions 9200-9250 of SEQ ID NO: 1.

[0111] In some embodiments the target nucleic acid is a region corresponding to positions 11505-11555 of SEQ ID NO: 1.

[0112] In some embodiments the target nucleic acid is a region corresponding to positions 15100-15150 of SEQ ID NO: 1.

[0113] In some embodiments the target nucleic acid is a region corresponding to positions 30590-30740 of SEQ ID NO: 1.

[0114] In some embodiments the target nucleic acid is a region corresponding to positions 46380-46430 of SEQ ID NO: 1.

The Oligonucleotides of the Invention

[0115] The invention relates to oligonucleotides capable of modulating expression of paternal UBE3A, in particular induction or up-regulation of paternally expressed UBE3A in neuronal cells . The modulation is achieved by hybridizing to a target nucleic acid located on the long non-coding RNA SNHG14 transcript downstream of SNORD109B. In certain embodiments the oligonucleotide of the invention hybridizes to a sub-sequence of the target nucleic acid of SEQ ID NO: 1 with a $\Delta G°$ below -10 kcal, such as with a $\Delta G°$ between -10 to -60 kcal, such as -12 to -40, such as from -15 to -30 kcal or-16 to -27 kcal such as -18 to -25 kcal.

[0116] The oligonucleotide of the invention is an antisense oligonucleotide which targets the pig, rhesus monkey and/or human SNHG14 transcript downstream of SNORD109B.

[0117] In some embodiments the antisense oligonucleotide of the invention is capable of modulating the expression of the target by removing, interfering with or decreasing the suppressor of the target. Preferably, the oligonucleotides of the invention induce UBE3A expression in a cell, in particular paternal UBE3A expression in a neuron, by degradation or removal of the SNHG14 transcript downstream of SNORD109B. In some embodiments the oligonucleotides of the invention are capable of increasing the expression of UBE3A by least 20% compared to the expression level of UBE3A in a neuronal cell treated with saline or a non-targeting oligonucleotide, more preferably by at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 80%, 100%, 120%, 150%, 160%, 170%, 180%, 190%, 200%, 210%, 220%, 230%, 240% or 250% compared to the expression level of UBE3A in a neuronal cell treated with saline or a non-targeting oligonucleotide. In additional embodiments the oligonucleotides of the invention are capable of decreasing the level of the SNHG14 transcript downstream of SNORD109B (in particular the part of the transcript that is antisense to the UBE3A pre-mRNA region) by at least 20% compared to the level of the SNHG14 transcript downstream of SNORD109B in a neuronal cell treated with saline or a non-targeting oligonucleotide, more preferably by at least 30%, 40%, 50%, 60%, 70%, 80%, 90% or 95% compared to the level of the SNHG14 transcript downstream of SNORD109B in a neuronal cell treated with saline or a non-targeting oligonucleotide, without reducing SNORD115 levels by more than 0%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 12%, 14%, 16%, 18%, 20%, 25% or 30% compared to the level of SNORD115 in a cell treated with saline or a non-targeting oligonucleotide. SNRPN and SNORD116 transcripts are located upstream from the SNORD115 transcript consequently if the SNORD115 transcript is not reduced by the oligonucleotide it is highly likely that the SNRPN and SNORD116 transcripts are also not reduced. In a further embodiment SNRPN and SNORD116 transcripts levels are not reduced by more than 0%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 12%, 14%, 16%, 18%, 20%, 25% or 30% compared to the level of SNRPN and SNORD116 in a cell treated with saline or a non-targeting oligonucleotide.

[0118] The target modulation is triggered by the hybridization between a contiguous nucleotide sequence of the oligonucleotide and the target nucleic acid. In some embodiments the oligonucleotide of the invention comprises mismatches between the oligonucleotide and the target nucleic acid. Despite mismatches hybridization to the target nucleic acid may still be sufficient to show a desired modulation of UBE3A expression. Reduced binding affinity resulting from mismatches may advantageously be compensated by increased number of nucleotides in the oligonucleotide and/or an increased number of modified nucleosides capable of increasing the binding affinity to the target, such as 2' modified nucleosides, including LNA, present within the oligonucleotide sequence.

[0119] An aspect of the present invention relates to an antisense oligonucleotide which comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 98% such as 100% complementarity to position 25278410 to 25419462 on human chromosome 15.

[0120] In some embodiments, the oligonucleotide comprises a contiguous sequence which is at least 98%, or 100% complementary with a region of the target nucleic acid shown as SEQ ID NO: 1, 2 or 3.

[0121] In a preferred embodiment the oligonucleotide of the invention, or contiguous nucleotide sequence thereof is fully complementary (100% complementary) to a region of the target nucleic acid shown as SEQ ID NO: 1, or in some embodiments may comprise one or two mismatches between the oligonucleotide and the target nucleic acid.

[0122] In some embodiments the oligonucleotide sequence is 100% complementary to a corresponding target nucleic acid region present in SEQ ID NO: 1 and SEQ ID NO: 2. In some embodiments the oligonucleotide sequence is 100% complementary to a corresponding target nucleic acid region present SEQ ID NO: 1, 2 and 3.

[0123] In some embodiments, the oligonucleotide comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary, such as 100% complementarity, to a corresponding target nucleic acid region present in SEQ ID NO: 1, wherein the target nucleic acid region is selected from the group consisting of region A1 to A3649 in table 1

Table 1: Regions of SEQ ID NO 1 which may be targeted using oligonucleotide of the invention

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
1	10	75	66	1218	50838	50864	27	2434	96887	96916	30
2	77	91	15	1219	50870	50884	15	2435	96928	96944	17
3	93	108	16	1220	50885	50911	27	2436	96946	96959	14
4	168	213	46	1221	50924	50937	14	2437	96970	96990	21
5	217	282	66	1222	50939	50974	36	2438	96992	97021	30
6	284	299	16	1223	50980	51008	29	2439	97023	97037	15
7	301	328	28	1224	51015	51030	16	2440	97039	97073	35
8	330	344	15	1225	51034	51047	14	2441	97075	97366	292
9	361	400	40	1226	51075	51089	15	2442	97368	97393	26
10	415	447	33	1227	51109	51123	15	2443	97420	97466	47
11	449	470	22	1228	51135	51172	38	2444	97469	97507	39
12	472	487	16	1229	51189	51216	28	2445	97513	97529	17
13	489	521	33	1230	51241	51260	20	2446	97531	97583	53
14	523	540	18	1231	51273	51294	22	2447	97585	97600	16
15	551	570	20	1232	51296	51312	17	2448	97602	97631	30
16	590	638	49	1233	51337	51357	21	2449	97633	97683	51
17	652	670	19	1234	51356	51381	26	2450	97685	97703	19
18	672	733	62	1235	51393	51465	73	2451	97705	97742	38
19	735	756	22	1236	51476	51494	19	2452	97787	97803	17
20	758	773	16	1237	51496	51515	20	2453	97805	97822	18
21	781	829	49	1238	51530	51544	15	2454	97824	97876	53
22	831	870	40	1239	51546	51572	27	2455	97878	97921	44
23	882	903	22	1240	51586	51600	15	2456	97923	97943	21
24	918	949	32	1241	51602	51617	16	2457	97945	97963	19

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
25	961	990	30	1242	51619	51677	59	2458	97965	97994	30
26	1007	1021	15	1243	51679	51700	22	2459	97995	98011	17
27	1019	1050	32	1244	51727	51741	15	2460	98014	98044	31
28	1052	1090	39	1245	51743	51821	79	2461	98039	98061	23
29	1092	1139	48	1246	51826	51859	34	2462	98055	98076	22
30	1147	1179	33	1247	51884	51912	29	2463	98077	98090	14
31	1175	1212	38	1248	51918	51936	19	2464	98079	98092	14
32	1220	1242	23	1249	51947	51979	33	2465	98085	98098	14
33	1245	1259	15	1250	52004	52017	14	2466	98100	98115	16
34	1265	1278	14	1251	52023	52048	26	2467	98113	98145	33
35	1285	1323	39	1252	52141	52167	27	2468	98142	98160	19
36	1317	1330	14	1253	52169	52188	20	2469	98162	98180	19
37	1337	1355	19	1254	52204	52225	22	2470	98188	98219	32
38	1357	1403	47	1255	52246	52262	17	2471	98215	98237	23
39	1405	1421	17	1256	52289	52306	18	2472	98227	98240	14
40	1423	1481	59	1257	52321	52339	19	2473	98232	98255	24
41	1486	1515	30	1258	52341	52360	20	2474	98255	98268	14
42	1521	1581	61	1259	52360	52428	69	2475	98264	98287	24
43	1611	1633	23	1260	52430	52504	75	2476	98292	98326	35
44	1631	1644	14	1261	52506	52567	62	2477	98373	98397	25
45	1635	1663	29	1262	52579	52594	16	2478	98399	98428	30
46	1669	1684	16	1263	52591	52610	20	2479	98442	98461	20
47	1685	1709	25	1264	52612	52642	31	2480	98480	98501	22
48	1711	1724	14	1265	52644	52667	24	2481	98499	98520	22

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
49	1726	1746	21	1266	52672	52686	15	2482	98524	98538	15
50	1754	1808	55	1267	52688	52702	15	2483	98537	98550	14
51	1819	1860	42	1268	52715	52753	39	2484	98545	98585	41
52	1862	1878	17	1269	52770	52783	14	2485	98595	98610	16
53	1896	1910	15	1270	52779	52792	14	2486	98599	98624	26
54	1923	1944	22	1271	52814	52845	32	2487	98644	98668	25
55	1946	1987	42	1272	52834	52857	24	2488	98678	98704	27
56	1985	2051	67	1273	52858	52885	28	2489	98703	98718	16
57	2053	2082	30	1274	52887	52943	57	2490	98736	98754	19
58	2088	2104	17	1275	52945	52962	18	2491	98778	98794	17
59	2106	2125	20	1276	52971	53019	49	2492	98802	98821	20
60	2132	2207	76	1277	53011	53036	26	2493	98845	98876	32
61	2209	2234	26	1278	53053	53066	14	2494	98878	98900	23
62	2247	2261	15	1279	53092	53112	21	2495	98900	98972	73
63	2263	2286	24	1280	53124	53151	28	2496	98961	98976	16
64	2290	2306	17	1281	53161	53175	15	2497	98974	98998	25
65	2308	2329	22	1282	53184	53220	37	2498	99011	99029	19
66	2347	2391	45	1283	53222	53243	22	2499	99033	99065	33
67	2398	2431	34	1284	53245	53260	16	2500	99067	99107	41
68	2447	2468	22	1285	53278	53304	27	2501	99151	99186	36
69	2470	2555	86	1286	53311	53346	36	2502	99188	99219	32
70	2565	2579	15	1287	53364	53386	23	2503	99222	99245	24
71	2579	2592	14	1288	53388	53404	17	2504	99254	99276	23
72	2589	2605	17	1289	53417	53431	15	2505	99288	99312	25

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
73	2594	2657	64	1290	53449	53463	15	2506	99314	99338	25
74	2672	2687	16	1291	53465	53484	20	2507	99367	99430	64
75	2692	2705	14	1292	53514	53527	14	2508	99444	99491	48
76	2703	2721	19	1293	53552	53567	16	2509	99496	99554	59
77	2770	2824	55	1294	53570	53591	22	2510	99570	99585	16
78	2826	2841	16	1295	53618	53644	27	2511	99587	99618	32
79	2838	2851	14	1296	53645	53667	23	2512	99620	99669	50
80	2843	2889	47	1297	53669	53684	16	2513	99679	99710	32
81	2896	2930	35	1298	53714	53742	29	2514	99720	99748	29
82	2930	2967	38	1299	53744	53764	21	2515	99750	99763	14
83	2965	2988	24	1300	53818	53843	26	2516	99768	99805	38
84	2984	3028	45	1301	53845	53860	16	2517	99818	99841	24
85	3024	3080	57	1302	53875	53889	15	2518	99855	99879	25
86	3081	3135	55	1303	53961	53991	31	2519	99881	99900	20
87	3140	3176	37	1304	53991	54013	23	2520	99902	99932	31
88	3168	3189	22	1305	54015	54055	41	2521	99934	99954	21
89	3197	3222	26	1306	54057	54081	25	2522	99959	100011	53
90	3212	3226	15	1307	54114	54135	22	2523	100011	100037	27
91	3221	3248	28	1308	54163	54178	16	2524	100057	100071	15
92	3243	3256	14	1309	54180	54193	14	2525	100073	100102	30
93	3250	3264	15	1310	54195	54254	60	2526	100104	100118	15
94	3266	3292	27	1311	54261	54290	30	2527	100131	100186	56
95	3326	3343	18	1312	54292	54307	16	2528	100188	100201	14
96	3345	3391	47	1313	54309	54327	19	2529	100194	100212	19

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
97	3400	3422	23	1314	54357	54372	16	2530	100214	100277	64
98	3424	3441	18	1315	54404	54420	17	2531	100279	100303	25
99	3434	3447	14	1316	54418	54439	22	2532	100309	100355	47
100	3443	3503	61	1317	54441	54466	26	2533	100349	100386	38
101	3495	3508	14	1318	54468	54512	45	2534	100379	100393	15
102	3505	3558	54	1319	54519	54532	14	2535	100388	100401	14
103	3589	3609	21	1320	54555	54572	18	2536	100403	100423	21
104	3611	3641	31	1321	54588	54601	14	2537	100452	100473	22
105	3662	3696	35	1322	54609	54633	25	2538	100508	100542	35
106	3698	3719	22	1323	54644	54688	45	2539	100548	100580	33
107	3723	3790	68	1324	54690	54721	32	2540	100582	100612	31
108	3810	3854	45	1325	54723	54761	39	2541	100614	100652	39
109	3858	3873	16	1326	54786	54802	17	2542	100695	100714	20
110	3902	3968	67	1327	54819	54835	17	2543	100736	100749	14
111	3971	4009	39	1328	54837	54912	76	2544	100751	100790	40
112	4005	4018	14	1329	54924	54941	18	2545	100808	100842	35
113	4011	4030	20	1330	54999	55017	19	2546	100844	100860	17
114	4032	4077	46	1331	55019	55035	17	2547	100862	100930	69
115	4082	4114	33	1332	55060	55073	14	2548	100939	100953	15
116	4123	4140	18	1333	55075	55100	26	2549	100955	100971	17
117	4150	4164	15	1334	55129	55171	43	2550	100973	101003	31
118	4166	4183	18	1335	55173	55188	16	2551	101021	101048	28
119	4185	4243	59	1336	55190	55203	14	2552	101057	101093	37
120	4248	4268	21	1337	55210	55230	21	2553	101109	101148	40

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
121	4284	4313	30	1338	55233	55281	49	2554	101145	101189	45
122	4317	4348	32	1339	55276	55289	14	2555	101194	101208	15
123	4364	4471	108	1340	55283	55320	38	2556	101210	101244	35
124	4473	4491	19	1341	55330	55379	50	2557	101256	101271	16
125	4494	4519	26	1342	55381	55423	43	2558	101277	101300	24
126	4521	4535	15	1343	55420	55441	22	2559	101310	101327	18
127	4545	4560	16	1344	55486	55502	17	2560	101329	101345	17
128	4567	4606	40	1345	55515	55533	19	2561	101374	101397	24
129	4616	4714	99	1346	55535	55553	19	2562	101409	101426	18
130	4725	4755	31	1347	55555	55569	15	2563	101453	101466	14
131	4757	4786	30	1348	55569	55588	20	2564	101474	101487	14
132	4788	4852	65	1349	55590	55611	22	2565	101481	101515	35
133	4856	4910	55	1350	55615	55663	49	2566	101518	101541	24
134	4912	4935	24	1351	55665	55678	14	2567	101542	101560	19
135	4937	4970	34	1352	55696	55713	18	2568	101554	101591	38
136	4972	5010	39	1353	55715	55738	24	2569	101593	101609	17
137	5058	5078	21	1354	55744	55774	31	2570	101635	101695	61
138	5080	5116	37	1355	55776	55794	19	2571	101707	101746	40
139	5110	5124	15	1356	55801	55823	23	2572	101748	101763	16
140	5135	5166	32	1357	55862	55906	45	2573	101774	101810	37
141	5168	5201	34	1358	55920	55933	14	2574	101812	101828	17
142	5203	5247	45	1359	55922	55947	26	2575	101819	101835	17
143	5261	5276	16	1360	55974	55993	20	2576	101829	101842	14
144	5278	5293	16	1361	55990	56031	42	2577	101842	101855	14

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
145	5314	5330	17	1362	56045	56073	29	2578	101857	101878	22
146	5332	5382	51	1363	56082	56114	33	2579	101880	101943	64
147	5398	5414	17	1364	56117	56140	24	2580	101947	101981	35
148	5427	5456	30	1365	56183	56214	32	2581	101988	102009	22
149	5458	5471	14	1366	56218	56236	19	2582	102022	102066	45
150	5487	5500	14	1367	56261	56282	22	2583	102068	102084	17
151	5506	5545	40	1368	56311	56336	26	2584	102100	102113	14
152	5561	5577	17	1369	56331	56345	15	2585	102115	102130	16
153	5580	5617	38	1370	56338	56358	21	2586	102132	102145	14
154	5607	5620	14	1371	56369	56390	22	2587	102192	102241	50
155	5619	5642	24	1372	56391	56431	41	2588	102269	102285	17
156	5644	5683	40	1373	56433	56451	19	2589	102312	102327	16
157	5685	5698	14	1374	56453	56473	21	2590	102357	102392	36
158	5713	5759	47	1375	56475	56498	24	2591	102407	102428	22
159	5756	5769	14	1376	56500	56546	47	2592	102430	102444	15
160	5784	5803	20	1377	56558	56581	24	2593	102460	102485	26
161	5801	5865	65	1378	56584	56597	14	2594	102487	102508	22
162	5873	5905	33	1379	56611	56647	37	2595	102532	102573	42
163	5907	5937	31	1380	56643	56657	15	2596	102595	102642	48
164	5939	5985	47	1381	56667	56691	25	2597	102653	102694	42
165	5987	6017	31	1382	56732	56759	28	2598	102701	102718	18
166	6016	6039	24	1383	56788	56805	18	2599	102720	102734	15
167	6028	6092	65	1384	56821	56845	25	2600	102736	102757	22
168	6102	6127	26	1385	56850	56882	33	2601	102799	102836	38

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
169	6127	6152	26	1386	56885	56906	22	2602	102847	102882	36
170	6151	6171	21	1387	56928	56942	15	2603	102890	102927	38
171	6178	6206	29	1388	56944	56959	16	2604	102938	102971	34
172	6217	6234	18	1389	56961	56975	15	2605	102982	103019	38
173	6224	6270	47	1390	56984	57002	19	2606	103014	103027	14
174	6272	6289	18	1391	57004	57041	38	2607	103027	103054	28
175	6291	6310	20	1392	57057	57082	26	2608	103065	103088	24
176	6312	6357	46	1393	57084	57122	39	2609	103090	103108	19
177	6367	6389	23	1394	57162	57222	61	2610	103098	103112	15
178	6396	6422	27	1395	57224	57246	23	2611	103117	103138	22
179	6440	6454	15	1396	57259	57284	26	2612	103152	103170	19
180	6456	6482	27	1397	57317	57332	16	2613	103174	103204	31
181	6484	6513	30	1398	57346	57369	24	2614	103206	103234	29
182	6505	6519	15	1399	57388	57423	36	2615	103240	103268	29
183	6518	6553	36	1400	57425	57440	16	2616	103286	103325	40
184	6552	6565	14	1401	57442	57455	14	2617	103327	103347	21
185	6557	6590	34	1402	57475	57492	18	2618	103349	103384	36
186	6596	6628	33	1403	57508	57522	15	2619	103386	103405	20
187	6640	6675	36	1404	57522	57546	25	2620	103422	103449	28
188	6686	6711	26	1405	57548	57576	29	2621	103451	103493	43
189	6714	6746	33	1406	57593	57634	42	2622	103495	103509	15
190	6781	6818	38	1407	57658	57675	18	2623	103511	103560	50
191	6832	6885	54	1408	57687	57771	85	2624	103565	103582	18
192	6889	6912	24	1409	57786	57803	18	2625	103585	103607	23

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
193	6920	6938	19	1410	57801	57819	19	2626	103631	103645	15
194	6940	6960	21	1411	57830	57858	29	2627	103653	103684	32
195	6954	6976	23	1412	57889	57911	23	2628	103683	103696	14
196	6998	7033	36	1413	57926	57945	20	2629	103691	103733	43
197	7035	7061	27	1414	57947	57972	26	2630	103738	103762	25
198	7071	7143	73	1415	58009	58028	20	2631	103752	103765	14
199	7159	7214	56	1416	58030	58060	31	2632	103755	103768	14
200	7253	7266	14	1417	58063	58091	29	2633	103758	103771	14
201	7268	7281	14	1418	58124	58146	23	2634	103790	103814	25
202	7283	7328	46	1419	58147	58162	16	2635	103803	103816	14
203	7329	7343	15	1420	58163	58198	36	2636	103830	103865	36
204	7338	7355	18	1421	58214	58292	79	2637	103900	103923	24
205	7345	7374	30	1422	58292	58309	18	2638	103912	103933	22
206	7374	7387	14	1423	58336	58429	94	2639	103945	103964	20
207	7383	7396	14	1424	58436	58457	22	2640	103990	104005	16
208	7389	7405	17	1425	58453	58501	49	2641	104024	104055	32
209	7399	7413	15	1426	58525	58553	29	2642	104058	104077	20
210	7420	7437	18	1427	58566	58579	14	2643	104086	104099	14
211	7427	7448	22	1428	58571	58584	14	2644	104095	104122	28
212	7450	7503	54	1429	58586	58601	16	2645	104124	104146	23
213	7495	7565	71	1430	58604	58630	27	2646	104148	104168	21
214	7561	7616	56	1431	58656	58682	27	2647	104162	104176	15
215	7618	7703	86	1432	58696	58713	18	2648	104173	104187	15
216	7717	7772	56	1433	58722	58744	23	2649	104201	104241	41

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
217	7776	7838	63	1434	58757	58771	15	2650	104234	104266	33
218	7852	7869	18	1435	58805	58979	175	2651	104268	104286	19
219	7882	7910	29	1436	58987	59073	87	2652	104288	104302	15
220	7919	7942	24	1437	59072	59123	52	2653	104304	104335	32
221	7944	7957	14	1438	59124	59150	27	2654	104340	104354	15
222	7959	7977	19	1439	59154	59234	81	2655	104356	104373	18
223	7979	7996	18	1440	59231	59276	46	2656	104375	104391	17
224	7998	8014	17	1441	59291	59413	123	2657	104393	104417	25
225	8030	8046	17	1442	59413	59458	46	2658	104426	104439	14
226	8059	8092	34	1443	59466	59511	46	2659	104448	104478	31
227	8100	8113	14	1444	59513	59533	21	2660	104480	104504	25
228	8115	8141	27	1445	59549	59764	216	2661	104519	104546	28
229	8143	8175	33	1446	59762	59825	64	2662	104549	104580	32
230	8179	8192	14	1447	59824	59907	84	2663	104604	104620	17
231	8187	8208	22	1448	59916	60004	89	2664	104620	104646	27
232	8205	8219	15	1449	60006	60030	25	2665	104654	104673	20
233	8210	8229	20	1450	60027	60040	14	2666	104675	104691	17
234	8231	8252	22	1451	60032	60100	69	2667	104689	104776	88
235	8254	8298	45	1452	60119	60188	70	2668	104829	104842	14
236	8302	8316	15	1453	60191	60227	37	2669	104838	104852	15
237	8306	8329	24	1454	60220	60287	68	2670	104934	104952	19
238	8331	8357	27	1455	60289	60314	26	2671	104956	104987	32
239	8400	8443	44	1456	60316	60554	239	2672	104993	105045	53
240	8443	8456	14	1457	60556	60575	20	2673	105041	105055	15

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
241	8445	8460	16	1458	60579	60593	15	2674	105047	105078	32
242	8472	8505	34	1459	60595	60638	44	2675	105090	105107	18
243	8494	8507	14	1460	60651	60690	40	2676	105101	105115	15
244	8554	8569	16	1461	60692	60724	33	2677	105109	105137	29
245	8571	8653	83	1462	60716	60799	84	2678	105149	105167	19
246	8659	8673	15	1463	60801	60872	72	2679	105163	105176	14
247	8675	8694	20	1464	60868	60881	14	2680	105185	105237	53
248	8696	8713	18	1465	60885	60912	28	2681	105230	105243	14
249	8736	8844	109	1466	60961	61009	49	2682	105233	105250	18
250	8847	8909	63	1467	61014	61042	29	2683	105260	105286	27
251	8915	8959	45	1468	61046	61059	14	2684	105288	105340	53
252	8961	8975	15	1469	61053	61066	14	2685	105345	105370	26
253	8993	9009	17	1470	61061	61084	24	2686	105372	105402	31
254	9024	9048	25	1471	61134	61164	31	2687	105441	105458	18
255	9050	9063	14	1472	61178	61199	22	2688	105460	105521	62
256	9089	9120	32	1473	61201	61229	29	2689	105526	105541	16
257	9127	9166	40	1474	61258	61284	27	2690	105543	105560	18
258	9191	9249	59	1475	61286	61304	19	2691	105562	105575	14
259	9257	9285	29	1476	61316	61332	17	2692	105582	105606	25
260	9288	9302	15	1477	61341	61354	14	2693	105616	105671	56
261	9331	9397	67	1478	61356	61383	28	2694	105677	105704	28
262	9399	9438	40	1479	61407	61440	34	2695	105703	105725	23
263	9437	9455	19	1480	61451	61468	18	2696	105746	105759	14
264	9483	9505	23	1481	61470	61497	28	2697	105750	105765	16

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
265	9507	9526	20	1482	61493	61506	14	2698	105776	105796	21
266	9583	9598	16	1483	61499	61529	31	2699	105798	105824	27
267	9600	9613	14	1484	61531	61558	28	2700	105827	105907	81
268	9628	9641	14	1485	61590	61615	26	2701	105924	105939	16
269	9653	9674	22	1486	61623	61640	18	2702	105941	105963	23
270	9676	9690	15	1487	61673	61877	205	2703	105990	106014	25
271	9745	9758	14	1488	61879	61898	20	2704	106017	106048	32
272	9752	9780	29	1489	61900	61941	42	2705	106039	106072	34
273	9796	9809	14	1490	61943	61962	20	2706	106061	106074	14
274	9811	9825	15	1491	61964	61983	20	2707	106073	106102	30
275	9832	9853	22	1492	62003	62017	15	2708	106092	106107	16
276	9877	9899	23	1493	62015	62080	66	2709	106114	106159	46
277	9901	9932	32	1494	62100	62124	25	2710	106161	106180	20
278	10000	10016	17	1495	62133	62146	14	2711	106197	106243	47
279	10029	10049	21	1496	62139	62175	37	2712	106237	106250	14
280	10051	10071	21	1497	62191	62237	47	2713	106243	106256	14
281	10089	10120	32	1498	62250	62270	21	2714	106247	106267	21
282	10111	10127	17	1499	62283	62316	34	2715	106273	106333	61
283	10122	10203	82	1500	62310	62358	49	2716	106335	106367	33
284	10211	10237	27	1501	62357	62397	41	2717	106369	106417	49
285	10239	10256	18	1502	62399	62413	15	2718	106419	106471	53
286	10258	10285	28	1503	62415	62470	56	2719	106486	106523	38
287	10287	10304	18	1504	62472	62501	30	2720	106525	106538	14
288	10306	10350	45	1505	62503	62541	39	2721	106552	106572	21

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
289	10352	10375	24	1506	62553	62609	57	2722	106584	106598	15
290	10381	10402	22	1507	62611	62656	46	2723	106609	106696	88
291	10412	10470	59	1508	62663	62690	28	2724	106698	106723	26
292	10474	10488	15	1509	62703	62735	33	2725	106725	106740	16
293	10508	10557	50	1510	62737	62759	23	2726	106743	106781	39
294	10565	10630	66	1511	62765	62789	25	2727	106783	106811	29
295	10632	10674	43	1512	62802	62816	15	2728	106826	106866	41
296	10698	10711	14	1513	62810	62824	15	2729	106875	106902	28
297	10701	10714	14	1514	62853	62868	16	2730	106916	106935	20
298	10704	10718	15	1515	62864	62878	15	2731	106942	106960	19
299	10720	10740	21	1516	62878	62907	30	2732	106991	107010	20
300	10742	10785	44	1517	62905	62937	33	2733	107019	107038	20
301	10786	10809	24	1518	62937	62951	15	2734	107040	107072	33
302	10811	10829	19	1519	62943	62956	14	2735	107079	107094	16
303	10832	10867	36	1520	62946	62960	15	2736	107087	107101	15
304	10869	10930	62	1521	62961	62988	28	2737	107090	107109	20
305	10932	10950	19	1522	62993	63006	14	2738	107113	107127	15
306	10959	10996	38	1523	63005	63019	15	2739	107129	107143	15
307	10998	11028	31	1524	63030	63049	20	2740	107154	107172	19
308	11037	11077	41	1525	63057	63076	20	2741	107174	107198	25
309	11079	11105	27	1526	63073	63088	16	2742	107210	107226	17
310	11115	11132	18	1527	63078	63125	48	2743	107226	107239	14
311	11134	11154	21	1528	63128	63152	25	2744	107237	107274	38
312	11156	11196	41	1529	63154	63170	17	2745	107296	107356	61

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
313	11206	11239	34	1530	63172	63196	25	2746	107358	107381	24
314	11241	11255	15	1531	63185	63223	39	2747	107383	107415	33
315	11266	11287	22	1532	63225	63245	21	2748	107417	107433	17
316	11299	11329	31	1533	63236	63254	19	2749	107435	107455	21
317	11331	11352	22	1534	63245	63261	17	2750	107457	107508	52
318	11358	11403	46	1535	63263	63276	14	2751	107510	107525	16
319	11405	11432	28	1536	63280	63295	16	2752	107527	107546	20
320	11434	11480	47	1537	63292	63336	45	2753	107559	107573	15
321	11482	11535	54	1538	63344	63368	25	2754	107586	107617	32
322	11539	11573	35	1539	63369	63396	28	2755	107643	107689	47
323	11584	11732	149	1540	63385	63398	14	2756	107694	107716	23
324	11731	11763	33	1541	63395	63417	23	2757	107744	107792	49
325	11765	11782	18	1542	63433	63451	19	2758	107790	107832	43
326	11784	11813	30	1543	63440	63453	14	2759	107834	107860	27
327	11815	11829	15	1544	63454	63470	17	2760	107864	107896	33
328	11831	11852	22	1545	63472	63511	40	2761	107898	107912	15
329	11854	11871	18	1546	63513	63539	27	2762	107914	107953	40
330	11866	11895	30	1547	63547	63603	57	2763	107967	107992	26
331	11930	11943	14	1548	63625	63651	27	2764	107994	108008	15
332	11975	12007	33	1549	63676	63692	17	2765	108010	108038	29
333	11996	12012	17	1550	63730	63746	17	2766	108065	108084	20
334	12017	12040	24	1551	63759	63775	17	2767	108113	108215	103
335	12050	12083	34	1552	63779	63833	55	2768	108220	108249	30
336	12088	12111	24	1553	63844	63883	40	2769	108253	108281	29

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
337	12133	12151	19	1554	63889	63907	19	2770	108283	108304	22
338	12161	12174	14	1555	63910	63938	29	2771	108317	108359	43
339	12179	12225	47	1556	63943	63962	20	2772	108361	108375	15
340	12238	12256	19	1557	64004	64033	30	2773	108386	108402	17
341	12265	12278	14	1558	64056	64087	32	2774	108421	108440	20
342	12296	12360	65	1559	64112	64132	21	2775	108538	108551	14
343	12362	12381	20	1560	64142	64158	17	2776	108561	108575	15
344	12384	12399	16	1561	64160	64191	32	2777	108577	108616	40
345	12400	12475	76	1562	64193	64209	17	2778	108618	108665	48
346	12487	12502	16	1563	64214	64227	14	2779	108677	108707	31
347	12504	12531	28	1564	64228	64241	14	2780	108735	108768	34
348	12533	12562	30	1565	64254	64278	25	2781	108762	108777	16
349	12564	12602	39	1566	64280	64298	19	2782	108780	108824	45
350	12627	12646	20	1567	64300	64338	39	2783	108842	108885	44
351	12655	12679	25	1568	64340	64355	16	2784	108907	108970	64
352	12681	12698	18	1569	64357	64380	24	2785	108983	109019	37
353	12700	12812	113	1570	64412	64434	23	2786	109021	109053	33
354	12828	12876	49	1571	64438	64456	19	2787	109055	109068	14
355	12877	12913	37	1572	64458	64488	31	2788	109070	109099	30
356	12932	12945	14	1573	64490	64517	28	2789	109097	109122	26
357	12936	12967	32	1574	64519	64538	20	2790	109113	109132	20
358	12988	13002	15	1575	64552	64572	21	2791	109125	109165	41
359	12996	13009	14	1576	64585	64608	24	2792	109167	109181	15
360	13018	13035	18	1577	64625	64642	18	2793	109183	109200	18

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
361	13031	13049	19	1578	64631	64644	14	2794	109214	109248	35
362	13056	13093	38	1579	64644	64683	40	2795	109256	109277	22
363	13096	13126	31	1580	64703	64716	14	2796	109281	109298	18
364	13128	13142	15	1581	64736	64751	16	2797	109298	109311	14
365	13144	13193	50	1582	64759	64773	15	2798	109300	109318	19
366	13201	13221	21	1583	64775	64806	32	2799	109324	109374	51
367	13223	13280	58	1584	64815	64831	17	2800	109377	109397	21
368	13282	13298	17	1585	64845	64878	34	2801	109399	109437	39
369	13300	13315	16	1586	64880	64904	25	2802	109446	109461	16
370	13307	13320	14	1587	64915	64937	23	2803	109463	109476	14
371	13315	13331	17	1588	64948	64971	24	2804	109472	109485	14
372	13351	13411	61	1589	64973	64994	22	2805	109478	109514	37
373	13422	13437	16	1590	64996	65017	22	2806	109516	109540	25
374	13439	13456	18	1591	65019	65055	37	2807	109556	109588	33
375	13461	13483	23	1592	65062	65109	48	2808	109601	109644	44
376	13485	13541	57	1593	65111	65138	28	2809	109661	109681	21
377	13543	13560	18	1594	65140	65179	40	2810	109683	109709	27
378	13574	13606	33	1595	65181	65195	15	2811	109707	109737	31
379	13618	13646	29	1596	65210	65230	21	2812	109739	109754	16
380	13778	13801	24	1597	65232	65248	17	2813	109754	109768	15
381	13994	14009	16	1598	65271	65296	26	2814	109770	109798	29
382	14508	14521	14	1599	65298	65319	22	2815	109810	109829	20
383	15049	15067	19	1600	65321	65371	51	2816	109859	109877	19
384	15069	15090	22	1601	65391	65413	23	2817	109879	109934	56

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
385	15102	15139	38	1602	65415	65436	22	2818	109955	109975	21
386	15142	15180	39	1603	65436	65454	19	2819	109975	109988	14
387	15182	15205	24	1604	65477	65490	14	2820	109994	110096	103
388	15238	15252	15	1605	65492	65520	29	2821	110103	110129	27
389	15254	15277	24	1606	65522	65552	31	2822	110131	110152	22
390	15292	15320	29	1607	65554	65579	26	2823	110153	110173	21
391	15322	15348	27	1608	65581	65594	14	2824	110175	110195	21
392	15343	15358	16	1609	65591	65606	16	2825	110192	110226	35
393	15362	15387	26	1610	65595	65616	22	2826	110297	110312	16
394	15399	15414	16	1611	65618	65632	15	2827	110301	110314	14
395	15416	15445	30	1612	65634	65657	24	2828	110308	110333	26
396	15459	15528	70	1613	65661	65716	56	2829	110335	110351	17
397	15537	15592	56	1614	65730	65747	18	2830	110353	110368	16
398	15610	15638	29	1615	65748	65807	60	2831	110376	110401	26
399	15640	15653	14	1616	65809	65829	21	2832	110418	110462	45
400	15655	15717	63	1617	65831	65844	14	2833	110464	110481	18
401	15719	15738	20	1618	65846	65859	14	2834	110531	110558	28
402	15757	15778	22	1619	65861	65891	31	2835	110571	110590	20
403	15783	15801	19	1620	65898	65920	23	2836	110599	110639	41
404	15818	15838	21	1621	65930	65963	34	2837	110630	110643	14
405	15835	15849	15	1622	65980	66060	81	2838	110641	110661	21
406	15840	15857	18	1623	66069	66085	17	2839	110668	110681	14
407	15856	15898	43	1624	66095	66108	14	2840	110683	110709	27
408	15900	15916	17	1625	66110	66126	17	2841	110717	110798	82

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
409	15931	15972	42	1626	66139	66173	35	2842	110804	110849	46
410	15988	16028	41	1627	66175	66191	17	2843	110853	110890	38
411	16030	16075	46	1628	66204	66226	23	2844	110928	110966	39
412	16103	16164	62	1629	66224	66263	40	2845	110971	111003	33
413	16207	16243	37	1630	66265	66278	14	2846	111000	111013	14
414	16233	16246	14	1631	66280	66320	41	2847	111015	111033	19
415	16255	16329	75	1632	66322	66345	24	2848	111035	111050	16
416	16349	16376	28	1633	66355	66371	17	2849	111062	111094	33
417	16378	16404	27	1634	66375	66407	33	2850	111092	111105	14
418	16399	16419	21	1635	66411	66424	14	2851	111107	111140	34
419	16421	16461	41	1636	66421	66441	21	2852	111161	111203	43
420	16463	16479	17	1637	66440	66460	21	2853	111209	111223	15
421	16481	16503	23	1638	66463	66482	20	2854	111224	111280	57
422	16506	16579	74	1639	66484	66501	18	2855	111275	111290	16
423	16582	16620	39	1640	66509	66527	19	2856	111283	111303	21
424	16622	16698	77	1641	66534	66548	15	2857	111305	111320	16
425	16700	16716	17	1642	66556	66569	14	2858	111311	111347	37
426	16723	16771	49	1643	66562	66593	32	2859	111355	111368	14
427	16786	16816	31	1644	66606	66637	32	2860	111357	111371	15
428	16835	16864	30	1645	66639	66665	27	2861	111360	111381	22
429	16865	16878	14	1646	66674	66690	17	2862	111373	111421	49
430	16872	16888	17	1647	66692	66720	29	2863	111412	111426	15
431	16890	16906	17	1648	66722	66742	21	2864	111451	111468	18
432	16904	16938	35	1649	66758	66786	29	2865	111467	111480	14

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
433	16965	17052	88	1650	66787	66802	16	2866	111482	111496	15
434	17054	17069	16	1651	66812	66862	51	2867	111486	111500	15
435	17071	17085	15	1652	66864	66885	22	2868	111497	111510	14
436	17083	17098	16	1653	66940	66953	14	2869	111531	111564	34
437	17088	17111	24	1654	66982	66997	16	2870	111580	111606	27
438	17124	17138	15	1655	67024	67084	61	2871	111616	111637	22
439	17140	17159	20	1656	67103	67118	16	2872	111658	111671	14
440	17181	17202	22	1657	67156	67185	30	2873	111674	111688	15
441	17202	17218	17	1658	67181	67195	15	2874	111692	111710	19
442	17229	17248	20	1659	67193	67206	14	2875	111712	111725	14
443	17250	17268	19	1660	67215	67229	15	2876	111727	111761	35
444	17332	17349	18	1661	67231	67271	41	2877	111781	111804	24
445	17363	17387	25	1662	67288	67301	14	2878	111811	111828	18
446	17389	17429	41	1663	67294	67345	52	2879	111831	111849	19
447	17450	17464	15	1664	67362	67379	18	2880	111856	111871	16
448	17482	17497	16	1665	67381	67397	17	2881	111901	111917	17
449	18104	18117	14	1666	67409	67448	40	2882	111919	111940	22
450	18418	18431	14	1667	67468	67481	14	2883	111942	111987	46
451	18613	18626	14	1668	67483	67510	28	2884	111984	112002	19
452	18620	18634	15	1669	67540	67561	22	2885	112004	112069	66
453	18707	18721	15	1670	67620	67640	21	2886	112070	112091	22
454	18841	18855	15	1671	67656	67672	17	2887	112093	112116	24
455	18875	18889	15	1672	67674	67749	76	2888	112118	112132	15
456	19282	19295	14	1673	67751	67764	14	2889	112139	112170	32

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
457	19310	19323	14	1674	67783	67801	19	2890	112180	112196	17
458	19454	19467	14	1675	67803	67828	26	2891	112204	112223	20
459	19774	19792	19	1676	67830	67848	19	2892	112236	112283	48
460	19794	19864	71	1677	67850	67868	19	2893	112329	112343	15
461	19862	19890	29	1678	67877	67918	42	2894	112345	112383	39
462	19892	19918	27	1679	67933	67961	29	2895	112385	112401	17
463	19907	19931	25	1680	67963	67978	16	2896	112404	112423	20
464	19927	19942	16	1681	67998	68026	29	2897	112463	112477	15
465	19932	19971	40	1682	68028	68046	19	2898	112485	112547	63
466	19973	20011	39	1683	68048	68082	35	2899	112563	112581	19
467	20022	20063	42	1684	68084	68112	29	2900	112583	112597	15
468	20080	20093	14	1685	68114	68130	17	2901	112607	112638	32
469	20131	20144	14	1686	68129	68155	27	2902	112640	112664	25
470	20240	20253	14	1687	68170	68192	23	2903	112683	112721	39
471	20448	20463	16	1688	68194	68237	44	2904	112730	112759	30
472	20495	20508	14	1689	68239	68261	23	2905	112773	112811	39
473	20532	20545	14	1690	68272	68286	15	2906	112811	112825	15
474	20600	20613	14	1691	68290	68373	84	2907	112828	112862	35
475	20617	20630	14	1692	68375	68419	45	2908	112882	112912	31
476	20960	20977	18	1693	68442	68487	46	2909	112914	112967	54
477	21412	21428	17	1694	68489	68547	59	2910	112968	112982	15
478	21465	21479	15	1695	68549	68592	44	2911	112984	113016	33
479	21489	21508	20	1696	68599	68614	16	2912	113044	113064	21
480	21797	21812	16	1697	68617	68657	41	2913	113074	113097	24

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
481	22015	22030	16	1698	68659	68686	28	2914	113111	113153	43
482	22144	22157	14	1699	68688	68735	48	2915	113169	113194	26
483	22153	22167	15	1700	68732	68747	16	2916	113198	113212	15
484	22265	22278	14	1701	68749	68786	38	2917	113214	113230	17
485	23110	23123	14	1702	68788	68830	43	2918	113232	113263	32
486	23114	23133	20	1703	68837	68879	43	2919	113265	113284	20
487	23286	23303	18	1704	68882	68899	18	2920	113306	113328	23
488	23364	23379	16	1705	68918	68942	25	2921	113330	113355	26
489	23478	23498	21	1706	68944	68968	25	2922	113357	113371	15
490	23544	23587	44	1707	68983	69007	25	2923	113404	113422	19
491	23589	23630	42	1708	69012	69027	16	2924	113421	113489	69
492	23658	23676	19	1709	69020	69064	45	2925	113533	113559	27
493	23678	23702	25	1710	69064	69077	14	2926	113561	113574	14
494	23704	23729	26	1711	69079	69114	36	2927	113595	113616	22
495	23731	23748	18	1712	69116	69196	81	2928	113648	113700	53
496	23740	23755	16	1713	69185	69198	14	2929	113702	113739	38
497	23744	23757	14	1714	69202	69219	18	2930	113762	113823	62
498	23750	23764	15	1715	69228	69246	19	2931	113825	113960	136
499	23767	23795	29	1716	69240	69282	43	2932	113962	114015	54
500	23802	23816	15	1717	69294	69317	24	2933	114017	114048	32
501	23818	23831	14	1718	69306	69324	19	2934	114045	114124	80
502	23855	23869	15	1719	69333	69346	14	2935	114151	114170	20
503	23906	23926	21	1720	69352	69366	15	2936	114182	114218	37
504	23928	23942	15	1721	69387	69431	45	2937	114230	114270	41

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
505	23994	24007	14	1722	69433	69447	15	2938	114272	114292	21
506	24005	24018	14	1723	69452	69480	29	2939	114296	114339	44
507	24023	24056	34	1724	69482	69497	16	2940	114354	114433	80
508	24074	24088	15	1725	69491	69504	14	2941	114440	114457	18
509	24088	24104	17	1726	69511	69564	54	2942	114459	114484	26
510	24112	24163	52	1727	69566	69628	63	2943	114478	114536	59
511	24199	24212	14	1728	69628	69642	15	2944	114538	114559	22
512	24231	24244	14	1729	69659	69681	23	2945	114567	114592	26
513	24237	24252	16	1730	69684	69697	14	2946	114594	114610	17
514	24254	24267	14	1731	69719	69744	26	2947	114612	114652	41
515	24281	24325	45	1732	69746	69763	18	2948	114681	114752	72
516	24327	24353	27	1733	69765	69792	28	2949	114775	114805	31
517	24355	24374	20	1734	69801	69828	28	2950	114803	114816	14
518	24376	24399	24	1735	69853	69901	49	2951	114807	114821	15
519	24401	24416	16	1736	69933	69949	17	2952	114823	114847	25
520	24442	24489	48	1737	69951	69966	16	2953	114868	114912	45
521	24492	24506	15	1738	69968	69983	16	2954	114947	114961	15
522	24498	24511	14	1739	69988	70061	74	2955	114974	114997	24
523	24538	24556	19	1740	70083	70100	18	2956	115001	115015	15
524	24546	24562	17	1741	70110	70154	45	2957	115004	115017	14
525	24591	24618	28	1742	70161	70199	39	2958	115019	115069	51
526	24620	24633	14	1743	70202	70225	24	2959	115060	115073	14
527	24635	24650	16	1744	70231	70246	16	2960	115072	115085	14
528	24665	24681	17	1745	70269	70295	27	2961	115087	115100	14

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
529	24687	24706	20	1746	70292	70327	36	2962	115102	115124	23
530	24709	24729	21	1747	70331	70349	19	2963	115132	115151	20
531	24731	24752	22	1748	70351	70371	21	2964	115154	115168	15
532	24756	24771	16	1749	70381	70403	23	2965	115188	115208	21
533	24773	24788	16	1750	70405	70420	16	2966	115219	115256	38
534	24793	24821	29	1751	70422	70483	62	2967	115258	115283	26
535	24823	24854	32	1752	70496	70533	38	2968	115285	115300	16
536	24856	24870	15	1753	70535	70578	44	2969	115331	115353	23
537	24873	24922	50	1754	70577	70639	63	2970	115355	115372	18
538	24933	24954	22	1755	70653	70667	15	2971	115380	115397	18
539	24965	24984	20	1756	70661	70674	14	2972	115399	115412	14
540	25019	25052	34	1757	70669	70695	27	2973	115426	115475	50
541	25054	25099	46	1758	70687	70705	19	2974	115496	115510	15
542	25112	25125	14	1759	70708	70744	37	2975	115521	115545	25
543	25133	25169	37	1760	70746	70764	19	2976	115555	115580	26
544	25171	25184	14	1761	70766	70779	14	2977	115582	115600	19
545	25186	25221	36	1762	70781	70832	52	2978	115602	115621	20
546	25236	25253	18	1763	70834	70851	18	2979	115653	115677	25
547	25246	25296	51	1764	70858	70887	30	2980	115692	115720	29
548	25298	25336	39	1765	70889	70902	14	2981	115722	115738	17
549	25332	25348	17	1766	70920	70933	14	2982	115769	115783	15
550	25349	25363	15	1767	70935	70964	30	2983	115792	115808	17
551	25388	25432	45	1768	70974	70987	14	2984	115819	115837	19
552	25439	25462	24	1769	71008	71028	21	2985	115846	115878	33

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
553	25509	25523	15	1770	71030	71046	17	2986	115888	115901	14
554	25525	25547	23	1771	71048	71073	26	2987	115916	115932	17
555	25578	25593	16	1772	71075	71106	32	2988	115943	115956	14
556	25587	25601	15	1773	71108	71133	26	2989	115967	115993	27
557	25604	25617	14	1774	71137	71152	16	2990	115996	116014	19
558	25633	25655	23	1775	71153	71170	18	2991	116027	116045	19
559	25672	25716	45	1776	71179	71192	14	2992	116105	116127	23
560	25725	25738	14	1777	71197	71224	28	2993	116126	116139	14
561	25764	25800	37	1778	71235	71251	17	2994	116141	116158	18
562	25802	25828	27	1779	71253	71311	59	2995	116171	116186	16
563	25831	25846	16	1780	71310	71329	20	2996	116194	116208	15
564	25851	25872	22	1781	71330	71364	35	2997	116257	116279	23
565	25877	25904	28	1782	71366	71386	21	2998	116318	116373	56
566	25921	25946	26	1783	71388	71410	23	2999	116375	116437	63
567	25943	25970	28	1784	71412	71433	22	3000	116439	116454	16
568	25972	25986	15	1785	71448	71472	25	3001	116456	116496	41
569	26051	26064	14	1786	71475	71491	17	3002	116500	116532	33
570	26068	26086	19	1787	71491	71553	63	3003	116534	116554	21
571	26113	26137	25	1788	71555	71581	27	3004	116556	116573	18
572	26139	26159	21	1789	71583	71624	42	3005	116575	116592	18
573	26182	26197	16	1790	71634	71700	67	3006	116596	116615	20
574	26243	26296	54	1791	71706	71725	20	3007	116617	116650	34
575	26298	26313	16	1792	71732	71747	16	3008	116650	116664	15
576	26327	26350	24	1793	71789	71804	16	3009	116666	116694	29

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
577	26366	26385	20	1794	71810	71824	15	3010	116775	116792	18
578	26387	26404	18	1795	71819	71834	16	3011	116794	116811	18
579	26397	26415	19	1796	71839	71872	34	3012	116813	116838	26
580	26416	26453	38	1797	71876	71889	14	3013	116840	116872	33
581	26447	26461	15	1798	71886	71908	23	3014	116890	116911	22
582	26457	26471	15	1799	71910	71924	15	3015	116921	116948	28
583	26481	26498	18	1800	71985	71999	15	3016	116952	116988	37
584	26502	26525	24	1801	72000	72021	22	3017	116990	117006	17
585	26528	26562	35	1802	72023	72047	25	3018	117008	117036	29
586	26564	26590	27	1803	72071	72158	88	3019	117059	117133	75
587	26590	26622	33	1804	72165	72192	28	3020	117187	117207	21
588	26624	26638	15	1805	72194	72234	41	3021	117204	117217	14
589	26687	26702	16	1806	72236	72255	20	3022	117209	117237	29
590	26706	26719	14	1807	72257	72281	25	3023	117239	117252	14
591	26717	26730	14	1808	72283	72299	17	3024	117255	117275	21
592	26729	26743	15	1809	72312	72329	18	3025	117277	117300	24
593	26767	26797	31	1810	72323	72336	14	3026	117337	117371	35
594	26796	26816	21	1811	72348	72395	48	3027	117373	117416	44
595	26831	26847	17	1812	72398	72411	14	3028	117418	117450	33
596	26837	26850	14	1813	72413	72455	43	3029	117456	117507	52
597	26877	26890	14	1814	72470	72503	34	3030	117518	117532	15
598	26900	26922	23	1815	72506	72541	36	3031	117534	117590	57
599	26911	26933	23	1816	72545	72558	14	3032	117582	117604	23
600	26933	26946	14	1817	72560	72586	27	3033	117593	117617	25

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
601	26938	26977	40	1818	72583	72597	15	3034	117621	117648	28
602	26979	26992	14	1819	72588	72602	15	3035	117640	117662	23
603	26981	27017	37	1820	72611	72636	26	3036	117664	117688	25
604	27023	27041	19	1821	72638	72688	51	3037	117690	117711	22
605	27039	27055	17	1822	72696	72736	41	3038	117728	117743	16
606	27075	27121	47	1823	72738	72761	24	3039	117747	117781	35
607	27138	27153	16	1824	72774	72799	26	3040	117784	117801	18
608	27163	27266	104	1825	72801	72886	86	3041	117792	117822	31
609	27270	27293	24	1826	72888	72903	16	3042	117824	117842	19
610	27325	27358	34	1827	72928	72958	31	3043	117850	117869	20
611	27363	27408	46	1828	72962	72990	29	3044	117890	117940	51
612	27419	27448	30	1829	73001	73014	14	3045	117936	117968	33
613	27450	27469	20	1830	73017	73053	37	3046	117970	117990	21
614	27471	27498	28	1831	73055	73078	24	3047	117989	118034	46
615	27510	27523	14	1832	73077	73090	14	3048	118034	118057	24
616	27535	27562	28	1833	73088	73121	34	3049	118061	118083	23
617	28098	28119	22	1834	73124	73153	30	3050	118086	118122	37
618	28136	28155	20	1835	73147	73172	26	3051	118122	118182	61
619	28169	28197	29	1836	73164	73203	40	3052	118172	118186	15
620	28199	28212	14	1837	73218	73257	40	3053	118197	118211	15
621	28221	28244	24	1838	73260	73273	14	3054	118216	118275	60
622	28271	28285	15	1839	73268	73281	14	3055	118291	118316	26
623	28400	28414	15	1840	73278	73291	14	3056	118318	118354	37
624	28441	28476	36	1841	73298	73313	16	3057	118373	118388	16

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
625	28490	28533	44	1842	73451	73465	15	3058	118391	118405	15
626	28535	28562	28	1843	73459	73472	14	3059	118407	118423	17
627	28575	28600	26	1844	73512	73567	56	3060	118425	118456	32
628	28621	28634	14	1845	73569	73611	43	3061	118465	118492	28
629	28650	28663	14	1846	73614	73645	32	3062	118498	118521	24
630	28674	28687	14	1847	73661	73713	53	3063	118533	118551	19
631	28681	28699	19	1848	73712	73727	16	3064	118553	118581	29
632	28713	28730	18	1849	73716	73731	16	3065	118587	118617	31
633	28736	28761	26	1850	73735	73748	14	3066	118620	118679	60
634	28763	28811	49	1851	73741	73760	20	3067	118687	118716	30
635	28821	28854	34	1852	73764	73782	19	3068	118731	118771	41
636	28856	28881	26	1853	73783	73801	19	3069	118779	118805	27
637	28883	28920	38	1854	73795	73829	35	3070	118816	118830	15
638	28922	28947	26	1855	73860	73873	14	3071	118832	118895	64
639	28979	29006	28	1856	73885	73904	20	3072	118910	119065	156
640	29008	29056	49	1857	73906	73919	14	3073	119067	119081	15
641	29078	29095	18	1858	73916	73945	30	3074	119095	119140	46
642	29098	29129	32	1859	73947	73961	15	3075	119170	119205	36
643	29122	29135	14	1860	73978	74018	41	3076	119210	119232	23
644	29131	29144	14	1861	74020	74046	27	3077	119230	119246	17
645	29144	29158	15	1862	74061	74082	22	3078	119236	119252	17
646	29160	29207	48	1863	74092	74158	67	3079	119255	119274	20
647	29209	29230	22	1864	74160	74177	18	3080	119271	119284	14
648	29234	29266	33	1865	74179	74209	31	3081	119290	119307	18

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
649	29268	29286	19	1866	74216	74245	30	3082	119320	119335	16
650	29301	29315	15	1867	74270	74287	18	3083	119357	119463	107
651	29304	29323	20	1868	74289	74305	17	3084	119465	119483	19
652	29330	29352	23	1869	74307	74368	62	3085	119485	119535	51
653	29344	29358	15	1870	74369	74411	43	3086	119550	119571	22
654	29347	29365	19	1871	74416	74461	46	3087	119577	119608	32
655	29377	29402	26	1872	74463	74479	17	3088	119610	119646	37
656	29402	29422	21	1873	74506	74541	36	3089	119648	119688	41
657	29424	29445	22	1874	74543	74636	94	3090	119713	119752	40
658	29443	29457	15	1875	74647	74704	58	3091	119743	119784	42
659	29447	29460	14	1876	74745	74770	26	3092	119786	119800	15
660	29462	29475	14	1877	74789	74813	25	3093	119822	119836	15
661	29491	29512	22	1878	74815	74838	24	3094	119830	119847	18
662	29514	29551	38	1879	74850	74877	28	3095	119849	119900	52
663	29547	29560	14	1880	74891	74923	33	3096	119912	119925	14
664	29553	29620	68	1881	74925	74940	16	3097	119960	119982	23
665	29625	29700	76	1882	74952	74969	18	3098	119984	120013	30
666	29714	29745	32	1883	74979	75001	23	3099	120038	120054	17
667	29774	29805	32	1884	75037	75066	30	3100	120057	120090	34
668	29816	29847	32	1885	75068	75088	21	3101	120092	120134	43
669	29875	29892	18	1886	75097	75123	27	3102	120138	120154	17
670	29894	29908	15	1887	75131	75149	19	3103	120157	120189	33
671	29897	29910	14	1888	75152	75189	38	3104	120187	120200	14
672	29917	29938	22	1889	75210	75252	43	3105	120191	120211	21

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
673	29939	29952	14	1890	75254	75276	23	3106	120225	120239	15
674	29961	29976	16	1891	75288	75310	23	3107	120242	120267	26
675	29974	29987	14	1892	75338	75357	20	3108	120271	120301	31
676	29978	30001	24	1893	75359	75372	14	3109	120320	120340	21
677	30006	30023	18	1894	75376	75397	22	3110	120363	120406	44
678	30025	30039	15	1895	75405	75432	28	3111	120406	120421	16
679	30043	30107	65	1896	75440	75470	31	3112	120414	120468	55
680	30145	30158	14	1897	75482	75501	20	3113	120457	120470	14
681	30149	30166	18	1898	75503	75540	38	3114	120487	120518	32
682	30173	30228	56	1899	75544	75560	17	3115	120545	120563	19
683	30230	30250	21	1900	75562	75576	15	3116	120567	120587	21
684	30251	30309	59	1901	75589	75610	22	3117	120589	120625	37
685	30321	30358	38	1902	75633	75646	14	3118	120619	120633	15
686	30359	30380	22	1903	75648	75679	32	3119	120650	120663	14
687	30382	30422	41	1904	75691	75709	19	3120	120676	120694	19
688	30428	30442	15	1905	75711	75724	14	3121	120703	120717	15
689	30455	30482	28	1906	75740	75764	25	3122	120721	120737	17
690	30484	30498	15	1907	75763	75776	14	3123	120755	120812	58
691	30516	30531	16	1908	75767	75790	24	3124	120816	120838	23
692	30533	30646	114	1909	75780	75794	15	3125	120843	120871	29
693	30654	30745	92	1910	75792	75808	17	3126	120873	120899	27
694	30745	30760	16	1911	75810	75829	20	3127	120903	120922	20
695	30752	30766	15	1912	75831	75863	33	3128	120933	120946	14
696	30788	30843	56	1913	75865	75880	16	3129	120936	120981	46

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
697	30845	30867	23	1914	75882	75922	41	3130	120983	121004	22
698	30869	30912	44	1915	75932	75998	67	3131	121006	121021	16
699	30906	30920	15	1916	76000	76026	27	3132	121023	121036	14
700	30934	30951	18	1917	76028	76045	18	3133	121035	121061	27
701	30962	30984	23	1918	76046	76082	37	3134	121063	121079	17
702	30989	31002	14	1919	76098	76413	316	3135	121081	121097	17
703	31010	31033	24	1920	76420	76442	23	3136	121105	121134	30
704	31036	31062	27	1921	76456	76477	22	3137	121138	121156	19
705	31092	31106	15	1922	76484	76558	75	3138	121155	121168	14
706	31128	31166	39	1923	76573	76592	20	3139	121158	121174	17
707	31168	31182	15	1924	76608	76622	15	3140	121166	121189	24
708	31189	31203	15	1925	76627	76663	37	3141	121194	121208	15
709	31205	31218	14	1926	76665	76683	19	3142	121201	121218	18
710	31224	31253	30	1927	76685	76698	14	3143	121213	121237	25
711	31256	31272	17	1928	76702	76716	15	3144	121246	121271	26
712	31274	31292	19	1929	76725	76744	20	3145	121298	121314	17
713	31294	31322	29	1930	76745	76761	17	3146	121311	121324	14
714	31324	31353	30	1931	76780	76796	17	3147	121327	121351	25
715	31357	31370	14	1932	76798	76812	15	3148	121359	121388	30
716	31373	31399	27	1933	76814	76832	19	3149	121390	121419	30
717	31403	31426	24	1934	76834	76859	26	3150	121446	121462	17
718	31445	31460	16	1935	76871	76934	64	3151	121468	121487	20
719	31463	31483	21	1936	77012	77034	23	3152	121499	121515	17
720	31485	31501	17	1937	77039	77055	17	3153	121517	121543	27

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
721	31494	31508	15	1938	77081	77094	14	3154	121545	121564	20
722	31507	31529	23	1939	77121	77184	64	3155	121575	121597	23
723	31531	31565	35	1940	77186	77200	15	3156	121599	121617	19
724	31567	31615	49	1941	77202	77225	24	3157	121619	121662	44
725	31630	31665	36	1942	77227	77247	21	3158	121664	121681	18
726	31675	31691	17	1943	77261	77317	57	3159	121683	121700	18
727	31703	31721	19	1944	77327	77340	14	3160	121702	121751	50
728	31729	31769	41	1945	77342	77366	25	3161	121773	121788	16
729	31770	31790	21	1946	77377	77394	18	3162	121790	121805	16
730	31795	31813	19	1947	77396	77439	44	3163	121807	121834	28
731	31815	31835	21	1948	77453	77468	16	3164	121836	121857	22
732	31837	31865	29	1949	77462	77593	132	3165	121859	121874	16
733	31876	31889	14	1950	77586	77599	14	3166	121877	121925	49
734	31920	31945	26	1951	77595	77641	47	3167	121923	121936	14
735	31962	31978	17	1952	77643	77728	86	3168	121928	121943	16
736	31983	32014	32	1953	77730	77768	39	3169	121962	121976	15
737	32029	32050	22	1954	77778	77816	39	3170	121978	121992	15
738	32058	32110	53	1955	77818	77835	18	3171	122004	122028	25
739	32129	32147	19	1956	77837	77855	19	3172	122030	122056	27
740	32166	32242	77	1957	77861	77876	16	3173	122046	122059	14
741	32244	32279	36	1958	77882	77898	17	3174	122052	122072	21
742	32296	32315	20	1959	77900	77924	25	3175	122080	122095	16
743	32334	32396	63	1960	77923	77936	14	3176	122099	122122	24
744	32398	32425	28	1961	77957	77970	14	3177	122143	122163	21

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
745	32427	32453	27	1962	77962	77985	24	3178	122169	122189	21
746	32459	32481	23	1963	77994	78022	29	3179	122258	122274	17
747	32475	32498	24	1964	78024	78056	33	3180	122289	122309	21
748	32490	32523	34	1965	78079	78128	50	3181	122311	122346	36
749	32519	32534	16	1966	78132	78158	27	3182	122357	122395	39
750	32525	32547	23	1967	78173	78213	41	3183	122446	122468	23
751	32542	32555	14	1968	78224	78265	42	3184	122471	122489	19
752	32559	32572	14	1969	78275	78332	58	3185	122491	122512	22
753	32574	32587	14	1970	78334	78440	107	3186	122526	122541	16
754	32595	32618	24	1971	78442	78489	48	3187	122543	122557	15
755	32613	32626	14	1972	78491	78505	15	3188	122579	122592	14
756	32627	32649	23	1973	78501	78514	14	3189	122606	122653	48
757	32651	32664	14	1974	78507	78537	31	3190	122663	122690	28
758	32655	32689	35	1975	78557	78570	14	3191	122728	122742	15
759	32693	32719	27	1976	78562	78623	62	3192	122757	122770	14
760	32721	32750	30	1977	78625	78665	41	3193	122779	122840	62
761	32752	32778	27	1978	78668	78684	17	3194	122842	122857	16
762	32780	32795	16	1979	78686	78759	74	3195	122900	122923	24
763	32797	32847	51	1980	78761	78787	27	3196	122933	122955	23
764	32881	32894	14	1981	78793	78814	22	3197	122968	123042	75
765	32891	32904	14	1982	78816	78854	39	3198	123055	123076	22
766	32896	32911	16	1983	78847	78860	14	3199	123094	123108	15
767	32927	32972	46	1984	78874	78909	36	3200	123114	123134	21
768	32986	33017	32	1985	78917	78944	28	3201	123143	123160	18

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
769	33019	33036	18	1986	78956	78978	23	3202	123162	123180	19
770	33038	33096	59	1987	78991	79008	18	3203	123184	123198	15
771	33102	33123	22	1988	79003	79032	30	3204	123200	123235	36
772	33132	33145	14	1989	79026	79040	15	3205	123237	123321	85
773	33150	33163	14	1990	79044	79072	29	3206	123314	123329	16
774	33166	33199	34	1991	79098	79158	61	3207	123342	123360	19
775	33214	33260	47	1992	79162	79182	21	3208	123356	123389	34
776	33262	33292	31	1993	79184	79228	45	3209	123391	123410	20
777	33294	33307	14	1994	79221	79235	15	3210	123412	123453	42
778	33316	33351	36	1995	79230	79262	33	3211	123455	123485	31
779	33360	33402	43	1996	79287	79333	47	3212	123488	123503	16
780	33412	33425	14	1997	79356	79392	37	3213	123506	123524	19
781	33427	33442	16	1998	79441	79476	36	3214	123526	123543	18
782	33439	33452	14	1999	79488	79522	35	3215	123545	123578	34
783	33443	33456	14	2000	79522	79539	18	3216	123598	123634	37
784	33460	33501	42	2001	79568	79583	16	3217	123654	123683	30
785	33503	33535	33	2002	79574	79601	28	3218	123685	123706	22
786	33542	33557	16	2003	79603	79618	16	3219	123710	123774	65
787	34168	34181	14	2004	79617	79639	23	3220	123803	123816	14
788	34370	34385	16	2005	79651	79683	33	3221	123818	123831	14
789	35422	35435	14	2006	79685	79724	40	3222	123896	123939	44
790	35627	35641	15	2007	79721	79736	16	3223	123941	123974	34
791	35685	35700	16	2008	79727	79782	56	3224	123976	124021	46
792	35837	35851	15	2009	79784	79812	29	3225	124026	124040	15

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
793	35849	35864	16	2010	79809	79834	26	3226	124042	124079	38
794	35866	35879	14	2011	79841	79861	21	3227	124091	124109	19
795	35974	35987	14	2012	79873	79923	51	3228	124158	124185	28
796	36009	36042	34	2013	79928	79948	21	3229	124238	124274	37
797	36044	36079	36	2014	79950	79986	37	3230	124319	124332	14
798	36081	36097	17	2015	79993	80019	27	3231	124335	124373	39
799	36099	36120	22	2016	80019	80063	45	3232	124394	124412	19
800	36119	36133	15	2017	80071	80088	18	3233	124419	124445	27
801	36147	36163	17	2018	80114	80160	47	3234	124450	124470	21
802	36171	36200	30	2019	80154	80183	30	3235	124472	124493	22
803	36216	36241	26	2020	80185	80212	28	3236	124499	124520	22
804	36245	36274	30	2021	80214	80232	19	3237	124522	124561	40
805	36265	36283	19	2022	80240	80266	27	3238	124564	124595	32
806	36295	36348	54	2023	80293	80312	20	3239	124607	124649	43
807	36352	36389	38	2024	80344	80380	37	3240	124662	124729	68
808	36383	36400	18	2025	80382	80420	39	3241	124750	124767	18
809	36402	36419	18	2026	80410	80423	14	3242	124769	124793	25
810	36475	36520	46	2027	80417	80438	22	3243	124812	124828	17
811	36522	36539	18	2028	80440	80456	17	3244	124853	124906	54
812	36541	36626	86	2029	80467	80499	33	3245	124923	124948	26
813	36652	36672	21	2030	80501	80527	27	3246	124958	124986	29
814	36675	36705	31	2031	80532	80561	30	3247	125023	125042	20
815	36707	36746	40	2032	80563	80599	37	3248	125032	125046	15
816	36780	36808	29	2033	80604	80692	89	3249	125065	125083	19

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
817	36810	36823	14	2034	80702	80737	36	3250	125073	125091	19
818	36825	36901	77	2035	80739	80795	57	3251	125093	125107	15
819	36903	36922	20	2036	80796	80871	76	3252	125132	125149	18
820	36924	36982	59	2037	80873	80891	19	3253	125139	125154	16
821	36999	37030	32	2038	80925	80961	37	3254	125151	125200	50
822	37056	37083	28	2039	80963	80992	30	3255	125201	125274	74
823	37091	37135	45	2040	81009	81068	60	3256	125314	125329	16
824	37194	37221	28	2041	81070	81150	81	3257	125331	125370	40
825	37238	37277	40	2042	81156	81199	44	3258	125372	125386	15
826	37280	37294	15	2043	81201	81225	25	3259	125411	125431	21
827	37298	37315	18	2044	81237	81253	17	3260	125433	125462	30
828	37325	37350	26	2045	81255	81271	17	3261	125475	125562	88
829	37363	37383	21	2046	81292	81351	60	3262	125564	125589	26
830	37377	37394	18	2047	81353	81371	19	3263	125605	125639	35
831	37384	37397	14	2048	81392	81422	31	3264	125641	125699	59
832	37390	37438	49	2049	81438	81483	46	3265	125719	125732	14
833	37456	37481	26	2050	81485	81503	19	3266	125737	125769	33
834	37478	37491	14	2051	81512	81526	15	3267	125815	125829	15
835	37481	37503	23	2052	81532	81554	23	3268	125834	125848	15
836	37506	37524	19	2053	81556	81593	38	3269	125850	125884	35
837	37526	37545	20	2054	81606	81664	59	3270	125899	125966	68
838	37540	37572	33	2055	81666	81698	33	3271	125967	125999	33
839	37574	37590	17	2056	81701	81720	20	3272	126026	126080	55
840	37601	37616	16	2057	81728	81776	49	3273	126097	126115	19

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
841	37621	37658	38	2058	81781	81810	30	3274	126130	126149	20
842	37673	37690	18	2059	81812	81847	36	3275	126151	126179	29
843	37703	37738	36	2060	81849	81893	45	3276	126186	126238	53
844	37740	37753	14	2061	81908	81934	27	3277	126241	126279	39
845	37764	37790	27	2062	81943	81964	22	3278	126275	126295	21
846	37800	37818	19	2063	81967	82034	68	3279	126297	126312	16
847	37820	37850	31	2064	82036	82134	99	3280	126320	126363	44
848	37888	37909	22	2065	82136	82154	19	3281	126376	126395	20
849	37911	37972	62	2066	82176	82197	22	3282	126406	126419	14
850	37986	38014	29	2067	82199	82250	52	3283	126420	126442	23
851	38016	38032	17	2068	82252	82269	18	3284	126467	126501	35
852	38034	38053	20	2069	82271	82293	23	3285	126503	126538	36
853	38055	38073	19	2070	82300	82314	15	3286	126566	126580	15
854	38075	38090	16	2071	82329	82343	15	3287	126584	126597	14
855	38092	38128	37	2072	82344	82357	14	3288	126620	126653	34
856	38141	38167	27	2073	82378	82407	30	3289	126654	126694	41
857	38171	38194	24	2074	82406	82422	17	3290	126697	126715	19
858	38213	38240	28	2075	82421	82443	23	3291	126764	126777	14
859	38264	38286	23	2076	82446	82469	24	3292	126792	126828	37
860	38288	38370	83	2077	82490	82507	18	3293	126842	126862	21
861	38394	38420	27	2078	82502	82523	22	3294	126866	126879	14
862	38452	38467	16	2079	82547	82576	30	3295	126881	126897	17
863	38471	38487	17	2080	82590	82603	14	3296	126906	126925	20
864	38477	38490	14	2081	82628	82647	20	3297	126956	126987	32

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
865	38494	38507	14	2082	82650	82666	17	3298	126989	127023	35
866	38536	38556	21	2083	82669	82683	15	3299	127026	127135	110
867	38580	38593	14	2084	82685	82716	32	3300	127142	127174	33
868	38602	38618	17	2085	82715	82736	22	3301	127176	127191	16
869	38628	38654	27	2086	82760	82785	26	3302	127193	127217	25
870	38693	38709	17	2087	82778	82791	14	3303	127229	127253	25
871	38709	38722	14	2088	82780	82818	39	3304	127255	127280	26
872	38711	38725	15	2089	82811	82825	15	3305	127294	127394	101
873	38740	38756	17	2090	82821	82864	44	3306	127396	127415	20
874	38749	38769	21	2091	82883	82915	33	3307	127417	127478	62
875	38772	38797	26	2092	82919	82935	17	3308	127491	127504	14
876	38827	38846	20	2093	82930	82946	17	3309	127506	127530	25
877	38860	38883	24	2094	82937	82957	21	3310	127542	127566	25
878	38885	38905	21	2095	82959	82972	14	3311	127582	127628	47
879	38911	38931	21	2096	82974	83000	27	3312	127654	127675	22
880	38933	38949	17	2097	83020	83036	17	3313	127681	127706	26
881	38962	39032	71	2098	83038	83088	51	3314	127706	127739	34
882	39034	39047	14	2099	83090	83115	26	3315	127769	127792	24
883	39049	39070	22	2100	83120	83140	21	3316	127808	127829	22
884	39075	39115	41	2101	83142	83155	14	3317	127839	127888	50
885	39127	39143	17	2102	83160	83186	27	3318	127900	127932	33
886	39148	39162	15	2103	83198	83215	18	3319	127943	127975	33
887	39164	39222	59	2104	83227	83246	20	3320	127988	128046	59
888	39218	39231	14	2105	83273	83339	67	3321	128048	128069	22

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
889	39224	39256	33	2106	83341	83385	45	3322	128068	128106	39
890	39265	39306	42	2107	83387	83400	14	3323	128105	128118	14
891	39297	39311	15	2108	83413	83426	14	3324	128121	128157	37
892	39308	39343	36	2109	83417	83449	33	3325	128159	128188	30
893	39345	39359	15	2110	83486	83520	35	3326	128190	128268	79
894	39361	39381	21	2111	83522	83565	44	3327	128279	128317	39
895	39370	39383	14	2112	83567	83581	15	3328	128321	128335	15
896	39383	39399	17	2113	83576	83670	95	3329	128342	128368	27
897	39417	39469	53	2114	83681	83701	21	3330	128374	128446	73
898	39490	39503	14	2115	83703	83716	14	3331	128444	128540	97
899	39500	39522	23	2116	83733	83817	85	3332	128546	128586	41
900	39535	39549	15	2117	83817	83830	14	3333	128588	128640	53
901	39551	39611	61	2118	83832	83853	22	3334	128642	128674	33
902	39628	39647	20	2119	83855	83871	17	3335	128675	128879	205
903	39649	39690	42	2120	83886	83926	41	3336	128881	128936	56
904	39707	39759	53	2121	83958	83974	17	3337	128934	129000	67
905	39773	39797	25	2122	83976	83991	16	3338	129002	129060	59
906	39799	39858	60	2123	83993	84031	39	3339	129074	129100	27
907	39872	39928	57	2124	84033	84067	35	3340	129107	129123	17
908	39930	39969	40	2125	84069	84102	34	3341	129125	129163	39
909	39973	39997	25	2126	84104	84121	18	3342	129168	129230	63
910	39998	40013	16	2127	84143	84233	91	3343	129264	129277	14
911	40015	40064	50	2128	84249	84281	33	3344	129284	129318	35
912	40067	40108	42	2129	84283	84403	121	3345	129320	129346	27

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
913	40110	40140	31	2130	84404	84432	29	3346	129357	129391	35
914	40147	40163	17	2131	84431	84444	14	3347	129393	129420	28
915	40154	40179	26	2132	84434	84490	57	3348	129447	129485	39
916	40181	40196	16	2133	84503	84520	18	3349	129489	129504	16
917	40232	40282	51	2134	84522	84555	34	3350	129514	129540	27
918	40284	40307	24	2135	84557	84572	16	3351	129550	129563	14
919	40309	40368	60	2136	84574	84597	24	3352	129559	129595	37
920	40381	40399	19	2137	84607	84626	20	3353	129606	129627	22
921	40431	40471	41	2138	84650	84675	26	3354	129633	129681	49
922	40479	40493	15	2139	84677	84700	24	3355	129683	129697	15
923	40484	40522	39	2140	84721	84753	33	3356	129699	129716	18
924	40524	40544	21	2141	84755	84807	53	3357	129706	129738	33
925	40547	40561	15	2142	84809	84826	18	3358	129757	129790	34
926	40577	40594	18	2143	84831	84849	19	3359	129792	129820	29
927	40586	40599	14	2144	84879	84893	15	3360	129812	129846	35
928	40616	40631	16	2145	84895	84915	21	3361	129851	129867	17
929	40634	40647	14	2146	84917	84961	45	3362	129869	129883	15
930	40674	40727	54	2147	85234	85247	14	3363	129885	129915	31
931	40738	40755	18	2148	85253	85267	15	3364	129917	129955	39
932	40749	40771	23	2149	85256	85351	96	3365	129957	130046	90
933	40780	40802	23	2150	85359	85374	16	3366	130042	130070	29
934	40811	40834	24	2151	85363	85376	14	3367	130110	130156	47
935	40847	40865	19	2152	85365	85381	17	3368	130158	130309	152
936	40861	40875	15	2153	85380	85414	35	3369	130311	130373	63

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
937	40869	40897	29	2154	85416	85454	39	3370	130375	130391	17
938	40899	40919	21	2155	85456	85484	29	3371	130407	130429	23
939	40921	40939	19	2156	85509	85545	37	3372	130439	130461	23
940	40942	40962	21	2157	85535	85550	16	3373	130475	130507	33
941	40967	40980	14	2158	85566	85584	19	3374	130512	130550	39
942	41008	41097	90	2159	85586	85610	25	3375	130552	130582	31
943	41099	41131	33	2160	85604	85627	24	3376	130584	130614	31
944	41133	41200	68	2161	85628	85665	38	3377	130616	130764	149
945	41202	41223	22	2162	85698	85723	26	3378	130766	130869	104
946	41225	41242	18	2163	85713	85728	16	3379	130871	131021	151
947	41266	41279	14	2164	85722	85735	14	3380	131033	131051	19
948	41275	41298	24	2165	85770	85785	16	3381	131092	131105	14
949	41300	41321	22	2166	85800	85813	14	3382	131112	131188	77
950	41325	41360	36	2167	85875	85888	14	3383	131194	131237	44
951	41367	41388	22	2168	85950	85963	14	3384	131233	131247	15
952	41403	41421	19	2169	86097	86125	29	3385	131236	131287	52
953	41439	41462	24	2170	86127	86142	16	3386	131292	131307	16
954	41481	41496	16	2171	86175	86198	24	3387	131314	131333	20
955	41508	41523	16	2172	86226	86242	17	3388	131373	131386	14
956	41531	41550	20	2173	86237	86302	66	3389	131396	131417	22
957	41552	41590	39	2174	86308	86327	20	3390	131419	131439	21
958	41590	41603	14	2175	86321	86334	14	3391	131429	131458	30
959	41612	41662	51	2176	86329	86382	54	3392	131481	131499	19
960	41664	41688	25	2177	86384	86400	17	3393	131676	131689	14

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
961	41685	41698	14	2178	86403	86417	15	3394	131729	131743	15
962	41691	41716	26	2179	86414	86437	24	3395	131745	131764	20
963	41718	41764	47	2180	86439	86455	17	3396	131785	131807	23
964	41761	41776	16	2181	86461	86478	18	3397	131809	131875	67
965	41778	41809	32	2182	86473	86487	15	3398	131877	131953	77
966	41798	41811	14	2183	86480	86517	38	3399	131955	131980	26
967	41838	41866	29	2184	86517	86531	15	3400	132020	132068	49
968	41872	41893	22	2185	86565	86583	19	3401	132086	132108	23
969	41885	41898	14	2186	86600	86632	33	3402	132118	132138	21
970	41912	41925	14	2187	86634	86651	18	3403	132152	132183	32
971	41914	41930	17	2188	86653	86678	26	3404	132185	132205	21
972	41923	41942	20	2189	86697	86756	60	3405	132219	132232	14
973	41933	41956	24	2190	86782	86796	15	3406	132234	132252	19
974	41962	41978	17	2191	86786	86809	24	3407	132261	132291	31
975	41997	42012	16	2192	86811	86855	45	3408	132319	132337	19
976	42026	42042	17	2193	86857	86891	35	3409	132345	132363	19
977	42035	42048	14	2194	86894	86908	15	3410	132365	132378	14
978	42037	42050	14	2195	86916	86933	18	3411	132414	132483	70
979	42048	42064	17	2196	86945	86959	15	3412	132504	132547	44
980	42056	42079	24	2197	86951	86965	15	3413	132549	132582	34
981	42081	42095	15	2198	86969	86990	22	3414	132584	132602	19
982	42096	42139	44	2199	87017	87057	41	3415	132616	132642	27
983	42141	42187	47	2200	87059	87073	15	3416	132643	132681	39
984	42190	42226	37	2201	87062	87076	15	3417	132685	132714	30

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
985	42232	42253	22	2202	87066	87089	24	3418	132736	132769	34
986	42255	42305	51	2203	87097	87121	25	3419	132771	132793	23
987	42307	42320	14	2204	87110	87134	25	3420	132809	132825	17
988	42347	42375	29	2205	87130	87155	26	3421	132827	132841	15
989	42389	42425	37	2206	87160	87194	35	3422	132861	132884	24
990	42427	42442	16	2207	87185	87198	14	3423	132882	132900	19
991	42452	42474	23	2208	87209	87260	52	3424	132899	132915	17
992	42482	42496	15	2209	87257	87270	14	3425	132917	132951	35
993	42495	42509	15	2210	87274	87287	14	3426	132940	132954	15
994	42536	42550	15	2211	87276	87294	19	3427	132958	132983	26
995	42566	42580	15	2212	87294	87328	35	3428	132985	133031	47
996	42590	42612	23	2213	87317	87333	17	3429	133032	133051	20
997	42646	42678	33	2214	87336	87360	25	3430	133042	133060	19
998	42683	42723	41	2215	87368	87418	51	3431	133051	133071	21
999	42735	42750	16	2216	87441	87460	20	3432	133073	133087	15
1000	42752	42817	66	2217	87462	87487	26	3433	133083	133104	22
1001	42843	42873	31	2218	87489	87518	30	3434	133097	133110	14
1002	42890	42939	50	2219	87520	87539	20	3435	133131	133199	69
1003	42938	42989	52	2220	87542	87570	29	3436	133198	133222	25
1004	42991	43005	15	2221	87572	87601	30	3437	133233	133249	17
1005	43007	43020	14	2222	87603	87644	42	3438	133251	133284	34
1006	43036	43055	20	2223	87642	87750	109	3439	133327	133429	103
1007	43057	43102	46	2224	87756	87776	21	3440	133431	133596	166
1008	43113	43145	33	2225	87778	87803	26	3441	133588	133602	15

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
1009	43147	43180	34	2226	87803	87837	35	3442	133598	133611	14
1010	43204	43221	18	2227	87872	87888	17	3443	133613	133628	16
1011	43221	43265	45	2228	87890	87917	28	3444	133628	133646	19
1012	43267	43296	30	2229	87949	87964	16	3445	133651	133670	20
1013	43311	43334	24	2230	87963	88008	46	3446	133666	133707	42
1014	43336	43361	26	2231	88010	88027	18	3447	133718	133742	25
1015	43371	43395	25	2232	88029	88046	18	3448	133743	133777	35
1016	43399	43423	25	2233	88048	88089	42	3449	133779	133794	16
1017	43425	43453	29	2234	88091	88108	18	3450	133821	133851	31
1018	43452	43468	17	2235	88110	88177	68	3451	133859	133880	22
1019	43470	43488	19	2236	88179	88192	14	3452	133890	133921	32
1020	43495	43522	28	2237	88194	88229	36	3453	133923	133974	52
1021	43525	43559	35	2238	88234	88259	26	3454	133982	133998	17
1022	43561	43584	24	2239	88261	88291	31	3455	134000	134036	37
1023	43590	43611	22	2240	88303	88328	26	3456	134065	134107	43
1024	43618	43650	33	2241	88328	88341	14	3457	134120	134173	54
1025	43670	43685	16	2242	88340	88354	15	3458	134165	134179	15
1026	43722	43774	53	2243	88356	88372	17	3459	134187	134200	14
1027	43776	43791	16	2244	88411	88446	36	3460	134207	134242	36
1028	43808	43835	28	2245	88448	88465	18	3461	134244	134258	15
1029	43835	43851	17	2246	88469	88511	43	3462	134260	134273	14
1030	43853	43868	16	2247	88518	88533	16	3463	134275	134299	25
1031	43923	43937	15	2248	88531	88557	27	3464	134314	134346	33
1032	43952	43987	36	2249	88547	88560	14	3465	134356	134371	16

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
1033	44011	44029	19	2250	88573	88593	21	3466	134365	134380	16
1034	44028	44070	43	2251	88597	88618	22	3467	134374	134420	47
1035	44072	44094	23	2252	88620	88690	71	3468	134445	134477	33
1036	44101	44130	30	2253	88692	88745	54	3469	134508	134523	16
1037	44137	44205	69	2254	88954	88973	20	3470	134531	134548	18
1038	44224	44244	21	2255	88988	89047	60	3471	134542	134555	14
1039	44246	44265	20	2256	89066	89091	26	3472	134568	134621	54
1040	44267	44318	52	2257	89098	89119	22	3473	134647	134667	21
1041	44316	44336	21	2258	89135	89149	15	3474	134679	134719	41
1042	44338	44359	22	2259	89151	89181	31	3475	134721	134824	104
1043	44361	44424	64	2260	89177	89193	17	3476	134826	134849	24
1044	44439	44474	36	2261	89223	89273	51	3477	134856	134869	14
1045	44476	44500	25	2262	89285	89300	16	3478	134877	134910	34
1046	44502	44519	18	2263	89315	89383	69	3479	134912	134966	55
1047	44539	44553	15	2264	89404	89442	39	3480	134960	134980	21
1048	44563	44578	16	2265	89444	89541	98	3481	134989	135012	24
1049	44585	44599	15	2266	89579	89639	61	3482	135014	135066	53
1050	44601	44617	17	2267	89660	89692	33	3483	135074	135093	20
1051	44640	44701	62	2268	89694	89741	48	3484	135108	135125	18
1052	44704	44723	20	2269	89773	89787	15	3485	135151	135260	110
1053	44741	44763	23	2270	89789	89817	29	3486	135264	135277	14
1054	44766	44846	81	2271	89826	89888	63	3487	135273	135310	38
1055	44870	44889	20	2272	89904	89922	19	3488	135321	135337	17
1056	44887	44905	19	2273	89937	89950	14	3489	135340	135365	26

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
1057	44920	44947	28	2274	89945	89958	14	3490	135360	135374	15
1058	44949	44966	18	2275	89956	89974	19	3491	135364	135386	23
1059	44994	45022	29	2276	89971	89985	15	3492	135388	135430	43
1060	45042	45059	18	2277	89979	89992	14	3493	135432	135447	16
1061	45061	45087	27	2278	89984	90000	17	3494	135498	135521	24
1062	45116	45154	39	2279	89999	90014	16	3495	135519	135545	27
1063	45156	45182	27	2280	90017	90041	25	3496	135559	135622	64
1064	45183	45198	16	2281	90036	90049	14	3497	135624	135647	24
1065	45210	45243	34	2282	90077	90093	17	3498	135656	135673	18
1066	45245	45320	76	2283	90099	90128	30	3499	135675	135704	30
1067	45331	45367	37	2284	90130	90155	26	3500	135721	135742	22
1068	45380	45399	20	2285	90157	90200	44	3501	135753	135796	44
1069	45415	45428	14	2286	90225	90256	32	3502	135815	135858	44
1070	45421	45486	66	2287	90258	90293	36	3503	135860	135880	21
1071	45488	45545	58	2288	90305	90318	14	3504	135883	135915	33
1072	45556	45576	21	2289	90320	90352	33	3505	135922	135965	44
1073	45578	45597	20	2290	90356	90370	15	3506	135979	135993	15
1074	45603	45650	48	2291	90400	90421	22	3507	135995	136036	42
1075	45652	45665	14	2292	90423	90461	39	3508	136051	136065	15
1076	45675	45715	41	2293	90464	90507	44	3509	136108	136165	58
1077	45749	45763	15	2294	90509	90530	22	3510	136173	136190	18
1078	45804	45826	23	2295	90529	90542	14	3511	136192	136287	96
1079	45839	45861	23	2296	90531	90567	37	3512	136289	136303	15
1080	45878	45910	33	2297	90569	90612	44	3513	136317	136346	30

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
1081	45926	45954	29	2298	90614	90730	117	3514	136375	136415	41
1082	45956	45975	20	2299	90732	90758	27	3515	136429	136470	42
1083	45977	45997	21	2300	90760	90885	126	3516	136472	136496	25
1084	45999	46020	22	2301	90887	90918	32	3517	136498	136532	35
1085	46046	46063	18	2302	90920	90946	27	3518	136542	136565	24
1086	46065	46088	24	2303	90938	90955	18	3519	136643	136657	15
1087	46097	46118	22	2304	90960	90973	14	3520	136674	136701	28
1088	46120	46142	23	2305	90965	90981	17	3521	136704	136719	16
1089	46144	46160	17	2306	90973	91000	28	3522	136715	136728	14
1090	46162	46185	24	2307	90997	91011	15	3523	136721	136737	17
1091	46204	46280	77	2308	91002	91019	18	3524	136737	136750	14
1092	46302	46326	25	2309	91059	91140	82	3525	136783	136810	28
1093	46328	46355	28	2310	91142	91157	16	3526	136824	136849	26
1094	46358	46377	20	2311	91157	91194	38	3527	136859	136896	38
1095	46379	46436	58	2312	91196	91231	36	3528	136898	136927	30
1096	46457	46471	15	2313	91233	91251	19	3529	136949	136983	35
1097	46473	46492	20	2314	91253	91274	22	3530	136985	137000	16
1098	46501	46541	41	2315	91296	91310	15	3531	137053	137071	19
1099	46543	46572	30	2316	91335	91367	33	3532	137077	137097	21
1100	46584	46626	43	2317	91406	91442	37	3533	137108	137164	57
1101	46655	46683	29	2318	91447	91477	31	3534	137166	137196	31
1102	46685	46702	18	2319	91489	91509	21	3535	137198	137221	24
1103	46704	46722	19	2320	91520	91621	102	3536	137223	137267	45
1104	46724	46763	40	2321	91623	91674	52	3537	137276	137359	84

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
1105	46784	46800	17	2322	91680	91703	24	3538	137360	137385	26
1106	46802	46827	26	2323	91715	91731	17	3539	137393	137440	48
1107	46830	46867	38	2324	91733	91771	39	3540	137438	137496	59
1108	46869	46887	19	2325	91773	91788	16	3541	137498	137518	21
1109	46889	46920	32	2326	91790	91805	16	3542	137523	137536	14
1110	46922	46947	26	2327	91807	91823	17	3543	137539	137572	34
1111	46976	47009	34	2328	91825	91859	35	3544	137584	137612	29
1112	47011	47030	20	2329	91861	91900	40	3545	137614	137628	15
1113	47032	47064	33	2330	91907	91926	20	3546	137630	137644	15
1114	47066	47092	27	2331	91928	91943	16	3547	137646	137669	24
1115	47108	47130	23	2332	91950	91980	31	3548	137702	137727	26
1116	47132	47168	37	2333	91982	91996	15	3549	137731	137745	15
1117	47170	47199	30	2334	91998	92011	14	3550	137759	137772	14
1118	47201	47222	22	2335	92010	92027	18	3551	137784	137819	36
1119	47238	47277	40	2336	92027	92067	41	3552	137832	137858	27
1120	47296	47350	55	2337	92069	92126	58	3553	137861	137876	16
1121	47352	47391	40	2338	92128	92321	194	3554	137878	137900	23
1122	47416	47440	25	2339	92323	92540	218	3555	137909	137925	17
1123	47452	47466	15	2340	92542	92558	17	3556	137924	137961	38
1124	47468	47523	56	2341	92566	92684	119	3557	137968	137981	14
1125	47522	47546	25	2342	92686	92726	41	3558	138011	138033	23
1126	47548	47567	20	2343	92728	92837	110	3559	138035	138077	43
1127	47569	47595	27	2344	92839	93032	194	3560	138079	138097	19
1128	47597	47634	38	2345	93034	93094	61	3561	138224	138238	15

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
1129	47657	47693	37	2346	93100	93209	110	3562	138232	138252	21
1130	47712	47731	20	2347	93211	93254	44	3563	138242	138256	15
1131	47749	47762	14	2348	93256	93323	68	3564	138255	138284	30
1132	47771	47825	55	2349	93325	93448	124	3565	138295	138326	32
1133	47827	47846	20	2350	93459	93477	19	3566	138328	138357	30
1134	47848	47872	25	2351	93475	93497	23	3567	138359	138389	31
1135	47874	47888	15	2352	93509	93530	22	3568	138403	138449	47
1136	47890	47909	20	2353	93532	93566	35	3569	138451	138492	42
1137	47911	47925	15	2354	93568	93601	34	3570	138500	138515	16
1138	47927	47952	26	2355	93606	93646	41	3571	138524	138548	25
1139	47961	47993	33	2356	93668	93716	49	3572	138555	138568	14
1140	48001	48016	16	2357	93718	93742	25	3573	138571	138589	19
1141	48051	48083	33	2358	93744	93788	45	3574	138589	138629	41
1142	48096	48158	63	2359	93790	93808	19	3575	138644	138680	37
1143	48158	48176	19	2360	93811	93832	22	3576	138697	138710	14
1144	48186	48201	16	2361	93874	93901	28	3577	138712	138729	18
1145	48213	48239	27	2362	93904	93986	83	3578	138744	138761	18
1146	48241	48256	16	2363	94021	94036	16	3579	138776	138801	26
1147	48258	48278	21	2364	94038	94079	42	3580	138860	138896	37
1148	48280	48339	60	2365	94073	94086	14	3581	138898	138923	26
1149	48341	48357	17	2366	94097	94116	20	3582	138925	138965	41
1150	48359	48377	19	2367	94118	94141	24	3583	138967	139008	42
1151	48379	48393	15	2368	94140	94219	80	3584	139010	139031	22
1152	48395	48488	94	2369	94242	94257	16	3585	139029	139043	15

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
1153	48492	48510	19	2370	94264	94335	72	3586	139034	139048	15
1154	48528	48549	22	2371	94337	94356	20	3587	139041	139056	16
1155	48550	48589	40	2372	94358	94378	21	3588	139055	139074	20
1156	48636	48658	23	2373	94373	94386	14	3589	139078	139094	17
1157	48683	48697	15	2374	94384	94403	20	3590	139084	139098	15
1158	48699	48762	64	2375	94405	94422	18	3591	139092	139116	25
1159	48762	48775	14	2376	94453	94497	45	3592	139133	139147	15
1160	48773	48832	60	2377	94497	94558	62	3593	139154	139173	20
1161	48873	48886	14	2378	94560	94605	46	3594	139175	139192	18
1162	48888	48914	27	2379	94630	94724	95	3595	139204	139229	26
1163	48916	48944	29	2380	94739	94752	14	3596	139231	139255	25
1164	48969	49008	40	2381	94755	94786	32	3597	139257	139270	14
1165	49010	49024	15	2382	94800	94815	16	3598	139272	139303	32
1166	49051	49110	60	2383	94872	94901	30	3599	139315	139335	21
1167	49116	49150	35	2384	94903	94953	51	3600	139337	139372	36
1168	49151	49184	34	2385	94955	95060	106	3601	139383	139397	15
1169	49187	49200	14	2386	95070	95085	16	3602	139399	139419	21
1170	49213	49230	18	2387	95093	95110	18	3603	139423	139437	15
1171	49233	49247	15	2388	95135	95149	15	3604	139435	139492	58
1172	49267	49284	18	2389	95154	95168	15	3605	139501	139518	18
1173	49297	49310	14	2390	95170	95210	41	3606	139508	139521	14
1174	49317	49369	53	2391	95227	95257	31	3607	139571	139586	16
1175	49371	49435	65	2392	95302	95318	17	3608	139588	139622	35
1176	49444	49458	15	2393	95311	95356	46	3609	139636	139655	20

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
1177	49467	49500	34	2394	95359	95401	43	3610	139657	139673	17
1178	49510	49538	29	2395	95403	95453	51	3611	139685	139699	15
1179	49540	49559	20	2396	95450	95463	14	3612	139724	139795	72
1180	49561	49584	24	2397	95475	95491	17	3613	139796	139811	16
1181	49591	49626	36	2398	95503	95553	51	3614	139818	139834	17
1182	49628	49646	19	2399	95555	95569	15	3615	139836	139857	22
1183	49653	49737	85	2400	95583	95609	27	3616	139856	139869	14
1184	49787	49802	16	2401	95634	95668	35	3617	139859	139882	24
1185	49817	49835	19	2402	95718	95738	21	3618	139891	139920	30
1186	49841	49860	20	2403	95727	95740	14	3619	139930	139952	23
1187	49862	49883	22	2404	95836	95849	14	3620	139965	139980	16
1188	49885	49905	21	2405	95851	95872	22	3621	139982	140011	30
1189	49921	49950	30	2406	95874	95888	15	3622	140013	140031	19
1190	49961	49979	19	2407	95890	95910	21	3623	140047	140072	26
1191	49995	50051	57	2408	95912	95925	14	3624	140074	140099	26
1192	50053	50071	19	2409	95938	95969	32	3625	140101	140119	19
1193	50073	50088	16	2410	95973	95990	18	3626	140121	140135	15
1194	50132	50158	27	2411	95992	96066	75	3627	140144	140158	15
1195	50167	50183	17	2412	96073	96087	15	3628	140157	140183	27
1196	50201	50226	26	2413	96103	96120	18	3629	140185	140210	26
1197	50226	50239	14	2414	96122	96167	46	3630	140231	140262	32
1198	50259	50313	55	2415	96169	96182	14	3631	140258	140272	15
1199	50323	50341	19	2416	96183	96211	29	3632	140264	140288	25
1200	50343	50396	54	2417	96213	96234	22	3633	140290	140325	36

(continued)

Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length	Reg. A	Position in SEQ ID NO 1		Length
	from	to			from	to			from	to	
1201	50390	50403	14	2418	96246	96279	34	3634	140339	140364	26
1202	50398	50448	51	2419	96300	96334	35	3635	140369	140402	34
1203	50451	50483	33	2420	96358	96375	18	3636	140428	140451	24
1204	50489	50507	19	2421	96377	96398	22	3637	140453	140510	58
1205	50526	50548	23	2422	96424	96467	44	3638	140512	140541	30
1206	50550	50569	20	2423	96496	96518	23	3639	140556	140621	66
1207	50575	50602	28	2424	96520	96535	16	3640	140626	140651	26
1208	50606	50621	16	2425	96540	96566	27	3641	140653	140724	72
1209	50617	50630	14	2426	96572	96592	21	3642	140726	140789	64
1210	50623	50641	19	2427	96604	96646	43	3643	140802	140825	24
1211	50634	50647	14	2428	96642	96655	14	3644	140837	140861	25
1212	50644	50663	20	2429	96648	96667	20	3645	140863	140896	34
1213	50665	50684	20	2430	96681	96728	48	3646	140903	140927	25
1214	50705	50730	26	2431	96730	96781	52	3647	140958	140993	36
1215	50732	50763	32	2432	96804	96829	26	3648	141001	141014	14
1216	50766	50799	34	2433	96831	96879	49	3649	141022	141053	32
1217	50797	50823	27								

[0124] In some embodiments, the oligonucleotide comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary, such as 100% complementarity, to a corresponding target nucleic acid region present in SEQ ID NO: 1, wherein the target nucleic acid region is selected from the group consisting of region B1 to B400 in table 2

Table 2: Regions of SEQ ID NO 1 which may be targeted using oligonucleotide of the invention

Reg.	Position in SEQ ID NO 1		Length	Reg.	Position in SEQ ID NO 1		Length	Reg.	Position in SEQ ID NO 1		Length
	To	From			To	From			To	From	
B1	225	238	14	B134	60006	60029	24	B267	92908	92921	14
B2	1163	1178	16	B135	60033	60071	39	B268	92923	92941	19
B3	2526	2539	14	B136	60139	60171	33	B269	92965	92986	22
B4	2805	2820	16	B137	60193	60215	23	B270	92988	93002	15
B5	3027	3040	14	B138	60212	60225	14	B271	93044	93059	16
B6	3208	3222	15	B139	60231	60244	14	B272	93061	93076	16
B7	3212	3225	14	B140	60246	60265	20	B273	93105	93122	18
B8	3228	3241	14	B141	60267	60282	16	B274	93142	93209	68
B9	3243	3256	14	B142	60292	60309	18	B275	93227	93241	15
B10	3810	3854	45	B143	60348	60361	14	B276	93288	93305	18
B11	4664	4680	17	B144	60358	60429	72	B277	93325	93344	20
B12	5516	5529	14	B145	60427	60517	91	B278	93398	93412	15
B13	5657	5671	15	B146	60519	60545	27	B279	93572	93586	15
B14	5661	5676	16	B147	60557	60575	19	B280	94509	94522	14
B15	5964	5977	14	B148	60580	60593	14	B281	95720	95738	19
B16	6217	6234	18	B149	60595	60622	28	B282	97050	97065	16
B17	6224	6237	14	B150	60675	60690	16	B283	97079	97098	20
B18	6408	6422	15	B151	60697	60713	17	B284	97127	97194	68
B19	7300	7313	14	B152	60727	60754	28	B285	97208	97230	23
B20	7399	7412	14	B153	60756	60799	44	B286	97232	97284	53
B21	7541	7564	24	B154	60801	60817	17	B287	97286	97311	26
B22	7626	7640	15	B155	60819	60855	37	B288	97313	97362	50
B23	7662	7694	33	B156	61423	61436	14	B289	97368	97383	16
B24	7791	7806	16	B157	61592	61605	14	B290	97426	97439	14

(continued)

Reg.	Position in SEQ ID NO 1		Length	Reg.	Position in SEQ ID NO 1		Length	Reg.	Position in SEQ ID NO 1		Length
	To	From			To	From			To	From	
B25	7853	7868	16	B158	61624	61637	14	B291	98077	98090	14
B26	8206	8219	14	B159	61673	61713	41	B292	98227	98240	14
B27	8443	8456	14	B160	61715	61731	17	B293	98232	98255	24
B28	8739	8752	14	B161	61733	61752	20	B294	99151	99164	14
B29	9197	9212	16	B162	61769	61794	26	B295	99405	99418	14
B30	10189	10203	15	B163	61805	61825	21	B296	99570	99583	14
B31	10754	10768	15	B164	62101	62114	14	B297	99733	99748	16
B32	10758	10771	14	B165	62302	62315	14	B298	101829	101842	14
B33	11790	11803	14	B166	62436	62449	14	B299	101882	101895	14
B34	11870	11883	14	B167	62664	62679	16	B300	101955	101968	14
B35	11993	12007	15	B168	62993	63006	14	B301	102202	102215	14
B36	B11996	12011	16	B169	63098	63111	14	B302	103310	103325	16
B37	12017	12040	24	B170	63347	63367	21	B303	103653	103666	14
B38	12095	12108	14	B171	63371	63396	26	B304	103908	103923	16
B39	12345	12358	14	B172	63385	63398	14	B305	103912	103928	17
B40	12721	12734	14	B173	63526	63539	14	B306	103917	103933	17
B41	13372	13386	15	B174	65032	65045	14	B307	104971	104984	14
B42	13489	13505	17	B175	66556	66569	14	B308	105217	105230	14
B43	15576	15590	15	B176	67158	67183	26	B309	105233	105250	18
B44	15617	15632	16	B177	67181	67194	14	B310	105443	105457	15
B45	15840	15853	14	B178	68007	68021	15	B311	105544	105559	16
B46	16041	16054	14	B179	68644	68657	14	B312	106047	106071	25
B47	16207	16222	16	B180	69294	69317	24	B313	106061	106074	14
B48	16308	16321	14	B181	69306	69323	18	B314	106093	106107	15

(continued)

Reg.	Position in SEQ ID NO 1		Length	Reg.	Position in SEQ ID NO 1		Length	Reg.	Position in SEQ ID NO 1		Length
	To	From			To	From			To	From	
B49	16349	16362	14	B182	69353	69366	14	B315	106114	106130	17
B50	16463	16479	17	B183	70497	70511	15	B316	106243	106256	14
B51	16528	16542	15	B184	71600	71613	14	B317	106251	106264	14
B52	16543	16556	14	B185	71887	71905	19	B318	106840	106855	16
B53	20495	20508	14	B186	72259	72272	14	B319	108113	108130	18
B54	20617	20630	14	B187	72589	72602	14	B320	108325	108338	14
B55	20960	20977	18	B188	72783	72796	14	B321	108856	108869	14
B56	21465	21479	15	B189	73528	73541	14	B322	109109	109122	14
B57	21491	21508	18	B190	73783	73800	18	B323	109113	109127	15
B58	23479	23496	18	B191	74907	74920	14	B324	109116	109132	17
B59	23741	23755	15	B192	75965	75981	17	B325	110301	110314	14
B60	25236	25249	14	B193	75983	75998	16	B326	110315	110328	14
B61	25323	25336	14	B194	76004	76020	17	B327	110317	110330	14
B62	25447	25462	16	B195	76110	76166	57	B328	112528	112546	19
B63	25588	25601	14	B196	76186	76205	20	B329	112607	112620	14
B64	25853	25867	15	B197	76234	76253	20	B330	114775	114788	14
B65	25885	25898	14	B198	76261	76280	20	B331	116322	116335	14
B66	26280	26293	14	B199	76369	76382	14	B332	116968	116981	14
B67	26388	26404	17	B200	77139	77152	14	B333	117788	117801	14
B68	26416	26450	35	B201	77409	77422	14	B334	118034	118057	24
B69	26687	26702	16	B202	77478	77524	47	B335	118230	118246	17
B70	26706	26719	14	B203	77526	77590	65	B336	118235	118248	14
B71	26783	26796	14	B204	77628	77641	14	B337	118870	118883	14
B72	27039	27052	14	B205	77688	77701	14	B338	119755	119784	30

(continued)

Reg.	Position in SEQ ID NO 1		Length	Reg.	Position in SEQ ID NO 1		Length	Reg.	Position in SEQ ID NO 1		Length
	To	From			To	From			To	From	
B73	27251	27265	15	B206	78275	78308	34	B339	119786	119800	15
B74	28683	28698	16	B207	78310	78332	23	B340	120363	120406	44
B75	29302	29315	14	B208	78340	78356	17	B341	120504	120517	14
B76	29304	29317	14	B209	78358	78371	14	B342	121161	121174	14
B77	29308	29321	14	B210	78373	78395	23	B343	121330	121347	18
B78	29532	29545	14	B211	78397	78440	44	B344	121338	121351	14
B79	29974	29987	14	B212	78442	78455	14	B345	123417	123430	14
B80	30054	30068	15	B213	78475	78489	15	B346	123464	123481	18
B81	30267	30281	15	B214	78696	78709	14	B347	125026	125042	17
B82	30623	30638	16	B215	78847	78860	14	B348	127046	127071	26
B83	30628	30641	14	B216	79493	79516	24	B349	127090	127103	14
B84	30814	30827	14	B217	79705	79718	14	B350	127311	127324	14
B85	30881	30894	14	B218	81009	81054	46	B351	127354	127367	14
B86	32459	32478	20	B219	81353	81367	15	B352	127363	127379	17
B87	37299	37315	17	B220	81970	81986	17	B353	127399	127412	14
B88	39083	39096	14	B221	81991	82006	16	B354	127863	127876	14
B89	39370	39383	14	B222	82042	82106	65	B355	128134	128148	15
B90	39659	39672	14	B223	82278	82291	14	B356	128280	128310	31
B91	40814	40831	18	B224	82716	82735	20	B357	128343	128368	26
B92	40851	40864	14	B225	84314	84328	15	B358	128444	128457	14
B93	41782	41795	14	B226	85628	85665	38	B359	128446	128469	24
B94	41873	41886	14	B227	86226	86239	14	B360	128498	128511	14
B95	42037	42050	14	B228	86237	86253	17	B361	128511	128524	14
B96	42048	42063	16	B229	86566	86579	14	B362	129892	129905	14

(continued)

Reg.	Position in SEQ ID NO 1		Length	Reg.	Position in SEQ ID NO 1		Length	Reg.	Position in SEQ ID NO 1		Length
	To	From			To	From			To	From	
B97	42096	42116	21	B230	86945	86959	15	B363	130261	130283	23
B98	42959	42973	15	B231	87337	87358	22	B364	130375	130388	14
B99	43165	43178	14	B232	87662	87675	14	B365	130415	130428	14
B100	45926	45939	14	B233	89424	89439	16	B366	130634	130650	17
B101	48163	48176	14	B234	89972	89985	14	B367	130667	130717	51
B102	52732	52745	14	B235	90782	90795	14	B368	130719	130764	46
B103	52984	53015	32	B236	90939	90953	15	B369	130783	130796	14
B104	54404	54420	17	B237	90942	90955	14	B370	130798	130820	23
B105	55294	55320	27	B238	90965	90981	17	B371	130840	130861	22
B106	55337	55350	14	B239	91101	91115	15	B372	130975	130994	20
B107	55420	55434	15	B240	92083	92096	14	B373	131112	131132	21
B108	55487	55501	15	B241	92164	92177	14	B374	131142	131161	20
B109	55623	55638	16	B242	92179	92192	14	B375	131233	131246	14
B110	56195	56214	20	B243	92194	92210	17	B376	131729	131743	15
B111	56584	56597	14	B244	92212	92236	25	B377	132754	132767	14
B112	57267	57282	16	B245	92245	92260	16	B378	132924	132937	14
B113	58126	58139	14	B246	92262	92302	41	B379	133174	133190	17
B114	58170	58183	14	B247	92304	92321	18	B380	133198	133212	15
B115	58295	58309	15	B248	92323	92366	44	B381	133207	133222	16
B116	58658	58671	14	B249	92375	92389	15	B382	133476	133489	14
B117	58906	58921	16	B250	92392	92405	14	B383	133479	133492	14
B118	58988	59005	18	B251	92407	92426	20	B384	133491	133531	41
B119	59024	59045	22	B252	92442	92459	18	B385	133533	133550	18
B120	59191	59207	17	B253	92497	92516	20	B386	133555	133594	40

(continued)

Reg.	Position in SEQ ID NO 1		Length	Reg.	Position in SEQ ID NO 1		Length	Reg.	Position in SEQ ID NO 1		Length
	To	From			To	From			To	From	
B121	59236	59251	16	B254	92578	92591	14	B387	134160	134173	14
B122	59298	59312	15	B255	92599	92612	14	B388	134165	134178	14
B123	59358	59378	21	B256	92614	92651	38	B389	134533	134546	14
B124	59400	59413	14	B257	92659	92684	26	B390	136724	136737	14
B125	59434	59447	14	B258	92686	92699	14	B391	137438	137463	26
B126	59589	59602	14	B259	92704	92726	23	B392	137878	137891	14
B127	59620	59642	23	B260	92731	92750	20	B393	138082	138097	16
B128	59718	59743	26	B261	92752	92774	23	B394	138233	138252	20
B129	59826	59841	16	B262	92780	92795	16	B395	138930	138943	14
B130	59843	59864	22	B263	92800	92813	14	B396	138947	138960	14
B131	59882	59906	25	B264	92839	92858	20	B397	138950	138963	14
B132	59930	59958	29	B265	92860	92891	32	B398	139502	139518	17
B133	59959	60004	46	B266	92893	92906	14	B399	139508	139521	14
								B400	140978	140991	14

[0125] In certain embodiments the oligonucleotide or contiguous nucleotide sequence is complementary to a region (or sub-sequence)(or sub-sequence) of the target nucleic acid, wherein the target nucleic acid region is selected from the group consisting of position 1589-10889, 46089-53989 and 60789-62489 of SEQ ID NO: 1.

[0126] In one embodiment the oligonucleotide comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90%, such as 100% complementary to a target nucleic acid sequence of position 55319 to 141053 of SEQ ID NO: 1.

[0127] In one embodiment the oligonucleotide comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90%, such as 100% complementary to a target nucleic acid sequence of position 1 to 55318 of SEQ ID NO: 1.

[0128] In some embodiments, the oligonucleotide comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary to a sub-sequence of the target nucleic acid selected from the group corresponding to positions : 55319-76274, 77483-77573, 92157-93403 and 97056-97354 of SEQ ID NO: 1.

[0129] In some embodiments the oligonucleotide a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary to a sub-sequence of the target nucleic acid selected from the group corresponding to positions: 60821-60849, 77567-77583, 92323-92339 and 97156-97172 of SEQ ID NO: 1.

[0130] In some embodiments the oligonucleotide a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary to a sub-sequence of the target nucleic acid corresponding to positions: 5218-5240 of SEQ ID NO: 1.

[0131] In some embodiments the oligonucleotide a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary to a sub-sequence of the target nucleic acid corresponding to positions: 5782-5803 of SEQ ID NO: 1.

[0132] In some embodiments the oligonucleotide a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary to a sub-sequence of the target nucleic acid corresponding to positions: 8113-8139 of SEQ ID NO: 1.

[0133] In some embodiments the oligonucleotide a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary to a sub-sequence of the target nucleic acid corresponding to positions: 9200-9250 of SEQ ID NO: 1.

[0134] In some embodiments the oligonucleotide a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary to a sub-sequence of the target nucleic acid corresponding to positions: 11505-11555 of SEQ ID NO: 1.

[0135] In some embodiments the oligonucleotide a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary to a sub-sequence of the target nucleic acid corresponding to positions: 13223-13242 of SEQ ID NO: 1.

[0136] In some embodiments the oligonucleotide a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary to a sub-sequence of the target nucleic acid corresponding to positions 15100-15150 of SEQ ID NO: 1.

[0137] In some embodiments the oligonucleotide a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary to a sub-sequence of the target nucleic acid corresponding to positions 15113-15180 of SEQ ID NO: 1.

[0138] In some embodiments the oligonucleotide a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary to a sub-sequence of the target nucleic acid corresponding to positions 29635-29705 of SEQ ID NO: 1.

[0139] In some embodiments the oligonucleotide a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary to a sub-sequence of the target nucleic acid corresponding to positions 30590-30740 of SEQ ID NO: 1.

[0140] In some embodiments the oligonucleotide a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary to a sub-sequence of the target nucleic acid corresponding to positions 39800-39855 of SEQ ID NO: 1.

[0141] In some embodiments the oligonucleotide a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary to a sub-sequence of the target nucleic acid to positions 44435-44460 of SEQ ID NO: 1.

[0142] In some embodiments the oligonucleotide a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary to a sub-sequence of the target nucleic acid to positions 45245-45270 of SEQ ID NO: 1.

[0143] In some embodiments the oligonucleotide a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary to a sub-sequence of the target nucleic acid to positions 46380-46430 of SEQ ID NO: 1.

[0144] In some embodiments the oligonucleotide a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary to a sub-sequence of the target nucleic acid to positions 68915-68940 of SEQ ID NO: 1.

[0145] In some embodiments, the oligonucleotide comprises or consists of 8 to 35 nucleotides in length, such as from 10 to 30, such as 11 to 22, such as from 12 to 18, such as from 13 to 17 or 14 to 16 contiguous nucleotides in length.

In a preferred embodiment, the oligonucleotide comprises or consists of 15 to20 nucleotides in length.

[0146] In some embodiments, the oligonucleotide or contiguous nucleotide sequence thereof comprises or consists of 22 or less nucleotides, such as 20 or less nucleotides, such as 18 or less nucleotides, such as 14, 15, 16 or 17 nucleotides. It is to be understood that any range given herein includes the range endpoints. Accordingly, if an oligonucleotide is said to include from 10 to 30 nucleotides, both 10 and 30 nucleotides are included.

[0147] In some embodiments, the contiguous nucleotide sequence comprises or consists of 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 a preferred embodiment, the oligonucleotide comprises or consists of 16, 17, 18 or 19 nucleotides in length.

[0148] In some embodiments, the antisense oligonucleotide or contiguous nucleotide sequence comprises or consists of of 10 to 30 nucleotides in length with at least 90% identity, preferably 100% identity to a sequence selected from the group consisting of SEQ ID NO: 4 to 150 (see motif sequences listed in table 3 in the Examples section).

[0149] In some embodiments, the antisense oligonucleotide or contiguous nucleotide sequence comprises or consists of of 10 to 30 nucleotides in length with at least 90% identity, preferably 100% identity to a sequence selected from the group consisting of SEQ ID NO: 4 to 818 (see motif sequences listed in table 3 in the Examples section).

[0150] In some embodiments, the antisense oligonucleotide or contiguous nucleotide sequence comprises or consists of of 10 to 30 nucleotides in length with at least 90% identity, preferably 100% identity to a sequence selected from the group consisting of SEQ ID NO: 4 to 678 (see motif sequences listed in table 3 in the Examples section).

[0151] In some embodiments, the antisense oligonucleotide or contiguous nucleotide sequence comprises or consists of of 10 to 30 nucleotides in length with at least 90% identity, preferably 100% identity to a sequence selected from the group consisting of SEQ ID NO: 166, 167, 167 or 169 (see motif sequences listed in table 3 in the Examples section).

[0152] In some embodiments, the antisense oligonucleotide or contiguous nucleotide sequence comprises or consists of of 10 to 30 nucleotides in length with at least 90% identity, preferably 100% identity to a sequence selected from the group consisting of SEQ ID NO: 570, 571 ,572, 679, 680, 681, 682 and 683 (see motif sequences listed in table 3 in the Examples section).

[0153] In some embodiments, the antisense oligonucleotide or contiguous nucleotide sequence comprises or consists of of 10 to 30 nucleotides in length with at least 90% identity, preferably 100% identity to a sequence selected from the group consisting of SEQ ID NO: 34, 186, 187, 188, 573, 574, 575, 576, 572, 684, 685, 686, 687, 688, 689, 690, 691, 692, 963, 964, 965 and 696 (see motif sequences listed in table 3 in the Examples section).

[0154] In some embodiments, the antisense oligonucleotide or contiguous nucleotide sequence comprises or consists of of 10 to 30 nucleotides in length with at least 90% identity, preferably 100% identity to a sequence selected from the group consisting of SEQ ID NO: 35, 199, 200, 201, 202, 203, 204, 205, 206, 207, 209 and 210 or SEQ ID NO: 582, 583 and 584 (see motif sequences listed in table 3 in the Examples section).

[0155] In some embodiments, the antisense oligonucleotide or contiguous nucleotide sequence comprises or consists of of 10 to 30 nucleotides in length with at least 90% identity, preferably 100% identity to a sequence selected from the group consisting of SEQ ID NO: 221, 222, 223, 224, 225, 585, 586, 587, 588, 589, 698, 699,700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717 and 718 (see motif sequences listed in table 3 in the Examples section).

[0156] In some embodiments, the antisense oligonucleotide or contiguous nucleotide sequence comprises or consists of of 10 to 30 nucleotides in length with at least 90% identity, preferably 100% identity to a sequence selected from the group consisting of SEQ ID NO: 236, 237, 238, 239, 240 and 590.

[0157] In some embodiments, the antisense oligonucleotide or contiguous nucleotide sequence comprises or consists of of 10 to 30 nucleotides in length with at least 90% identity, preferably 100% identity to a sequence selected from the group consisting of SEQ ID NO: 241, 591 and 719 (see motif sequences listed in table 3 in the Examples section).

[0158] In some embodiments, the antisense oligonucleotide or contiguous nucleotide sequence comprises or consists of of 10 to 30 nucleotides in length with at least 90% identity, preferably 100% identity to a sequence selected from the group consisting of SEQ ID NO: 46, 47,48, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304,305, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626,627, 628, 629, 630, 631, 632, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 800, 800, 800, 800, 801, 801, 802, 803, 804, 805, 806 and 807 (see motif sequences listed in table 3 in the Examples section).

[0159] In some embodiments, the antisense oligonucleotide or contiguous nucleotide sequence comprises or consists of of 10 to 30 nucleotides in length with at least 90% identity, preferably 100% identity to a sequence selected from the group consisting of SEQ ID NO: 331, 332, 638, 639, 640, 808, 809, 810 ,811 ,812, 813, 814 and 815 (see motif sequences listed in table 3 in the Examples section).

[0160] In some embodiments, the antisense oligonucleotide or contiguous nucleotide sequence comprises or consists of of 10 to 30 nucleotides in length with at least 90% identity, preferably 100% identity to a sequence selected from the group consisting of SEQ ID NO: 409, 410, 411, 642, 643, 644, 645, 646, 816, 818 and 818 (see motif sequences listed in table 3 in the Examples section).

[0161] It is understood that the contiguous nucleobase sequences (motif sequence) can be modified to for example increase nuclease resistance and/or binding affinity to the target nucleic acid. Modifications are described in the definitions and in the "Oligonucleotide design" section. Table 3 lists preferred designs of each motif sequence.

Oligonucleotide design

[0162] Oligonucleotide design refers to the pattern of nucleoside sugar modifications in the oligonucleotide sequence. The oligonucleotides of the invention comprise sugar-modified nucleosides and may also comprise DNA or RNA nucleosides. In some embodiments, the oligonucleotide comprises sugar-modified nucleosides and DNA nucleosides. Incorporation of modified nucleosides into the oligonucleotide of the invention may enhance the affinity of the oligonucleotide for the target nucleic acid. In that case, the modified nucleosides can be referred to as affinity enhancing modified nucleotides.

[0163] In an embodiment, the oligonucleotide comprises at least 1 modified nucleoside, such as at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15 or at least 16 modified nucleosides. In an embodiment the oligonucleotide comprises from 1 to 10 modified nucleosides, such as from 2 to 9 modified nucleosides, such as from 3 to 8 modified nucleosides, such as from 4 to 7 modified nucleosides, such as 6 or 7 modified nucleosides. In some embodiments, at least 1 of the modified nucleosides is a locked nucleic acid (LNA), such as at least 2, such as at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 of the modified nucleosides are LNA. In a still further embodiment all the modified nucleosides are LNA.

[0164] In an embodiment, the oligonucleotide of the invention may comprise modifications, which are independently selected from these three types of modifications (modified sugar, modified nucleobase and modified internucleoside linkage) or a combination thereof. Preferably the oligonucleotide comprises one or more sugar modified nucleosides, such as 2' sugar modified nucleosides. Preferably the oligonucleotide of the invention comprise the one or more 2' sugar modified nucleoside independently selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA, 2'-amino-DNA, 2'-fluoro-DNA, arabino nucleic acid (ANA), 2'-fluoro-ANA and LNA nucleosides. Even more preferably the the one or more modified nucleoside is LNA.

[0165] In a further embodiment the oligonucleotide comprises at least one modified internucleoside linkage. In a preferred embodiment the the internucleoside linkages within the contiguous nucleotide sequence are phosphorothioate or boranophosphate internucleoside linkages.

[0166] In some embodiments, the oligonucleotide of the invention comprise at least one modified nucleoside which is a 2'-MOE-RNA, such as 2, 3, 4, 5, 6, 7, 8, 9 or 10 2'-MOE-RNA nucleoside units. In some embodiments, at least one of said modified nucleoside is 2'-fluoro DNA, such as 2, 3, 4, 5, 6, 7, 8, 9 or 10 2'-fluoro-DNA nucleoside units.

[0167] In some embodiments, the oligonucleotide of the invention comprises at least one LNA unit, such as 1, 2, 3, 4, 5, 6, 7, or 8 LNA units, such as from 2 to 6 LNA units, such as from 3 to 7 LNA units, 4 to 8 LNA units or 3, 4, 5, 6 or 7 LNA units. In some embodiments, all the modified nucleosides are LNA nucleosides. In a further embodiment, the oligonucleotide 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 a further embodiment, all LNA cytosine units are 5-methyl-cytosine. In a preferred embodiment the oligonucleotide or contiguous nucleotide sequence has at least 1 LNA unit at the 5' end and at least 2 LNA units at the 3' end of the nucleotide sequence.

[0168] In some embodiments, the oligonucleotide of the invention comprises at least one LNA unit and at least one 2' substituted modified nucleoside.

[0169] In some embodiments of the invention, the oligonucleotide comprise both 2' sugar modified nucleosides and DNA units. Preferably the oligonucleotide comprise both LNA and DNA units.

[0170] Preferably, the combined total of LNA and DNA units is 8-30, such as 10 - 25, preferably 12-22, such as 12 - 18, even more preferably 11-16. In some embodiments of the invention, the nucleotide sequence of the oligonucleotide, such as the contiguous nucleotide sequence consists of at least one or two LNA units and the remaining nucleotide units are DNA units. In some embodiments the oligonucleotide comprises only LNA nucleosides and naturally occurring nucleosides (such as RNA or DNA, most preferably DNA nucleosides), optionally with modified internucleoside linkages such as phosphorothioate.

[0171] In an embodiment of the invention the oligonucleotide of the invention is capable of recruiting RNase H.

Gapmer design

[0172] In a preferred embodiment the oligonucleotide of the invention has a gapmer design or structure also referred herein merely as "Gapmer". In a gapmer structure the oligonucleotide comprises at least three distinct structural regions a 5'-flank, a gap and a 3'-flank, F-G-F' in '5 -> 3' orientation. In this design, flanking regions F and F' (also termed wing regions) comprise a contiguous stretch of modified nucleosides, which are complementary to the UBE3A target nucleic acid, while the gap region, G, comprises a contiguous stretch of nucleotides which are capable of recruiting a nuclease, preferably an endonuclease such as RNase, for example RNase H, when the oligonucleotide is in duplex with the target nucleic acid. Nucleosides which are capable of recruiting a nuclease, in particular RNase H, can be selected from the group consisting of DNA, alpha-L-oxy-LNA, 2'-Flouro-ANA and UNA. Regions F and F', flanking the 5' and 3' ends of region G, preferably comprise non-nuclease recruiting nucleosides (nucleosides with a 3' endo structure), more preferably one or more affinity enhancing modified nucleosides. In some embodiments, the 3' flank comprises at least one LNA nucleoside, preferably at least 2 LNA nucleosides. In some embodiments, the 5' flank comprises at least one LNA nucleoside. In some embodiments both the 5' and 3' flanking regions comprise a LNA nucleoside. In some embodiments all the nucleosides in the flanking regions are LNA nucleosides. In other embodiments, the flanking regions may comprise both LNA nucleosides and other nucleosides (mixed flanks), such as DNA nucleosides and/or non-LNA modified nucleosides, such as 2' substituted nucleosides. In this case the gap is defined as a contiguous sequence of at least 5 RNase H recruiting nucleosides (nucleosides with a 2' endo structure, preferably DNA) flanked at the 5' and 3' end by an affinity enhancing modified nucleoside, preferably LNA, such as beta-D-oxy-LNA. Consequently, the nucleosides of the 5' flanking region and the 3' flanking region which are adjacent to the gap region are modified nucleosides, preferably non-nuclease recruiting nucleosides. In oligonucleotides with mixed flanks where the flanks comprise DNA the 5' and 3' nucleosides are modified nucleosides.

Region F

[0173] Region F (5' flank or 5' wing) attached to the '5 end of region G comprises, contains or consists of at least one modified nucleoside such as at least 2, at least 3, at least 4, at least 5, at least 6, at least 7 modified nucleosides. In an embodiment region F comprises or consists of from 1 to 7 modified nucleosides, such as from 2 to 6 modified nucleosides, such as from 2 to 5 modified nucleosides, such as from 2 to 4 modified nucleosides, such as from 1 to 3 modified nucleosides, such as 1, 2, 3 or 4 modified nucleosides. In a further embodiment further additional nucleosides may be attached to the '5 end of region F, representing a region D preferably comprising 1, 2 or 3 nucleoside units, such as DNA nucleosides. Region D can take the function of a biocleavable (B) linker described in the definition of "Linkers ".

[0174] In some embodiments, the modified nucleosides in region F have a 3' endo structure.

[0175] In an embodiment, one or more of the modified nucleosides in region F are 2' modified nucleosides.

[0176] In a further embodiment one or more of the 2' modified nucleosides in region F are selected from 2'-O-alkyl-RNA units, 2'-O-methyl-RNA, 2'-amino-DNA units, 2'-fluoro-DNA units, 2'-alkoxy-RNA, MOE units, LNA units, arabino nucleic acid (ANA) units and 2'-fluoro-ANA units.

[0177] In one embodiment of the invention all the modified nucleosides in region F are LNA nucleosides. In a further embodiment the LNA nucleosides in region F are independently selected from the group consisting of oxy-LNA, thio-LNA, amino-LNA, cET, and/or ENA, in either the beta-D or alpha-L configurations or combinations thereof. In a preferred embodiment region F has at least 1 beta-D-oxy LNA unit, at the 5' end of the contiguous sequence.

Region G

[0178] Region G (gap region) preferably comprise, contain or consist of at least 4, such as at least 5, such as at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15 or at least 16 consecutive nucleosides capable of recruiting the aforementioned nuclease, in particular RNaseH. In a further embodiment region G comprise, contain or consist of from 5 to 12, or from 6 to 10 or from 7 to 9, such as 8 consecutive nucleotide units capable of recruiting aforementioned nuclease.

[0179] The nucleoside units in region G, which are capable of recruiting nuclease are in an embodiment selected from the group consisting of DNA, alpha-L-LNA, C4' alkylated DNA (as described in PCT/EP2009/050349 and Vester et al., Bioorg. Med. Chem. Lett. 18 (2008) 2296 - 2300), arabinose derived nucleosides like ANA and 2'F-ANA (Mangos et al. 2003 J. AM. CHEM. SOC. 125, 654-661), UNA (unlocked nucleic acid) (as described in Fluiter et al., Mol. Biosyst., 2009, 10, 1039). UNA is unlocked nucleic acid, typically where the bond between C2 and C3 of the ribose has been removed, forming an unlocked "sugar" residue.

[0180] In a still further embodiment at least one nucleoside unit in region G is a DNA nucleoside unit, such as from 1 to 16 DNA units, such as 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 DNA units, preferably from 2 to 13 DNA units, such as from 4 to 12 DNA units, more preferably from 5 to 11, or from 10 to 16, 11 to 15 or 12 to 14 DNA units. In some embodiments, region G consists of 100% DNA units. In a preferred embodiment G consists of , most preferably 10, 11, 12, 13, 14 or 15 DNA units.

[0181] In further embodiments the region G may consist of a mixture of DNA and other nucleosides capable of mediating RNase H cleavage. Region G may consist of at least 50% DNA, more preferably 60 %, 70% or 80 % DNA, and even more preferred 90% or 95% DNA.

[0182] In a still further embodiment at least one nucleoside unit in region G is an alpha-L-LNA nucleoside unit, such as at least one alpha-L-LNA unit, such as 2, 3, 4, 5, 6, 7, 8 or 9 alpha-L-LNA units. In a further embodiment, region G comprises the least one alpha-L-LNA is alpha-L-oxy-LNA unit. In a further embodiment region G comprises a combination of DNA and alpha-L-LNA nucleoside units.

[0183] In some embodiments the size of the contiguous sequence in region G may be longer, such as 15, 16, 17, 18, 19 or 20 nucleoside units.

[0184] In some embodiments, nucleosides in region G have a 2' endo structure.

Region F'

[0185] Region F' (3' flank or 3' wing) attached to the '3 end of region G comprises, contains or consists of at least one modified nucleoside such as at least 2, at least 3, at least 4, at least 5, at least 6, at least 7 modified nucleosides. In an embodiment region F' comprise or consist of from 1 to 7 modified nucleosides, such as from 2 to 6 modified nucleoside, such as from 2 to 4 modified nucleosides, such as from 1 to 3 modified nucleosides, such as 1, 2, 3 or 4 modified nucleosides. In a further embodiment further additional nucleosides attached to the '3 end of region F', representing a region D', preferably comprising 1, 2 or 3 nucleoside units, such as DNA nucleosides. Region D' can take the function of a biocleavable (B) linker described, in the section "Linkers".

[0186] In some embodiments, the modified nucleosides in region F' have a 3' endo structure.

[0187] In a preferred embodiment, modified nucleosides in region F' is LNA.

[0188] In a further embodiment modified nucleosides in region F' are selected from 2'-O-alkyl-RNA units, 2'-O-methyl-RNA, 2'-amino-DNA units, 2'-fluoro-DNA units, 2'-alkoxy-RNA, MOE units, LNA units, arabino nucleic acid (ANA) units and 2'-fluoro-ANA units.

[0189] In one embodiment of the invention all the modified nucleosides in region F' are LNA nucleosides. In a further embodiment the LNA nucleosides in region F' are independently selected from the group consisting of oxy-LNA, thio-LNA, amino-LNA, cET and/or ENA, in either the beta-D or alpha-L configurations or combinations thereof. In a preferred embodiment region F' has at least 2 beta-D-oxy LNA unit, at the 3' end of the contiguous sequence.

Region D and D'

[0190] Region D and D' can be attached to the 5' end of region F or the 3' end of region F', respectively.

[0191] Region D or D' may independently comprise 1, 2, 3, 4 or 5 additional nucleotides, which may be complementary or non-complementary to the target nucleic acid. In this respect the oligonucleotide of the invention, may in some embodiments comprise a contiguous nucleotide sequence capable of modulating the target which is flanked at the 5' and/or 3' end by additional nucleotides. Such additional nucleotides may serve as a nuclease susceptible biocleavable linker (see definition of linkers). In some embodiments the additional 5' and/or 3' end nucleotides are linked with phosphodiester linkages, and may be DNA or RNA. In another embodiment, the additional 5' and/or 3' end nucleotides are modified nucleotides which may for example be included to enhance nuclease stability or for ease of synthesis. In an embodiment of the oligonucleotide of the invention, comprises a region D and/or D' in addition to the contiguous nucleotide sequence.

[0192] The gapmer oligonucleotide of the present invention can be represented by the following formulae:

F-G-F'; in particular F_{1-7}-G_{4-12}-F'_{1-7}
D-F-G-F', in particular D_{1-3}-F_{1-7}-G_{4-12}-F'_{1-7}
F-G-F'-D', in particular F_{1-7}-G_{4-12}-F'_{1-7}-D'_{1-3}
D-F-G-F'-D', in particular D_{1-3}-F_{1-7}-G_{4-12}-F'_{1-7}-D'_{1-3}

[0193] The preferred number and types of nucleosides in regions F, G and F', D and D' have been described above. The design of the individual oligonucleotide may also have profound impact on the properties of the oligonucleotide in its use for modulating expression of UBE3A.

[0194] In some embodiments the oligonucleotide is a gapmer consisting of 14, 15, 16, 17, 18, 19 or 20 nucleotides in length, wherein each of regions F and F' independently consists of 2, 3 or 4 modified nucleoside units complementary to a part of the human SNHG14 long non-coding RNA which is antisense to the UBE3A pre-mRNA (the target nucleic acid) and region G consists of 10, 11, 12 ,13, 14 or 15 nucleoside units, capable of recruiting nuclease when in duplex with the target nucleic acid.

[0195] In a further embodiments, the oligonucleotide is a gapmer wherein each of regions F and F' independently consists of 2, 3, 4 or 5 modified nucleoside units, such as nucleoside units containing a 2'-O-methoxyethyl-ribose sugar (2'-MOE) or nucleoside units containing a 2'-fluoro-deoxyribose sugar and/or LNA units, and region G consists of 9, 10, 11, 12,13, 14 or 15 nucleoside units, such as DNA units or other nuclease recruiting nucleosides such as alpha-L-LNA or a mixture of DNA and nuclease recruiting nucleosides.

[0196] In a further specific embodiment, the oligonucleotide is a gapmer wherein each of regions F and F' region consists of two LNA units each, and region G consists of 10, 11, 12, 13, 14 or 15 nucleoside units, preferably DNA units. Specific gapmer designs of this nature include 2-10-2, 2-11-2, 2-12-2, 2-13-2, 2-14-2 and 2-15-2.

[0197] In a further specific embodiment, the oligonucleotide is a gapmer wherein each of regions F and F' independently consists of three LNA units, and region G consists of 10, 11, 12,13, 14 or 15 nucleoside units, preferably DNA units. Specific gapmer designs of this nature include 3-10-3, 3-11-3, 3-12-3, 3-13-3, 3-14-3 and 3-15-3.

[0198] In a further specific embodiment, the oligonucleotide is a gapmer wherein each of regions F and F' consists of four LNA units each, and region G consists of 10, 11, 12,13, 14 or 15 nucleoside units, preferably DNA units. Specific gapmer designs of this nature include 4-10-4, 4-11-4, 4-12-4, 4-13-4, 4-14-4 and 4-15-4.

[0199] Specific gapmer designs of this nature include F-G-F' designs selected from a group consisting of a gap with 10 nucleosides and independently 1 to 4 modified nucleosides in the wings including 1-10-1, 2-10-1, 1-10-2, 1-10-3, 3-10-1, 1-10-4, 4-10-1, 2-10-2, 2-10-3, 3-10-2, 2-10-4, 4-10-2, 3-10-3, 3-10-4, 4-10-3 and 4-10-4 gapmers.

[0200] Specific gapmer designs of this nature include F-G-F' designs selected from a group consisting of a gap with 11 nucleosides and independently 1 to 4 modified nucleosides in the wings including, 1-11-1, 2-11-1, 1-11-2, 1-11-3, 3-11-1, 1-11-4, 4-11-1, 2-11-2, 2-11-3, 3-11-2, 2-11-4, 4-11-2, 3-11-3, 3-11-4, 4-11-3 and 4-11-4 gapmers.

[0201] Specific gapmer designs of this nature include F-G-F' designs selected from a group consisting of a gap with 12 nucleosides including, 1-12-1, 2-12-1, 1-12-2, 1-12-3, 3-12-1, 1-12-4, 4-12-1, 2-12-2, 2-12-3, 3-12-2, 2-12-4, 4-12-2, 3-12-3, 3-12-4, 4-12-3 and 4-12-4 gapmers.

[0202] Specific gapmer designs of this nature include F-G-F' designs selected from a group consisting of a gap with 13 nucleosides and independently 1 to 4 modified nucleosides in the wings including 1-13-1, 1-13-2, 1-13-3, 3-13-1, 1-13-4, 4-13-1,2-13-1, 2-13-2, 2-13-3, 3-13-2, 2-13-4, , 4-13-2, 3-13-3, 3-13-4, 4-13-3, and 4-13-4 gapmers.

[0203] Specific gapmer designs of this nature include F-G-F' designs selected from a group consisting of a gap with 14 nucleosides and independently 1 to 4 modified nucleosides in the wings including 1-14-1, 1-14-2, 2-14-1, 1-14-3, 3-14-1, 1-14-4, 4-14-1, 2-14-2, 2-14-3, 3-14-2 2-14-4, 4-14-2, 3-14-3, 3-14-4 and 4-14-3 gapmers.

[0204] Specific gapmer designs of this nature include F-G-F' designs selected from a group consisting of a gap with 15 nucleosides and independently 1 to 4 modified nucleosides in the wings including 1-15-1, 1-15-2, 2-15-1, 1-15-3, 3-15-1, 1-15-4, 4-15-1, 2-15-2, 2-15-3, 3-15-2 2-15-4, 4-15-2, 3-15-3, 3-15-4 and 4-15-3 gapmers.

[0205] Specific gapmer designs of this nature include F-G-F' designs selected from a group consisting of a gap with 16 nucleosides and independently 1 to 4 modified nucleosides in the wings including 1-16-1, 1-16-2, 2-16-1, 1-15-3, 3-16-1, 1-16-4, 4-16-1, 2-16-2, 2-16-3, 3-16-2 2-16-4, 4-16-2, 3-16-3, 3-16-4 and 4-16-3 gapmers.

[0206] In some embodiments the F-G-F' design is selected from 2-10-4, 3-10-3 and 4-10-2.

[0207] In some embodiments the F-G-F' design is selected from 2-11-4, 3-11-2, 3-11-3 and 4-11-2.

[0208] In some embodiments the F-G-F' design is selected from 2-12-2, 2-12-3, 2-12-4, 3-12-2, 3-12-3, and 4-12-2.

[0209] In some embodiments the F-G-F' design is selected from 2-13-2, 2-13-3, 2-13-4, 3-13-3 and 4-13-2.

[0210] In some embodiments the F-G-F' design is selected from 2-14-2, 2-14-4, 3-14-3 and 4-14-2.

[0211] In some embodiments the F-G-F' design is selected from 2-15-2 and 2-16-2.

[0212] In some embodiments the F-G-F' design is selected from the designs indicated in table 3.

[0213] In all instances the F-G-F' design may further include region D and/or D', which may have 1, 2 or 3 nucleoside units, such as DNA units. Preferably, the nucleosides in region F and F' are modified nucleosides, while nucleotides in region G are preferably unmodified nucleosides.

[0214] In each design, the preferred modified nucleoside is LNA.

[0215] In another embodiment all the internucleoside linkages in the gap in a gapmer are phosphorothioate and/or boranophosphate linkages. In another embodiment all the internucleoside linkages in the flanks (F and F' region) in a gapmer are phosphorothioate and/or boranophosphate linkages. In another preferred embodiment all the internucleoside linkages in the D and D' region in a gapmer are phosphodiester linkages.

[0216] For specific gapmers as disclosed herein, when the cytosine (C) residues are annotated as 5-methyl-cytosine, in various embodiments, one or more of the C's present in the oligonucleotide may be unmodified C residues.

[0217] Further gapmer designs are disclosed in WO2004/046160 and WO2007/146511.

[0218] For certain embodiments of the invention, the oligonucleotide is selected from the group of oligonucleotide compounds in table 3.

[0219] For certain embodiments of the invention, the oligonucleotide is selected from the group of oligonucleotide compounds with CMP-ID-NO: 4_1 to 150_2.

[0220] For certain embodiments of the invention, the oligonucleotide is selected from the group of oligonucleotide compounds with CMP-ID-NO: 4_1 to 678_1.

[0221] For certain embodiments of the invention, the oligonucleotide is selected from the group of oligonucleotide compounds with CMP-ID-NO: 4_1 to 818_1 (see oligonucleotide sequences listed in table 3 in the Examples section).

[0222] For certain embodiments of the invention, the oligonucleotide is an oligonucleotide compound with CMP-ID-

NO: 155_1 or 165_1.

[0223] For certain embodiments of the invention, the oligonucleotide is selected from the group of oligonucleotide compounds with CMP-ID-NO: 169_52, 169_50 or 169_56.

[0224] For certain embodiments of the invention, the oligonucleotide is selected from the group of oligonucleotide compounds with CMP-ID-NO: 172_1, 272_1, 572_7, 572_6 or 572_5.

[0225] For certain embodiments of the invention, the oligonucleotide is an oligonucleotide compound with CMP-ID-NO: 175_1.

[0226] For certain embodiments of the invention, the oligonucleotide is an oligonucleotide compound with CMP-ID-NO: 178_1.

[0227] For certain embodiments of the invention, the oligonucleotide is selected from the group of oligonucleotide compounds with CMP-ID-NO: 573_8, 186_1 or 187_1.

[0228] For certain embodiments of the invention, the oligonucleotide is an oligonucleotide compound with CMP-ID-NO: 186_1.

[0229] For certain embodiments of the invention, the oligonucleotide is selected from the group of oligonucleotide compounds with CMP-ID-NO: 200_1, 204_1, 206_1, 35_2 or 209_1.

[0230] For certain embodiments of the invention, the oligonucleotide is selected from the group of oligonucleotide compounds with CMP-ID-NO: 585_1, 585_8, 586_9, 586_5, 586_8, 586_4 or 586_6.

[0231] For certain embodiments of the invention, the oligonucleotide is an oligonucleotide compound with CMP-ID-NO: 233_1.

[0232] For certain embodiments of the invention, the oligonucleotide is an oligonucleotide compound with CMP-ID-NO: 237_8 or 590_13.

[0233] For certain embodiments of the invention, the oligonucleotide is an oligonucleotide compound with CMP-ID-NO: 220_1.

[0234] For certain embodiments of the invention, the oligonucleotide is selected from the group of oligonucleotide compounds with CMP-ID-NO: 591_1, 592_2, 592_4 or 241_9.

[0235] For certain embodiments of the invention, the oligonucleotide is selected from the group of oligonucleotide compounds with CMP-ID-NO: 597_4, 598_4, 39_1 or 602_1.

[0236] For certain embodiments of the invention, the oligonucleotide is an oligonucleotide compound with CMP-ID-NO: 39_1.

[0237] For certain embodiments of the invention, the oligonucleotide is an oligonucleotide compound with CMP-ID-NO: 611_7.

[0238] For certain embodiments of the invention, the oligonucleotide is an oligonucleotide compound with CMP-ID-NO: 271_1 or 278_1.

[0239] For certain embodiments of the invention, the oligonucleotide is selected from the group of oligonucleotide compounds with CMP-ID-NO: 616_4, 621_2, 621_1, 622_3, 622_5, 622_4, 624_3, 624_5, 287_1, 625_6, 626_7, 626_8, 626_9, 48_1, 631_6, 631_1, 303_1, 304_6 or 304_10.

[0240] For certain embodiments of the invention, the oligonucleotide is an oligonucleotide compound with CMP-ID-NO: 636_8.

[0241] For certain embodiments of the invention, the oligonucleotide is selected from the group of oligonucleotide compounds with CMP-ID-NO: 638_8, 639_5, 331_1 or 640_4.

[0242] For certain embodiments of the invention, the oligonucleotide is selected from the group of oligonucleotide compounds with CMP-ID-NO: 359_1, 361_1, 361_5, 362_1 or 641_5.

[0243] For certain embodiments of the invention, the oligonucleotide is selected from the group of oligonucleotide compounds with CMP-ID-NO: 378_1, 379_1, 399_1.

[0244] For certain embodiments of the invention, the oligonucleotide is selected from the group of oligonucleotide compounds with CMP-ID-NO: 403_1, 405_1, 642_12, 642_13, 644_3 or 646_16.

[0245] For certain embodiments of the invention, the oligonucleotide is an oligonucleotide compound with CMP-ID-NO: 85_1 or 425_5.

[0246] For certain embodiments of the invention, the oligonucleotide is an oligonucleotide compound with CMP-ID-NO: 116_1.

[0247] For certain embodiments of the invention, the oligonucleotide is an oligonucleotide compound with CMP-ID-NO: 123_1 or 124_1.

[0248] For certain embodiments of the invention, the oligonucleotide is an oligonucleotide compound with CMP-ID-NO: 126_2.

Method of manufacture

[0249] In a further aspect, the invention provides methods for manufacturing the oligonucleotides of the invention comprising reacting nucleotide units and thereby forming covalently linked contiguous nucleotide units comprised in the oligonucleotide. Preferably, the method uses phophoramidite chemistry (see for example Caruthers et al, 1987, Methods in Enzymology vol. 154, pages 287-313). In a further embodiment the method further comprises reacting the contiguous nucleotide sequence with a conjugating moiety (ligand). In a further aspect a method is provided for manufacturing the composition of the invention, comprising mixing the oligonucleotide or conjugated oligonucleotide of the invention with a pharmaceutically acceptable diluent, solvent, carrier, salt and/or adjuvant.

Pharmaceutical Composition

[0250] In a further aspect, the invention provides pharmaceutical compositions comprising any of the aforementioned oligonucleotides and/or oligonucleotide conjugates and a pharmaceutically acceptable diluent, carrier, salt and/or adjuvant. A pharmaceutically acceptable diluent includes phosphate-buffered saline (PBS) and pharmaceutically acceptable salts include, but are not limited to, sodium and potassium salts.

[0251] WO 2007/031091 provides suitable and preferred examples of pharmaceutically acceptable diluents, carriers and adjuvants. Suitable dosages, formulations, administration routes, compositions, dosage forms, combinations with other therapeutic agents, pro-drug formulations are also provided in WO2007/031091.

[0252] Oligonucleotides or oligonucleotide conjugates of the invention may be mixed with pharmaceutically acceptable active or inert substances for the preparation of pharmaceutical compositions or formulations. Compositions and methods for the formulation of pharmaceutical compositions are dependent upon a number of criteria, including, but not limited to, route of administration, extent of disease, or dose to be administered.

[0253] In some embodiments, the oligonucleotide or oligonucleotide conjugate of the invention is a prodrug. In particular with respect to oligonucleotide conjugates the conjugate moiety is cleaved of the oligonucleotide once the prodrug is delivered to the site of action, e.g. the target cell.

Applications

[0254] The oligonucleotides of the invention may be utilized as research reagents for, for example, therapeutics and prophylaxis.

[0255] In research, such oligonucleotides may be used to specifically modulate the synthesis of UBE3A protein in cells (e.g. *in vitro* cell cultures) and experimental animals thereby facilitating functional analysis of the target or an appraisal of its usefulness as a target for therapeutic intervention. The target modulation is achieved by degrading or inhibiting a modulator of the gene or mRNA producing the protein.

[0256] For therapeutics, an animal or a human, suspected of having a disease or disorder, which can be treated by modulating the expression of UBE3A.

[0257] Described herein are methods for treating or preventing a disease, comprising administering a therapeutically or prophylactically effective amount of an oligonucleotide, an oligonucleotide conjugate or a pharmaceutical composition of the invention to a subject suffering from or susceptible to the disease.

[0258] The invention relates to an oligonucleotide, a composition or a conjugate as defined herein for use as a medicament.

[0259] The oligonucleotide, oligonucleotide conjugate or a pharmaceutical composition according to the invention is typically administered in an effective amount.

[0260] The invention also provides for the use of the oligonucleotide or oligonucleotide 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.

[0261] The disease or disorder, as referred to herein, is associated with expression of UBE3A. In some embodiments the disease or disorder may be associated with a mutation in the maternal UBE3A gene. In some embodiments, the target nucleic acid is a regulator of the paternal UBE3A gene.

[0262] The methods of the invention are preferably employed for treatment or prophylaxis against diseases caused by abnormal levels and/or activity of UBE3A. The disease may in particular be caused by reduced levels and/or activity of UBE3A protein.

[0263] The invention further relates to use of an oligonucleotide, oligonucleotide conjugate or a pharmaceutical composition as defined herein for the manufacture of a medicament for the treatment of abnormal levels and/or activity of UBE3A, in particular low levels and/or activity of UBE3A.

[0264] The invention relates to oligonucleotides, oligonucleotide conjugates or pharmaceutical compositions for use in the treatment of Angelman symdrome.

Administration

[0265] The oligonucleotides or pharmaceutical compositions of the present invention may be administered topical (such as, to the skin, inhalation, ophthalmic or otic) or enteral (such as, orally or through the gastrointestinal tract) or parenteral (such as, intravenous, subcutaneous, intra-muscular, intracerebral, intracerebroventricular or intrathecal).

[0266] In a preferred embodiment the oligonucleotide or pharmaceutical compositions of the present invention are administered by a parenteral route including intravenous, intraarterial, subcutaneous, intraperitoneal or intramuscular injection or infusion, intrathecal or intracranial, e.g., intracerebral or intraventricular, administration. In one embodiment the active oligonucleotide or oligonucleotide conjugate is administered intracerebral or intracerebroventricular. In another embodiment the active oligonucleotide or oligonucleotide conjugate is administered intrathecal.

[0267] The invention also provides for the use of the oligonucleotide or oligonucleotide conjugate of the invention as described for the manufacture of a medicament wherein the medicament is in a dosage form for intrathecal administration.

[0268] The invention also provides for the use of the oligonucleotide or oligonucleotide conjugate of the invention as described for the manufacture of a medicament wherein the medicament is in a dosage form for intracerebral or intraventricular administration.

[0269] The invention also provides for the use of the oligonucleotide or oligonucleotide conjugate of the invention as described for the manufacture of a medicament wherein the medicament is in a dosage form for intracerebroventricular administration.

Combination therapies

[0270] In some embodiments the oligonucleotide, oligonucleotide conjugate or pharmaceutical composition of the invention is for use in a combination treatment with another therapeutic agent. The therapeutic agent can for example be anticonvulsant medication.

EXAMPLES

Materials and methods

[0271]

Table 3: List of oligonucleotides or contiguous nucleobase sequences complementary to SEQ ID NO: 1 (motif sequences indicated by SEQ ID NO), oligonucleotide designs made from these, as well as specific oligonucleotide compounds (indicated by CMP ID NO) designed based on the motif sequence.

Seq ID NO	Motif	Design	Compound	CMP ID NO	∆G°	Start SEQ ID NO 1
4	AACTTCATCAATATTTCCC	3-13-3	AACttcatcaatatttCCC	4_1	-23,36	1677
4	AACTTCATCAATATTTCCC	2-15-2	AActtcatcaatatttcCC	4_2	-19,60	1677
5	ACTTCATCAATATTTCCC	3-12-3	ACTtcatcaatatttCCC	5_1	-23,80	1677
5	ACTTCATCAATATTTCCC	2-14-2	ACttcatcaatatttcCC	5_2	-20,24	1677
6	CAACTTCATCAATATTTCCC	2-14-4	CAacttcatcaatattTCCC	6_1	-25,64	1677
6	CAACTTCATCAATATTTCCC	2-16-2	CAacttcatcaatatttcCC	6_2	-22,28	1677
7	CAACTTCATCAATATTTCC	4-13-2	CAACttcatcaatatttCC	7_1	-21,47	1678
7	CAACTTCATCAATATTTCC	2-15-2	CAacttcatcaatatttCC	7_2	-19,46	1678
8	CCAACTTCATCAATATTTCC	3-14-3	CCAacttcatcaatattTCC	8_1	-25,64	1678
9	CCCAACTTCATCAATATTTC	4-14-2	CCCAacttcatcaatattTC	9_1	-25,64	1679
10	ACCCAACTTCATCAATATTT	2-16-2	ACccaacttcatcaatatTT	10_1	-20,05	1680
11	CCCAACTTCATCAATATTT	4-13-2	CCCAacttcatcaatatTT	11_1	-23,96	1680
11	CCCAACTTCATCAATATTT	2-15-2	CCcaacttcatcaatatTT	11_2	-20,28	1680
12	ACCCAACTTCATCAATATT	4-13-2	ACCCaacttcatcaataTT	12_1	-23,64	1681
12	ACCCAACTTCATCAATATT	2-15-2	ACccaacttcatcaataTT	12_2	-19,18	1681
13	CCCAACTTCATCAATATT	4-12-2	CCCAacttcatcaataTT	13_1	-23,09	1681
13	CCCAACTTCATCAATATT	2-14-2	CCcaacttcatcaataTT	13_2	-19,41	1681
14	TACCCAACTTCATCAATAT	2-15-2	TAcccaacttcatcaatAT	14_1	-19,31	1682
15	TACCCAACTTCATCAATA	2-14-2	T AcccaacttcatcaaT A	15_1	-19,14	1683
16	TTACCCAACTTCATCAATA	2-15-2	TT acccaacttcatcaaTA	16_1	-19,74	1683
17	TTTACCCAACTTCATCAAT	4-13-2	TTTAcccaacttcatcaAT	17_1	-21,68	1684
17	TTTACCCAACTTCATCAAT	2-15-2	TTtacccaacttcatcaAT	17_2	-19,22	1684
18	ATACTTTACCCAACTTCAT	3-13-3	ATActttacccaacttCAT	18_1	-23,44	1688

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
18	ATACTTTACCCAACTTCAT	2-15-2	ATactttacccaacttcAT	18_2	-20,13	1688
19	TACTTTACCCAACTTCAT	3-12-3	TACtttacccaacttCAT	19_1	-22,78	1688
19	TACTTTACCCAACTTCAT	2-14-2	TActttacccaacttcAT	19_2	-19,30	1688
20	TTATACTTTACCCAACTTCA	2-16-2	TTatactttacccaacttCA	20_1	-21,40	1689
21	TCACTGTTCTGACTTT	3-10-3	TCActgttctgacTTT	21_1	-19,11	1712
22	TTCAATCTCTATCTCATCAT	2-16-2	TTcaatctctatctcatcAT	22_1	-19,42	4169
23	CTTCAATCTCTATCTCATCA	4-14-2	CTTCaatctctatctcatCA	23_1	-24,21	4170
23	CTTCAATCTCTATCTCATCA	2-16-2	CTtcaatctctatctcatCA	23_2	-22,04	4170
24	TTCAATCTCTATCTCATCA	2-15-2	TTcaatctctatctcatCA	24_1	-19,44	4170
25	CTTCAATCTCTATCTCATC	2-15-2	CTtcaatctctatctcaTC	25_1	-19,87	4171
26	ACTTCAATCTCTATCTCAT	3-13-3	ACTtcaatctctatctCAT	26_1	-22,36	4172
26	ACTTCAATCTCTATCTCAT	2-15-2	ACttcaatctctatctcAT	26_2	-19,08	4172
27	CACTTCAATCTCTATCTCAT	2-16-2	CActtcaatctctatctcAT	27_1	-20,98	4172
28	ACTTCAATCTCTATCTCA	2-12-4	ACttcaatctctatCTCA	28_1	-21,96	4173
28	ACTTCAATCTCTATCTCA	2-14-2	ACttcaatctctatctCA	28_2	-19,10	4173
29	CACTTCAATCTCTATCTCA	2-13-4	CActtcaatctctatCT CA	29_1	-23,86	4173
29	CACTTCAATCTCTATCTCA	2-15-2	CActtcaatctctatctCA	29_2	-21,00	4173
30	ACACTTCAATCTCTATCTC	2-15-2	ACacttcaatctctatcTC	30_1	-19,38	4174
31	TACACTTCAATCTCTATCTC	2-14-4	T Acacttcaatctcta TCTC	31_1	-23,31	4174
31	TACACTTCAATCTCTATCTC	2-16-2	TAcacttcaatctctatcTC	31_2	-20,53	4174
32	TACACTTCAATCTCTATCT	4-13-2	T ACActtcaatctctatCT	32_1	-22,34	4175
33	CTTTGTCTCTCTTTACT	2-13-2	CTttgtctctctttaCT	33_1	-19,36	4374
34	TATACCTTTCTTTAACCC	3-12-3	TATacctttctttaaCCC	34_1	-24,89	8118
34	TATACCTTTCTTTAACCC	2-14-2	TAtacctttctttaacCC	34_2	-20,83	8118

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
34	TATACCTTTCTTTAACCC	1-3-1-7-1-1-1-1-2	TataCctttcttTaAcCC	34_3	-21,63	8116
34	TATACCTTTCTTTAACCC	1-4-1-6-1-3-2	TatacCtttcttTaacCC	34_4	-21,31	8116
34	TATACCTTTCTTTAACCC	1-2-1-1-1-7-2-1-2	TatAcCtttctttAAcCC	34_5	-21,51	8116
34	TATACCTTTCTTTAACCC	2-3-1-7-1-2-2	TAtacCtttctttAacCC	34_6	-21,84	8116
34	TATACCTTTCTTTAACCC	2-13-3	TAtacctttctttaaCCC	34_7	-23,21	8116
35	TGTTTATACCCTTTCC	2-12-2	TGtttataccctttCC	35_1	-20,33	9212
35	TGTTTATACCCTTTCC	4-10-2	TGTTtataccctttCC	35_2	-22,69	9212
36	TCTCCTTTATGACTCC	2-10-4	TCtcctttatgaCTCC	36_1	-23,29	10839
37	CTTCTCCTTTATGACTC	2-13-2	CTtctcctttatgacTC	37_1	-19,26	10840
38	CCATTTATTTCCATTTATT	4-13-2	CCATttatttccatttaTT	38_1	-22,32	15567
38	CCATTTATTTCCATTTATT	2-15-2	CCatttatttccatttaTT	38_2	-19,61	15567
38	CCATTTATTTCCATTTATT	1-2-1-9-2-1-3	CcaTttatttccaTTtATT	38_3	-20,02	15567
38	CCATTTATTTCCATTTATT	1-1-1-1-1-8-1-1-1-1-2	CcAtTtatttccaTtTaTT	38_4	-18,95	15567
38	CCATTTATTTCCATTTATT	2-2-1-8-1-3-2	CCatTtatttccaTttaTT	38_5	-20,35	15567
38	CCATTTATTTCCATTTATT	1-2-3-6-1-3-3	CcaTTTatttccAtttATT	38_6	-20,87	15567
39	CTTTCCATTTATTTCCATTT	2-14-4	CTttccatttatttccATTT	39_1	-23,14	15570
39	CTTTCCATTTATTTCCATTT	1-13-1-1-1-1-2	CtttccatttatttCcAtTT	39_2	-20,96	15570
39	CTTTCCATTTATTTCCATTT	1-13-1-3-2	CtttccatttatttCcatTT	39_3	-20,91	15570
39	CTTTCCATTTATTTCCATTT	1-3-1-1-1-11-2	CtttCcAtttatttccatTT	39_4	-20,96	15570
39	CTTTCCATTTATTTCCATTT	1-1-1-3-1-9-1-1-2	CtTtccAtttatttccAtTT	39_5	-20,54	15570
40	TCTTTCCATTTATTTCCATT	2-14-4	TCtttccatttatttcCATT	40_1	-24,62	15571
40	TCTTTCCATTTATTTCCATT	2-13-1-1-3	TCtttccatttatttCcATT	40_2	-23,39	15571
40	TCTTTCCATTTATTTCCATT	2-13-1-2-2	TCtttccatttatttCcaTT	40_3	-22,53	15571
40	TCTTTCCATTTATTTCCATT	2-14-1-1-2	TCtttccatttatttcCaTT	40_4	-22,34	15571

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
40	TCTTTCCATTTATTTCCATT	2-3-1-11-3	TCtttCcatttatttccATT	40_5	-23,39	15571
40	TCTTTCCATTTATTTCCATT	2-4-1-10-3	TCtttcCatttatttccATT	40_6	-23,20	15571
40	TCTTTCCATTTATTTCCATT	2-3-1-12-2	TCtttCcatttatttccaTT	40_7	-22,53	15571
40	TCTTTCCATTTATTTCCATT	2-4-1-11-2	TCtttcCatttatttccaTT	40_8	-22,34	15571
41	ATTACCCATCCGTTCT	2-12-2	ATtacccatccgttCT	41_1	-21,15	21965
42	GCATTAGGCACATTACAT	3-12-3	GCAttaggcacattaCAT	42_1	-23,96	22211
43	ATTATTATTTAACCTTCCTA	2-16-2	ATtattatttaaccttccTA	43_1	-19,28	30451
44	ACATTATTATTTAACCTTCC	4-14-2	ACATtattatttaaccttCC	44_1	-22,84	30453
44	ACATTATTATTTAACCTTCC	2-16-2	ACattattatttaaccttCC	44_2	-20,13	30453
45	CATTATTATTTAACCTTCC	4-13-2	CATTattatttaaccttCC	45_1	-22,04	30453
45	CATTATTATTTAACCTTCC	2-15-2	CAttattatttaaccttCC	45_2	-19,55	30453
46	CCTCTGCTTATAACTTT	2-13-2	CCtctgcttataactTT	46_1	-19,15	30699
47	CTACTATACTTTCCTCT	2-11-4	CTactatactttcCTCT	47_1	-22,32	30711
48	GTTCTACTATACTTTCC	4-11-2	GTTCtactatactttCC	48_1	-21,69	30714
48	GTTCTACTATACTTTCC	2-13-2	GTtctactatactttCC	48_2	-19,21	30714
48	GTTCTACTATACTTTCC	1-2-1-7-2-2-2	GttCtactataCTttCC	48_3	-20,83	30712
48	GTTCTACTATACTTTCC	2-9-1-3-2	GTtctactatactttCC	48_4	-20,20	30712
48	GTTCTACTATACTTTCC	1-2-1-9-1-1-2	GttCtactatactTtCC	48_5	-18,95	30712
48	GTTCTACTATACTTTCC	2-1-1-10-3	GTtCtactatacttTCC	48_6	-21,18	30712
48	GTTCTACTATACTTTCC	1-3-1-10-2	GttcTactatactttCC	48_7	-18,61	30712
49	CACCTGATAACAGACCCT	3-12-3	CACctgataacagacCCT	49_1	-26,38	36068
50	CACCTGATAACAGACC	3-10-3	CACctgataacagACC	50_1	-21,10	36070
51	CCCACCAAAGGATATATT	3-12-3	CCCaccaaaggatatATT	51_1	-23,47	37208
52	ACCAGCTACAGGAACCTC	3-12-3	ACCagctacaggaacCTC	52_1	-26,57	46132

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
53	CTATATCTCACTCCTATTT	4-13-2	CTATatctcactcctatTT	53_1	-23,07	48143
53	CTATATCTCACTCCTATTT	2-13-4	CTatatctcactcctATTT	53_2	-22,12	48143
54	CTATATCTCACTCCTATT	2-14-2	CTatatctcactcctaTT	54_1	-19,40	48144
54	CTATATCTCACTCCTATT	2-12-4	CTatatctcactccTATT	54_2	-22,28	48144
54	CTATATCTCACTCCTATT	3-12-3	CTAtatctcactcctATT	54_3	-21,44	48144
55	CTACTATATCTCACTCCTAT	2-16-2	CTactatatctcactcctAT	55_1	-22,00	48145
55	CTACTATATCTCACTCCTAT	2-14-4	CTactatatctcactcCTAT	55_2	-25,54	48145
56	TACTATATCTCACTCCTAT	2-13-4	TActatatctcactcCTAT	56_1	-23,29	48145
57	CTACTATATCTCACTCCTA	2-15-2	CTactatatctcactccTA	57_1	-21,91	48146
58	TACTATATCTCACTCCTA	2-14-2	TActatatctcactccTA	58_1	-19,66	48146
58	TACTATATCTCACTCCTA	2-12-4	T ActatatctcactCCT A	58_2	-23,59	48146
58	TACTATATCTCACTCCTA	3-12-3	TACtatatctcactcCTA	58_3	-22,62	48146
59	CTACTATATCTCACTCCT	2-14-2	CTactatatctcactcCT	59_1	-21,25	48147
59	CTACTATATCTCACTCCT	4-12-2	CTACtatatctcactcCT	59_2	-23,87	48147
60	CTACTATATCTCACTCC	2-13-2	CTactatatctcactCC	60_1	-20,13	48148
60	CTACTATATCTCACTCC	2-11-4	CTactatatctcaCTCC	60_2	-23,00	48148
60	CTACTATATCTCACTCC	3-11-3	CTActatatctcacTCC	60_3	-22,56	48148
61	CCTACTATATCTCACTC	2-11-4	CCtactatatctcACTC	61_1	-21,93	48149
62	CTCCTACTATATCTCACTC	4-13-2	CTCCtactatatctcacTC	62_1	-25,69	48149
63	TCCTACTATATCTCACTC	3-12-3	TCCtactatatctcaCTC	63_1	-23,88	48149
64	CTCCTACTATATCTCACT	4-12-2	CTCCtactatatctcaCT	64_1	-24,87	48150
64	CTCCTACTATATCTCACT	3-12-3	CTCctactatatctcACT	64_2	-22,93	48150
65	TTTCCTCTCCTACTATATC	2-15-2	TTtcctctcctactataTC	65_1	-21,23	48155
66	ATCCATATCCTTTCCT	3-10-3	ATCcatatcctttCCT	66_1	-24,02	48168

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
67	CATCCATATCCTTTCCT	4-11-2	CATCcatatcctttcCT	67_1	-24,94	48168
68	ATCATCCATATCCTTTCC	4-12-2	ATCAtccatatcctttCC	68_1	-25,69	48169
69	CATCATCCATATCCTTTC	4-12-2	CAT CatccatatccttT C	69_1	-23,32	48170
69	CATCATCCATATCCTTTC	2-14-2	C AtcatccatatccttT C	69_2	-20,72	48170
69	CATCATCCATATCCTTTC	2-12-4	CAtcatccatatccTTTC	69_3	-22,56	48170
70	TACATCATCCATATCCTTTC	2-16-2	TAcatcatccatatcctttTC	70_1	-22,45	48170
70	TACATCATCCATATCCTTTC	4-14-2	T ACAtcatccatatcctttTC	70_2	-25,00	48170
70	TACATCATCCATATCCTTTC	2-14-4	TAcatcatccatatccTTTC	70_3	-24,29	48170
71	ACATCATCCATATCCTTT	3-12-3	ACAtcatccatatccTTT	71_1	-22,11	48171
72	CATCATCCATATCCTTT	2-13-2	CAtcatccatatcctTT	72_1	-19,04	48171
72	CATCATCCATATCCTTT	4-11-2	CATCatccatatcctTT	72_2	-21,64	48171
73	TACATCATCCATATCCTTT	2-15-2	TAcatcatccatatcctTT	73_1	-20,76	48171
73	TACATCATCCATATCCTTT	2-13-4	TAcatcatccatatcCTTT	73_2	-23,36	48171
73	TACATCATCCATATCCTTT	3-13-3	TACatcatccatatccTTT	73_3	-22,88	48171
74	ATACATCATCCATATCCTT	2-15-2	ATacatcatccatatccTT	74_1	-20,80	48172
74	ATACATCATCCATATCCTT	4-13-2	ATACatcatccatatccTT	74_2	-23,12	48172
75	TACATCATCCATATCCTT	2-14-2	TAcatcatccatatccTT	75_1	-19,97	48172
75	TACATCATCCATATCCTT	4-12-2	TACAtcatccatatccTT	75_2	-22,52	48172
76	TATACATCATCCATATCCTT	2-16-2	TAtacatcatccatatccTT	76_1	-21,36	48172
77	ATACATCATCCATATCCT	3-12-3	ATAcatcatccatatCCT	77_1	-24,15	48173
77	ATACATCATCCATATCCT	2-14-2	ATacatcatccatatcCT	77_2	-20,55	48173
77	ATACATCATCCATATCCT	2-13-3	ATacatcatccatatCCT	77_3	-22,92	48173
78	ATATACATCATCCATATCCT	2-16-2	ATatacatcatccatatcCT	78_1	-22,04	48173
79	TACATCATCCATATCCT	2-11-4	TAcatcatccataTCCT	79_1	-23,21	48173

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
79	TACATCATCCATATCCT	2-13-2	TAcatcatccatatcCT	79_2	-19,71	48173
79	TACATCATCCATATCCT	4-11-2	TACAtcatccatatcCT	79_3	-22,27	48173
80	TATACATCATCCATATCCT	2-15-2	TAtacatcatccatatcCT	80_1	-21,11	48173
80	TATACATCATCCATATCCT	3-13-3	TATacatcatccatatCCT	80_2	-25,15	48173
80	TATACATCATCCATATCCT	4-13-2	TATAcatcatccatatcCT	80_3	-24,01	48173
81	ATACATCATCCATATCC	3-11-3	ATAcatcatccataTCC	81_1	-21,79	48174
82	ATATACATCATCCATATCC	4-13-2	ATATacatcatccatatCC	82_1	-23,73	48174
82	ATATACATCATCCATATCC	2-15-2	ATatacatcatccatatCC	82_2	-20,93	48174
83	TATACATCATCCATATCC	2-14-2	TAtacatcatccatatCC	83_1	-20,00	48174
83	TATACATCATCCATATCC	4-12-2	TATAcatcatccatatCC	83_2	-22,90	48174
84	TATATACATCATCCATATCC	2-16-2	TAtatacatcatccatatCC	84_1	-21,49	48174
84	TATATACATCATCCATATCC	4-14-2	TATAtacatcatccatatCC	84_2	-24,29	48174
85	GCTTCATATTTCTCCA	2-12-2	GCttcatatttctcCA	85_1	-20,44	49345
85	GCTTCATATTTCTCCA	2-11-3	GCttcatatttctcCA	85_2	-22,81	49345
86	CATCTTGTTCTTTACCT	2-13-2	CAtcttgttctttacCT	86_1	-19,67	49581
87	TATATTCACCATTGCC	2-10-4	TAtattcaccatTGCC	87_1	-22,70	49724
88	CCTTATATTCACCATTG	2-13-2	CCttatattcaccatTG	88_1	-19,44	49726
88	CCTTATATTCACCATTG	2-11-4	CCttatattcaccATTG	88_2	-21,25	49726
89	CCTCCTTATATTCACC	4-10-2	CCTCcttatattcaCC	89_1	-24,64	49730
90	CCCTTCCTTTATTCAA	3-10-3	CCCttcctttattCAA	90_1	-23,86	50189
91	CCTTACTGTTAAATCCT	2-13-2	CCttactgttaaatcCT	91_1	-19,81	50475
92	CAGGCAGATAACCTCCAA	3-12-3	CAGgcagataacctcCAA	92_1	-25,31	52419
93	CAGCAGGCAGATAACCTC	3-12-3	CAGcaggcagataacCTC	93_1	-25,88	52422
94	CGAATCTTGACATACAGG	3-12-3	CGAatcttgacatacAGG	94_1	-21,47	53955

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
95	CTCATACTTGCTTTAAT	4-11-2	CTCAtacttgctttaAT	95_1	-19,10	60821
95	CTCATACTTGCTTTAAT	2-13-2	CTcatacttgctttaAT	95_2	-16,35	60821
96	ACATCTCATACTTGCTT	2-11-4	ACatctcatacttGCTT	96_1	-21,31	60825
96	ACATCTCATACTTGCTT	2-13-2	ACatctcatacttgcTT	96_2	-17,66	60825
96	ACATCTCATACTTGCTT	2-12-3	ACatctcatacttgCTT	96_3	-19,52	60825
97	ACATCTCATACTTGCT	2-10-4	ACatctcatactTGCT	97_1	-21,18	60826
97	ACATCTCATACTTGCT	2-12-2	ACatctcatacttgCT	97_2	-17,70	60826
97	ACATCTCATACTTGCT	2-11-3	ACatctcatacttGCT	97_3	-19,49	60826
97	ACATCTCATACTTGCT	4-10-2	ACA T ctcatacttgCT	97_4	-20,48	60826
98	TACATCTCATACTTGCT	2-11-4	TAcatctcatactTGCT	98_1	-22,33	60826
98	TACATCTCATACTTGCT	2-13-2	TAcatctcatacttgCT	98_2	-18,85	60826
98	TACATCTCATACTTGCT	4-11-2	TACAtctcatacttgCT	98_3	-21,40	60826
99	CCTACATCTCATACTTGC	3-12-3	CCTacatctcatactTGC	99_1	-26,29	60827
99	CCTACATCTCATACTTGC	2-14-2	CCtacatctcatacttGC	99_2	-22,98	60827
99	CCTACATCTCATACTTGC	2-13-3	CCtacatctcatactTGC	99_3	-24,67	60827
99	CCTACATCTCATACTTGC	2-12-4	CCtacatctcatacTTGC	99_4	-25,70	60827
100	CTACATCTCATACTTGC	3-11-3	CTAcatctcatactTGC	100_1	-22,33	60827
100	CTACATCTCATACTTGC	2-13-2	CT acatctcatacttGC	100_2	-19,41	60827
100	CTACATCTCATACTTGC	2-12-3	CTacatctcatactTGC	100_3	-21,10	60827
101	TACATCTCATACTTGC	3-10-3	TACatctcatactTGC	101_1	-19,94	60827
101	TACATCTCATACTTGC	2-12-2	TAcatctcatacttGC	101_2	-17,15	60827
101	TACATCTCATACTTGC	2-11-3	TAcatctcatactTGC	101_3	-18,85	60827
101	TACATCTCATACTTGC	4-10-2	T ACAtctcatacttGC	101_4	-19,71	60827
102	CCTACATCTCATACTTG	4-11-2	CCTAcatctcatactTG	102_1	-22,52	60828

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
102	CCTACATCTCATACTTG	2-13-2	CCtacatctcatactTG	102_2	-19,67	60828
102	CCTACATCTCATACTTG	3-12-2	CCTacatctcatactTG	102_3	-21,29	60828
102	CCTACATCTCATACTTG	3-11-3	CCTacatctcatacTTG	102_4	-22,31	60828
103	ACCTACATCTCATACTT	3-11-3	ACCtacatctcataCTT	103_1	-21,93	60829
103	ACCTACATCTCATACTT	2-13-2	ACctacatctcatacTT	103_2	-17,76	60829
103	ACCTACATCTCATACTT	2-11-4	ACctacatctcatACTT	103_3	-20,03	60829
103	ACCTACATCTCATACTT	3-12-2	ACCtacatctcatacTT	103_4	-20,26	60829
104	CCTACATCTCATACTT	3-10-3	CCTacatctcataCTT	104_1	-21,50	60829
104	CCTACATCTCATACTT	2-12-2	CCtacatctcatacTT	104_2	-18,21	60829
104	CCTACATCTCATACTT	2-10-4	CCtacatctcatACTT	104_3	-20,48	60829
105	TACCTACATCTCATACTT	4-12-2	TACCtacatctcatacTT	105_1	-22,49	60829
105	TACCTACATCTCATACTT	2-14-2	TAcctacatctcatacTT	105_2	-18,81	60829
105	TACCTACATCTCATACTT	2-13-3	T AcctacatctcataCTT	105_3	-20,48	60829
105	TACCTACATCTCATACTT	2-12-4	T AcctacatctcatACTT	105_4	-21,08	60829
106	TTACCTACATCTCATACTT	3-13-3	TTAcctacatctcataCTT	106_1	-22,30	60829
106	TTACCTACATCTCATACTT	2-15-2	TTacctacatctcatacTT	106_2	-19,40	60829
106	TTACCTACATCTCATACTT	2-14-3	TTacctacatctcataCTT	106_3	-21,08	60829
106	TTACCTACATCTCATACTT	2-13-4	TTacctacatctcatACTT	106_4	-21,67	60829
107	ACCTACATCTCATACT	4-10-2	ACCTacatctcataCT	107_1	-21,72	60830
107	ACCTACATCTCATACT	2-12-2	ACctacatctcataCT	107_2	-17,61	60830
107	ACCTACATCTCATACT	3-11-2	ACCtacatctcataCT	107_3	-20,10	60830
107	ACCTACATCTCATACT	2-10-4	ACctacatctcaTACT	107_4	-20,11	60830
108	TACCTACATCTCATACT	4-11-2	TACCtacatctcataCT	108_1	-22,34	60830
108	TACCTACATCTCATACT	2-13-2	TAcctacatctcataCT	108_2	-18,66	60830

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
108	TACCTACATCTCATACT	3-12-2	TACctacatctcataCT	108_3	-19,85	60830
108	TACCTACATCTCATACT	3-11-3	TACctacatctcatACT	108_4	-20,44	60830
109	TTACCTACATCTCATACT	2-12-4	TTacctacatctcaTACT	109_1	-21,75	60830
109	TTACCTACATCTCATACT	2-14-2	TTacctacatctcataCT	109_2	-19,25	60830
109	TTACCTACATCTCATACT	3-13-2	TTAcctacatctcataCT	109_3	-20,48	60830
109	TTACCTACATCTCATACT	3-12-3	TTAcctacatctcatACT	109_4	-21,08	60830
110	TTACCTACATCTCATAC	3-11-3	TTAcctacatctcaTAC	110_1	-19,50	60831
110	TTACCTACATCTCATAC	2-13-2	TTacctacatctcatAC	110_2	-16,37	60831
111	GTTACCTACATCTCATA	2-11-4	GTtacctacatctCATA	111_1	-21,69	60832
111	GTTACCTACATCTCATA	2-13-2	GTtacctacatctcaTA	111_2	-18,74	60832
111	GTTACCTACATCTCATA	3-12-2	GTTacctacatctcaTA	111_3	-19,98	60832
112	GTTACCTACATCTCAT	3-10-3	GTTacctacatctCAT	112_1	-20,69	60833
112	GTTACCTACATCTCAT	2-12-2	GTtacctacatctcAT	112_2	-17,37	60833
113	ATATACCCAAAGGCACCT	3-12-3	ATAtacccaaaggcaCCT	113_1	-25,99	62200
114	TCTACTCATCCTTTAACTCA	2-14-4	TCtactcatcctttaaCTCA	114_1	-25,63	62251
115	CCTTAATCTGTATCACT	2-13-2	CCttaatctgtatcaCT	115_1	-19,58	62286
116	CCATACACAGCACATA	2-12-2	CCatacacagcacaTA	116_1	-19,04	62424
117	CTCCATACACAGCACAT	2-13-2	CTccatacacagcacAT	117_1	-20,08	62425
118	CAGAATAATTCTCCTCC	2-13-2	CAgaataattctcctCC	118_1	-19,86	62441
119	GTCCTACATATATACC	4-10-2	GTCCtacatatataCC	119_1	-22,09	66380
120	TGCTTCCTTACTAACC	4-10-2	TGCTtccttactaaCC	120_1	-23,93	66701
120	TGCTTCCTTACTAACC	2-12-2	TGcttccttactaaCC	120_2	-20,10	66701
121	CCCTTTGTAATCATCT	4-10-2	CCCTttgtaatcatCT	121_1	-23,44	66838
122	TCCCTTTGTAATCATCT	2-13-2	TCcctttgtaatcatCT	122_1	-19,97	66838

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
123	CTGCCATCAATACCAT	2-12-2	CTgccatcaataccAT	123_1	-19,14	68918
124	TCACTGCCATCAATACC	2-13-2	TCactgccatcaataCC	124_1	-21,35	68920
125	ATTCTTACTTTATTCCTCA	2-15-2	ATtcttactttattcctCA	125_1	-20,16	70033
126	TCACTTTCCAGATATCA	4-11-2	TCACtttccagatatCA	126_1	-21,61	77567
126	TCACTTTCCAGATATCA	2-13-2	TCactttccagatatCA	126_2	-18,65	77567
127	TCCTTCAAATTCCACATAC	3-13-3	TCCttcaaattccacaTAC	127_1	-24,09	82053
128	ACATGTCCCTTTATATT	4-11-2	ACATgtccctttataTT	128_1	-20,87	92323
128	ACATGTCCCTTTATATT	2-13-2	ACatgtccctttataTT	128_2	-17,66	92323
128	ACATGTCCCTTTATATT	3-12-2	ACAtgtccctttataTT	128_3	-19,13	92323
128	ACATGTCCCTTTATATT	3-11-3	ACAtgtccctttatATT	128_4	-20,03	92323
129	ACATGTCCCTTTATAT	3-10-3	ACAtgtccctttaTAT	129_1	-20,11	92324
129	ACATGTCCCTTTATAT	2-12-2	ACatgtccctttatAT	129_2	-16,74	92324
130	CCAAGAAAGGAGCAAGCT	3-12-3	CCAagaaaggagcaaGCT	130_1	-25,26	97146
131	TCCAAGAAAGGAGCAAGC	3-12-3	TCCaagaaaggagcaAGC	131_1	-24,12	97147
132	CTCATCCCTCCAAGAAA	4-11-2	CTCAtccctccaagaAA	132_1	-22,58	97156
132	CTCATCCCTCCAAGAAA	2-13-2	CTcatccctccaagaAA	132_2	-19,83	97156
132	CTCATCCCTCCAAGAAA	3-12-2	CTCatccctccaagaAA	132_3	-21,11	97156
133	TCATCCCTCCAAGAAA	4-10-2	TCATccctccaagaAA	133_1	-20,41	97156
133	TCATCCCTCCAAGAAA	2-12-2	TCatccctccaagaAA	133_2	-17,63	97156
133	TCATCCCTCCAAGAAA	3-11-2	TCAtccctccaagaAA	133_3	-19,09	97156
133	TCATCCCTCCAAGAAA	3-10-3	TCAtccctccaagAAA	133_4	-19,81	97156
134	CACCTCCCTATTACATAAA	4-13-2	CACCtccctattacataAA	134_1	-24,18	100018
134	CACCTCCCTATTACATAAA	2-15-2	CAcctccctattacataAA	134_2	-20,51	100018
135	CACCTCCCTATTACATAA	4-12-2	CACCtccctattacatAA	135_1	-23,75	100019

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
135	CACCTCCCTATTACATAA	2-14-2	CAcctccctatta catAA	135_2	-20,07	100019
136	CCTCCCTATTACATAA	2-12-2	CCtccctattacatAA	136_1	-18,40	100019
137	CTAAATCTTCCAATTCATA	2-15-2	CTaaatcttccaattcaTA	137_1	-18,12	106139
138	TATCCCTTGATTATCCT	2-13-2	TAtcccttgattatcCT	138_1	-20,68	109406
139	CCTCTTTGTCAAATACT	2-13-2	CCtctttgtcaaataCT	139_1	-19,30	110768
140	CAGCTTATTTACCTCTT	2-13-2	CAgcttatttacctcTT	140_1	-19,30	114828
141	ACTCTTTACCTCTAACACT	4-13-2	ACTCtttacctctaacaCT	141_1	-24,26	117468
142	TTACTCTTTACCTCTAACAC	3-14-3	TTActctttacctctaaCAC	142_1	-23,23	117469
143	CCAACCTAATACCTTAATA	2-15-2	CCaacctaataccttaaTA	143_1	-20,27	118639
144	TACCAACCTAATACCTTAA	2-15-2	TAccaacctaataccttAA	144_1	-18,32	118641
145	CCAATACCCACAAACC	3-10-3	CCAatacccacaaACC	145_1	-23,17	124162
145	CCAATACCCACAAACC	2-12-2	CCaatacccacaaaCC	145_2	-20,85	124162
146	CCATTATTCTACTTTGT	3-11-3	CCAttattctactttTGT	146_1	-21,79	125501
146	CCATTATTCTACTTTGT	2-13-2	CCattattctactttGT	146_2	-18,63	125501
147	CATTTCCTTATCTTCACA	2-14-2	CAtttccttatcttcaCA	147_1	-20,39	125529
148	TCATTTCCTTATCTTCACA	4-13-2	TCATttccttatcttcaCA	148_1	-24,13	125529
149	AATAATTCCTCATTTCCT	2-14-2	AAtaattcctcatttcCT	149_1	-18,01	125539
150	ACAATAATTCCTCATTTCC	3-13-3	ACAataattcctcattTCC	150_1	-22,71	125540
150	ACAATAATTCCTCATTTCC	2-15-2	ACaataattcctcatttCC	150_2	-20,23	125540
151	TATTGAACCAATTCTA	3-10-3	TATtgaaccaattCTA	151_1	-16,93	4806
152	CATATTGAACCAATTC	4-10-2	CATAttgaaccaatTC	152_1	-16,32	4808
153	TCATATTGAACCAATT	4-10-2	TCATattgaaccaaTT	153_1	-16,14	4809
154	CATCATATTGAACCAA	2-10-4	CAtcatattgaaCCAA	154_1	-17,65	4811
155	TCATCATATTGAACCA	3-10-3	TCAtcatattgaaCCA	155_1	-19,40	4812

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
156	CACAATCAACAACAAATA	4-12-2	CACAatcaacaacaaaTA	156_1	-16,16	4972
157	TACACAATCAACAACAAAT	4-13-2	TACAcaatcaacaacaaAT	157_1	-16,76	4973
158	CTGTACACAATCAACA	4-10-2	CTGTacacaatcaaCA	158_1	-19,05	4979
159	CACTAATAATTCACTTT	4-11-2	CACTaataattcactTT	159_1	-16,39	5058
160	CAACATTATTGACACT	2-10-4	CAacattattgaCACT	160_1	-17,17	5071
161	AAACTTTCCCAACATTAT	2-12-4	AAactttcccaacaTTAT	161_1	-18,69	5078
162	TCCTATATTCTCTTAAA	4-11-2	TCCTatattctcttaAA	162_1	-18,58	5094
163	TTTCCTATATTCTCTTA	4-11-2	TTTCctatattctctTA	163_1	-18,69	5096
164	CAAGTTTCCTATATTCT	4-11-2	CAAGtttcctatattCT	164_1	-19,97	5100
165	CAAGTTTCCTATATTC	4-10-2	CAAGtttcctatatTC	165_1	-17,47	5101
166	CATTCTATCTGCCAAA	2-10-4	CAttctatctgcCAAA	166_1	-18,36	5218
167	CCATTCTATCTGCCAAA	2-11-4	CCattctatctgcCAAA	167_1	-22,08	5218
168	TATAGCCATTCTATCT	4-10-2	TAT AgccattctatCT	168_1	-20,63	5224
169	TTATAGCCATTCTATCT	4-11-2	TTATagccattctatCT	169_1	-20,82	5224
169	TTATAGCCATTCTATCT	1-10-3-1-2	TtatagccattCTAtCT	169_2	-20,51	5224
169	TTATAGCCATTCTATCT	2-9-1-2-3	TTatagccattCtaTCT	169_3	-20,12	5224
169	TTATAGCCATTCTATCT	1-1-1-8-2-1-3	TtAtagccattCTaTCT	169_4	-20,59	5224
169	TTATAGCCATTCTATCT	1-3-1-6-2-2-2	TtatAgccattCT atCT	169_5	-19,97	5224
169	TTATAGCCATTCTATCT	3-8-1-3-2	TTAtagccattCtatCT	169_6	-20,13	5224
169	TTATAGCCATTCTATCT	1-10-2-2-2	TtatagccattCTatCT	169_7	-19,37	5224
169	TTATAGCCATTCTATCT	2-9-1-1-4	TTatagccattCtATCT	169_8	-21,02	5224
169	TTATAGCCATTCTATCT	1-1-1-8-1-1-4	TtAtagccattCtATCT	169_9	-19,88	5224
169	TTATAGCCATTCTATCT	1-2-1-7-1-1-4	TtaTagccattCtATCT	169_10	-20,65	5224
169	TTATAGCCATTCTATCT	1-3-1-6-1-1-4	TtatAgccattCtATCT	169_11	-20,38	5224

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
169	TTATAGCCATTCTATCT	1-10-1-1-4	TtatagccattCtATCT	169_12	-19,78	5224
169	TTATAGCCATTCTATCT	3-8-1-1-1-1-2	TTAtagccattCtAtCT	169_13	-20,22	5224
169	TTATAGCCATTCTATCT	2-1-1-7-1-1-1-1-2	TTaTagccattCtAtCT	169_14	-19,96	5224
169	TTATAGCCATTCTATCT	2-2-1-6-1-1-1-1-2	TTatAgccattCtAtCT	169_15	-19,69	5224
169	TTATAGCCATTCTATCT	2-9-1-1-1-1-2	TTatagccattCtAtCT	169_16	-19,09	5224
169	TTATAGCCATTCTATCT	1-2-2-6-1-1-1-1-2	TtaTAgccattCtAtCT	169_17	-20,35	5224
169	TTATAGCCATTCTATCT	1-2-1-7-1-1-1-1-2	TtaTagccattCtAtCT	169_18	-18,72	5224
169	TTATAGCCATTCTATCT	1-3-1-6-1-1-1-1-2	TtatAgccattCtAtCT	169_19	-18,45	5224
169	TTATAGCCATTCTATCT	2-2-1-6-1-2-3	TTatAgccattCtaTCT	169_20	-20,71	5224
169	TTATAGCCATTCTATCT	1-1-2-7-1-2-3	TtATagccattCtaTCT	169_21	-20,65	5224
169	TTATAGCCATTCTATCT	1-1-1-1-1-6-1-2-3	TtAtAgccattCtaTCT	169_22	-19,57	5224
169	TTATAGCCATTCTATCT	1-1-1-8-1-2-3	TtAtagccattCtaTCT	169_23	-18,98	5224
169	TTATAGCCATTCTATCT	4-7-1-3-2	TTATagccattCtatCT	169_24	-21,80	5224
169	TTATAGCCATTCTATCT	3-1-1-6-1-3-2	TT AtAgccattCtatCT	169_25	-20,72	5224
169	TTATAGCCATTCTATCT	2-1-1-7-1-3-2	TTaTagccattCtatCT	169_26	-19,86	5224
169	TTATAGCCATTCTATCT	2-2-1-6-1-3-2	TTatAgccattCtatCT	169_27	-19,59	5224
169	TTATAGCCATTCTATCT	2-9-1-3-2	TTatagccattCtatCT	169_28	-18,99	5224
169	TTATAGCCATTCTATCT	1-1-3-6-1-3-2	TtATAgccattCtatCT	169_29	-21,16	5224
169	TTATAGCCATTCTATCT	1-1-2-7-1-3-2	TtATagccattCtatCT	169_30	-19,53	5224
169	TTATAGCCATTCTATCT	1-1-1-1-1-6-1-3-2	TtAtAgccattCtatCT	169_31	-18,45	5224
169	TTATAGCCATTCTATCT	1-2-2-6-1-3-2	TtaTAgccattCtatCT	169_32	-20,25	5224
169	TTATAGCCATTCTATCT	1-2-1-7-1-3-2	TtaTagccattCtatCT	169_33	-18,62	5224
169	TTATAGCCATTCTATCT	1-3-1-6-1-3-2	TtatAgccattCtatCT	169_34	-18,35	5224
169	TTATAGCCATTCTATCT	1-1-1-9-5	TtAtagccattcTATCT	169_35	-20,88	5224

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
169	TTATAGCCATTCTATCT	2-10-2-1-2	TTatagccattcTAtCT	169_36	-20,09	5224
169	TTATAGCCATTCTATCT	1-1-1-9-2-1-2	TtAtagccattcTAtCT	169_37	-18,95	5224
169	TTATAGCCATTCTATCT	1-2-1-8-2-1-2	TtaTagccattcTAtCT	169_38	-19,72	5224
169	TTATAGCCATTCTATCT	1-3-1-7-2-1-2	TtatAgccattcTAtCT	169_39	-19,44	5224
169	TTATAGCCATTCTATCT	1-11-2-1-2	TtatagccattcTAtCT	169_40	-18,85	5224
169	TTATAGCCATTCTATCT	3-9-1-1-3	TTAtagccattcTaTCT	169_41	-21,21	5224
169	TTATAGCCATTCTATCT	1-1-1-9-1-1-3	TtAtagccattcTaTCT	169_42	-18,94	5224
169	TTATAGCCATTCTATCT	3-9-1-2-2	TTAtagccattcTatCT	169_43	-20,09	5224
169	TTATAGCCATTCTATCT	1-2-1-8-1-2-2	TtaTagccattcTatCT	169_44	-18,58	5224
169	TTATAGCCATTCTATCT	1-3-1-7-1-2-2	TtatAgccattcTatCT	169_45	-18,31	5224
169	TTATAGCCATTCTATCT	1-1-1-10-4	TtAtagccattctATCT	169_46	-18,90	5224
169	TTATAGCCATTCTATCT	3-10-1-1-2	TTAtagccattctAtCT	169_47	-19,24	5224
169	TTATAGCCATTCTATCT	2-11-1-1-2	TTatagccattctAtCT	169_48	-18,11	5224
169	TTATAGCCATTCTATCT	1-2-2-8-1-1-2	TtaTAgccattctAtCT	169_49	-19,37	5224
169	TTATAGCCATTCTATCT	3-1-1-10-2	TTAtAgccattctatCT	169_50	-19,74	5224
169	TTATAGCCATTCTATCT	3-12-2	TTAtagccattctatCT	169_51	-19,15	5224
169	TTATAGCCATTCTATCT	2-1-2-10-2	TTaTAgccattctatCT	169_52	-20,51	5224
169	TTATAGCCATTCTATCT	2-1-1-11-2	TTaTagccattctatCT	169_53	-18,88	5224
169	TTATAGCCATTCTATCT	2-2-1-10-2	TTatAgccattctatCT	169_54	-18,61	5224
169	TTATAGCCATTCTATCT	2-13-2	TTatagccattctatCT	169_55	-18,02	5224
169	TTATAGCCATTCTATCT	1-1-3-10-2	TtATAgccattctatCT	169_56	-20,18	5224
169	TTATAGCCATTCTATCT	1-1-2-11-2	TtATagccattctatCT	169_57	-18,55	5224
169	TTATAGCCATTCTATCT	2-9-3-1-2	TTatagccattCTAtCT	169_58	-21,75	5224
169	TTATAGCCATTCTATCT	1-1-1-8-2-2-2	TtAtagccattCTatCT	169_59	-19,47	5224

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
169	TTATAGCCATTCTATCT	1-2-2-6-2-2-2	TtaTAgccattCTatCT	169_60	-21,87	5224
169	TTATAGCCATTCTATCT	1-1-3-6-1-1-1-1-2	TtATAgccattCtAtCT	169_61	-21,25	5224
169	TTATAGCCATTCTATCT	3-8-1-2-3	TTAtagccattCtaTCT	169_62	-21,25	5224
170	ATTTAAATTTCCAAACATT	2-13-4	ATttaaatttccaaaCATT	170_1	-16,82	5427
171	GCTAATTTAAATTTCC	4-10-2	GCTAatttaaatttCC	171_1	-18,50	5434
172	ATCAATATCTTCTCAC	3-10-3	ATCaatatcttctCAC	172_1	-17,10	5785
173	TATCAATATCTTCTCA	2-10-4	TAtcaatatcttCTCA	173_1	-17,55	5786
174	CTACAAATTCAATTTACT	2-12-4	CTacaaattcaattTACT	174_1	-17,38	6341
175	TCTTACTCTGACTTTCCA	2-14-2	TCttactctgactttcCA	175_1	-21,47	6694
176	TCTTACTCTGACTTTCC	2-12-3	TCttactctgactTTCC	176_1	-21,53	6695
177	AAATTTCCAAACCTTTC	2-11-4	AAatttccaaaccTTTC	177_1	-16,30	6958
178	CTTCTTGTTTATCCCAA	2-11-4	CTtcttgtttatcCCAA	178_1	-22,77	7159
179	TTCTTGTTTATCCCAA	2-10-4	TTcttgtttatcCCAA	179_1	-20,17	7159
180	ATGCTTCTAACTAACA	4-10-2	ATGCttctaactaaCA	180_1	-19,21	7720
181	CTTTAATGCTTCTAACT	4-11-2	CTTTaatgcttctaaCT	181_1	-18,49	7724
182	CCTTTAATGCTTCTAAC	2-11-4	CCtttaatgcttcTAAC	182_1	-20,06	7725
183	CTTTAATGCTTCTAAC	2-10-4	CTttaatgcttcTAAC	183_1	-16,07	7725
184	TTCCTTTAATGCTTCTA	4-11-2	TTCCtttaatgcttcTA	184_1	-21,59	7727
185	TATACCTTTCTTTAACCCT	2-15-2	TAtacctttctttaaccCT	185_1	-22,03	8117
186	ATACCTTTCTTTAACCC	4-11-2	ATACctttctttaacCC	186_1	-22,68	8118
187	TTATACCTTTCTTTAACC	4-12-2	TTATacctttctttaaCC	187_1	-21,52	8119
188	TTTATACCTTTCTTTAAC	2-12-4	TTtatacctttcttTAAC	188_1	-17,01	8120
189	TCAAGAATTCTCTCCTT	2-11-4	TCaagaattctctCCTT	189_1	-21,29	8571
190	TTCAAGAATTCTCTCC	2-10-4	TTcaagaattctCTCC	190_1	-19,38	8573

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
191	CTTCAAGAATTCTCTC	2-10-4	CTtcaagaattcTCTC	191_1	-18,00	8574
192	TCTTCAAGAATTCTCT	2-10-4	TCttcaagaattCTCT	192_1	-18,46	8575
193	ATCTTCAAGAATTCTC	3-10-3	ATCttcaagaattCTC	193_1	-17,04	8576
194	TTTCTTACTATCTTCA	4-10-2	TTTCttactatcttCA	194_1	-17,47	8585
195	CCTTTAGCATTTCTATT	2-11-4	CCtttagcatttcTATT	195_1	-21,72	8819
196	TCCTTTAGCATTTCTAT	3-11-3	TCCtttagcatttcTAT	196_1	-22,39	8820
197	GTTCTCTTTATTTCTTCT	2-12-4	GTtctctttatttcTTCT	197_1	-21,76	8887
198	TTTACTGTCAACTCCT	2-10-4	TTtactgtcaacTCCT	198_1	-20,83	9150
199	TTTCCAATGAATCTAT	2-10-4	TTtccaatgaatCTAT	199_1	-16,61	9201
200	CCTTTCCAATGAATCTA	2-11-4	CCtttccaatgaaTCTA	200_1	-22,34	9202
201	CTTTCCAATGAATCTA	2-10-4	CTttccaatgaaTCTA	201_1	-18,34	9202
202	CCTTTCCAATGAATCT	3-10-3	CCTttccaatgaaTCT	202_1	-21,30	9203
203	TTATACCCTTTCCAAT	2-10-4	TTataccctttcCAAT	203_1	-19,61	9209
204	GTTTATACCCTTTCCAA	3-11-3	GTTtataccctttcCAA	204_1	-21,88	9210
205	TTTATACCCTTTCCAA	2-10-4	TTtatacccttttCCAA	205_1	-20,50	9210
206	GTTTATACCCTTTCCA	2-11-3	GTttatacccttttCCA	206_1	-22,69	9211
207	TGTTTATACCCTTTCCA	3-12-2	TGTttataccctttcCA	207_1	-22,80	9211
208	ACTGTTTATACCCTTTCC	2-14-2	ACtgtttatacccttttCC	208_1	-22,96	9212
208	ACTGTTTATACCCTTTCC	1-11-1-3-2	ActgtttataccCtttCC	208_2	-22,45	9212
208	ACTGTTTATACCCTTTCC	1-2-1-10-1-1-2	ActGtttatacccctTtCC	208_3	-22,17	9212
208	ACTGTTTATACCCTTTCC	1-2-1-1-1-10-2	ActGtTtatacccttttCC	208_4	-22,17	9212
208	ACTGTTTATACCCTTTCC	1-2-1-12-2	ActGtttatacccttttCC	208_5	-21,87	9212
208	ACTGTTTATACCCTTTCC	1-3-1-11-2	ActgTttatacccttttCC	208_6	-22,22	9212
208	ACTGTTTATACCCTTTCC	1-15-2	ActgtttatacccttttCC	208_7	-21,56	9212

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
209	ACTGTTTATACCCTTTC	4-11-2	ACTGtttatacccttTC	209_1	-21,65	9213
209	ACTGTTTATACCCTTTC	1-11-1-2-2	ActgtttataccCttTC	209_2	-18,25	9213
209	ACTGTTTATACCCTTTC	1-1-1-8-1-1-1-1-2	AcTgtttatacCcTtTC	209_3	-19,56	9213
209	ACTGTTTATACCCTTTC	1-2-1-9-4	ActGtttatacccTTTC	209_4	-19,51	9213
209	ACTGTTTATACCCTTTC	1-3-1-6-1-2-3	ActgTttatacCctTTC	209_5	-19,51	9213
209	ACTGTTTATACCCTTTC	2-9-1-3-2	ACtgtttatacCcttTC	209_6	-19,43	9213
209	ACTGTTTATACCCTTTC	1-2-1-7-1-3-2	ActGtttatacCcttTC	209_7	-18,35	9213
209	ACTGTTTATACCCTTTC	1-3-1-8-1-1-2	ActgTttatacccTtTC	209_8	-18,53	9213
209	ACTGTTTATACCCTTTC	1-11-1-1-3	ActgtttataccCtTTC	209_9	-19,06	9213
209	ACTGTTTATACCCTTTC	2-10-1-2-2	ACtgtttataccCttTC	209_10	-19,64	9213
210	AACTGTTTATACCCTTT	4-11-2	AACTgtttatacccttTT	210_1	-19,51	9214
211	TATGACTCCAATAATC	3-10-3	TATgactccaataATC	211_1	-16,57	10832
212	CTCCTTTATGACTCCAA	4-11-2	CTCCtttatgactccAA	212_1	-22,74	10837
213	CTCCTTTATGACTCCA	3-11-2	CTCctttatgactcCA	213_1	-21,50	10838
214	CCATTATTTCTTAAATA	4-11-2	CCATtatttcttaaaTA	214_1	-17,56	10877
215	ATTTCATATTACTAACTA	2-12-4	ATttcatattactaACTA	215_1	-16,64	11434
216	CATTTCATATTACTAACT	3-12-3	CATttcatattactaACT	216_1	-17,70	11435
217	TCATTTCATATTACTAAC	4-12-2	TCATttcatattactaAC	217_1	-16,72	11436
218	ATCATTTCATATTACTA	3-11-3	ATCatttcatattaCTA	218_1	-17,23	11438
219	TTATCATTTCATATTACT	4-12-2	TTATcatttcatattaCT	219_1	-17,77	11439
220	TGTACTTTCCTTTACCA	2-13-2	TGtactttcctttacCA	220_1	-20,37	11464
221	TATACACCATCATTATA	4-11-2	TATAcaccatcattaTA	221_1	-18,48	11507
222	TTATACACCATCATTAT	3-11-3	TTAtacaccatcatTAT	222_1	-17,83	11508
223	TATTTATACACCATCAT	3-11-3	TATttatacaccatCAT	223_1	-18,54	11511

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
224	TTATTTATACACCATC	2-10-4	TTatttatacacCATC	224_1	-16,60	11513
225	AATTATTTATACACCAT	2-11-4	AAttatttatacaCCAT	225_1	-16,82	11514
226	CATGACACTTACATAA	3-10-3	CATgacacttacaTAA	226_1	-16,26	11736
227	AGTTCACTACTATTAC	3-10-3	AGTtcactactatTAC	227_1	-17,55	12361
228	ATAAGCTTACCTCATA	2-10-4	ATaagcttacctCATA	228_1	-19,32	12794
229	TATAAGCTTACCTCAT	3-10-3	TATaagcttacctCAT	229_1	-19,32	12795
230	ATATAAGCTTACCTCA	4-10-2	ATATaagcttacctCA	230_1	-19,32	12796
231	CTTCCCTTTGATAACAT	3-11-3	CTTccctttgataaCAT	231_1	-21,19	12894
232	TTCCCTTTGATAACAT	4-10-2	TTCCctttgataacAT	232_1	-19,27	12894
233	CCTTCCCTTTGATAACA	2-12-3	CCttccctttgataACA	233_1	-23,06	12895
234	CTTCCCTTTGATAACA	4-10-2	CTTCcctttgataaCA	234_1	-20,51	12895
235	CCTTCCCTTTGATAAC	3-11-2	CCTtccctttgataAC	235_1	-20,96	12896
236	TTGATTCAATTCCCTTA	2-11-4	TTgattcaattccCTTA	236_1	-20,48	13223
236	TTGATTCAATTCCCTTA	2-9-1-1-1-1-2	TTgattcaattCcCtTA	236_2	-19,54	13223
236	TTGATTCAATTCCCTTA	2-10-1-1-3	TTgattcaattcCcTTA	236_3	-19,59	13223
236	TTGATTCAATTCCCTTA	2-1-1-8-1-2-2	TTgAttcaattcCctTA	236_4	-19,06	13223
236	TTGATTCAATTCCCTTA	2-2-1-7-1-2-2	TTgaTtcaattcCctTA	236_5	-19,00	13223
236	TTGATTCAATTCCCTTA	2-9-1-3-2	TTgattcaattCcctTA	236_6	-18,65	13223
236	TTGATTCAATTCCCTTA	1-2-2-6-2-2-2	TtgATtcaattCCctTA	236_7	-21,37	13223
236	TTGATTCAATTCCCTTA	2-1-1-7-1-1-1-1-2	TTgAttcaattCcCtTA	236_8	-20,04	13223
236	TTGATTCAATTCCCTTA	1-1-2-7-1-1-1-1-2	TtGAttcaattCcCtTA	236_9	-20,10	13223
236	TTGATTCAATTCCCTTA	1-2-1-9-4	TtgAttcaattccCTTA	236_10	-19,67	13223
236	TTGATTCAATTCCCTTA	1-3-1-6-1-1-1-1-2	TtgaTtcaattCcCtTA	236_11	-18,67	13223
236	TTGATTCAATTCCCTTA	2-10-1-2-2	TTgattcaattcCctTA	236_12	-18,56	13223

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
236	TTGATTCAATTCCCTTA	1-2-2-7-2-1-2	TtgATtcaattcCCtTA	236_13	-21,49	13223
236	TTGATTCAATTCCCTTA	1-1-2-8-1-2-2	TtGAttcaattcCctTA	236_14	-19,13	13223
236	TTGATTCAATTCCCTTA	2-11-1-1-2	TTgattcaattccCtTA	236_15	-18,77	13223
236	TTGATTCAATTCCCTTA	1-1-1-1-1-8-1-1-2	TtGaTtcaattccCtTA	236_16	-18,07	13223
236	TTGATTCAATTCCCTTA	1-1-2-7-2-2-2	TtGAttcaattCCctTA	236_17	-21,50	13223
236	TTGATTCAATTCCCTTA	1-2-1-7-1-1-4	TtgAttcaattCcCTTA	236_18	-20,44	13223
236	TTGATTCAATTCCCTTA	3-8-1-1-1-1-2	TTGattcaattCcCtTA	236_19	-20,60	13223
236	TTGATTCAATTCCCTTA	2-2-1-6-1-3-2	TTgaTtcaattCcctTA	236_20	-19,09	13223
236	TTGATTCAATTCCCTTA	2-2-1-7-2-1-2	TTgaTtcaattcCCtTA	236_21	-21,49	13223
237	ATTGATTCAATTCCCTT	2-11-4	ATtgattcaattcCCTT	237_1	-21,28	13224
237	ATTGATTCAATTCCCTT	3-8-3-1-2	ATTgattcaatTCCcTT	237_2	-22,78	13224
237	ATTGATTCAATTCCCTT	1-1-1-8-3-1-2	AtTgattcaatTCCcTT	237_3	-21,02	13224
237	ATTGATTCAATTCCCTT	1-2-1-8-2-1-2	AttGattcaattCCcTT	237_4	-19,40	13224
237	ATTGATTCAATTCCCTT	1-3-1-7-2-1-2	AttgAttcaattCCcTT	237_5	-19,74	13224
237	ATTGATTCAATTCCCTT	1-2-1-7-2-1-3	AttGattcaatTCcCTT	237_6	-19,67	13224
237	ATTGATTCAATTCCCTT	2-2-1-7-1-1-3	ATtgAttcaattCcCTT	237_7	-20,27	13224
237	ATTGATTCAATTCCCTT	1-1-1-9-1-1-3	AtT gattcaattCcCTT	237_8	-19,32	13224
237	ATTGATTCAATTCCCTT	1-3-1-7-1-1-3	AttgAttcaattCcCTT	237_9	-19,02	13224
237	ATTGATTCAATTCCCTT	1-1-1-1-1-7-2-1-2	AtTgAttcaattCCcTT	237_10	-20,53	13224
237	ATTGATTCAATTCCCTT	1-2-2-7-2-1-2	AttGAttcaattCCcTT	237_11	-21,11	13224
237	ATTGATTCAATTCCCTT	1-2-1-8-1-1-3	AttGattcaattCcCTT	237_12	-18,68	13224
237	ATTGATTCAATTCCCTT	1-1-2-8-1-2-2	AtTGattcaattCccTT	237_13	-18,81	13224
237	ATTGATTCAATTCCCTT	3-10-1-1-2	ATTgattcaattcCcTT	237_14	-19,42	13224
237	ATTGATTCAATTCCCTT	1-1-2-9-4	AtTGattcaattcCCTT	237_15	-21,89	13224

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
237	ATTGATTCAATTCCCTT	2-2-1-8-1-1-2	ATtgAttcaattcCcTT	237_16	-18,61	13224
237	ATTGATTCAATTCCCTT	1-2-2-6-3-1-2	AttGAttcaatTCCcTT	237_17	-22,09	13224
237	ATTGATTCAATTCCCTT	1-1-1-8-2-1-3	AtTgattcaatTCcCTT	237_18	-20,30	13224
237	ATTGATTCAATTCCCTT	1-1-1-9-2-1-2	AtTgattcaattCCcTT	237_19	-20,03	13224
237	ATTGATTCAATTCCCTT	1-1-1-1-1-7-1-1-3	AtT gAttcaattCcCTT	237_20	-19,82	13224
237	ATTGATTCAATTCCCTT	3-1-1-8-1-1-2	ATTgAttcaattcCcTT	237_21	-19,92	13224
238	TTGATTCAATTCCCTT	2-10-4	TTgattcaattcCCTT	238_1	-20,52	13224
239	TATTGATTCAATTCCCT	2-11-4	TAttgattcaattCCCT	239_1	-22,82	13225
239	TATTGATTCAATTCCCT	3-9-2-1-2	TATtgattcaatTCcCT	239_2	-21,17	13225
239	TATTGATTCAATTCCCT	2-9-1-1-1-1-2	TAttgattcaaTtCcCT	239_3	-19,37	13225
239	TATTGATTCAATTCCCT	1-1-2-7-3-1-2	TaTTgattcaaTTCcCT	239_4	-21,49	13225
239	TATTGATTCAATTCCCT	1-3-1-6-3-1-2	TattGattcaaTTCcCT	239_5	-19,90	13225
239	TATTGATTCAATTCCCT	2-9-1-2-3	TAttgattcaaTtcCCT	239_6	-20,89	13225
239	TATTGATTCAATTCCCT	1-10-1-2-3	TattgattcaaTtcCCT	239_7	-19,76	13225
239	TATTGATTCAATTCCCT	1-1-1-1-1-8-1-1-2	T a TtGattcaattCcCT	239_8	-18,41	13225
239	TATTGATTCAATTCCCT	1-2-2-8-1-1-2	TatTGattcaattCcCT	239_9	-19,66	13225
239	TATTGATTCAATTCCCT	1-2-1-9-1-1-2	TatTgattcaattCcCT	239_10	-18,60	13225
239	TATTGATTCAATTCCCT	2-2-1-10-2	TAttGattcaattccCT	239_11	-18,33	13225
239	TATTGATTCAATTCCCT	1-12-4	TattgattcaattCCCT	239_12	-21,69	13225
239	TATTGATTCAATTCCCT	2-1-1-9-1-1-2	TAtTgattcaattCcCT	239_13	-19,73	13225
239	TATTGATTCAATTCCCT	2-12-3	TAttgattcaattcCCT	239_14	-20,45	13225
239	TATTGATTCAATTCCCT	1-2-1-10-3	TatTgattcaattcCCT	239_15	-20,11	13225
239	TATTGATTCAATTCCCT	1-1-3-10-2	TaTTGattcaattccCT	239_16	-19,84	13225
239	TATTGATTCAATTCCCT	1-1-1-1-1-6-3-1-2	TaTtGattcaaTTCcCT	239_17	-20,34	13225

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
239	TATTGATTCAATTCCCT	2-2-1-6-1-1-1-1-2	TAttGattcaaTtCcCT	239_18	-19,54	13225
239	TATTGATTCAATTCCCT	2-1-1-8-2-1-2	TAtTgattcaatTCcCT	239_19	-20,72	13225
239	TATTGATTCAATTCCCT	1-1-2-9-1-1-2	TaTTgattcaattCcCT	239_20	-19,55	13225
239	TATTGATTCAATTCCCT	2-1-1-10-3	TAtTgattcaattcCCT	239_21	-21,24	13225
240	TATTGATTCAATTCCC	3-10-3	TATtgattcaattCCC	240_1	-20,58	13226
241	GCACATTCTTTCTATAC	3-11-3	GCAcattctttctaTAC	241_1	-21,17	15115
241	GCACATTCTTTCTATAC	1-1-3-6-2-2-2	GcACAttctttCTatAC	241_2	-20,68	15115
241	GCACATTCTTTCTATAC	1-1-1-1-1-6-1-2-3	GcAcAttctttCtaTAC	241_3	-18,46	15115
241	GCACATTCTTTCTATAC	1-1-2-7-1-2-3	GcACattctttCtaTAC	241_4	-19,49	15115
241	GCACATTCTTTCTATAC	2-9-1-3-2	GCacattctttCtatAC	241_5	-18,68	15115
241	GCACATTCTTTCTATAC	1-1-3-8-4	GcACAttctttctATAC	241_6	-20,89	15115
241	GCACATTCTTTCTATAC	2-2-1-9-3	GCacAttctttctaTAC	241_7	-19,66	15115
241	GCACATTCTTTCTATAC	2-1-1-11-2	GCaCattctttctatAC	241_8	-18,39	15115
241	GCACATTCTTTCTATAC	1-1-3-9-3	GcACAttctttctaTAC	241_9	-19,98	15115
241	GCACATTCTTTCTATAC	3-12-2	GCAcattctttctatAC	241_10	-19,27	15115
241	GCACATTCTTTCTATAC	1-1-1-1-1-6-1-1-4	GcAcAttctttCtATAC	241_11	-19,36	15115
241	GCACATTCTTTCTATAC	3-8-1-1-1-1-2	GCAcattctttCtAtAC	241_12	-20,34	15115
241	GCACATTCTTTCTATAC	2-1-1-7-1-2-3	GCaCattctttCtaTAC	241_13	-21,27	15115
241	GCACATTCTTTCTATAC	1-2-2-8-4	GcaCAttctttctATAC	241_14	-20,33	15115
241	GCACATTCTTTCTATAC	1-1-3-10-2	GcACAttctttctatAC	241_15	-18,08	15115
242	GAATTTCAACTACTAT	2-10-4	GAatttcaactaCTAT	242_1	-16,13	15258
243	CCATTTATTTCCATTTAT	3-12-3	CCAtttatttccattTAT	243_1	-21,92	15568
244	TTTCCATTTATTTCCATTT	4-13-2	TTTCcatttatttccatTT	244_1	-20,93	15570
244	TTTCCATTTATTTCCATTT	1-4-1-7-1-1-4	TttccAtttatttCcATTT	244_2	-20,48	15570

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
244	TTTCCATTTATTTCCATTT	2-1-1-10-2-1-2	TTtCcatttatttcCAtTT	244_3	-21,47	15570
244	TTTCCATTTATTTCCATTT	1-2-1-1-1-7-1-3-2	TttCcAtttatttCcatTT	244_4	-19,43	15570
244	TTTCCATTTATTTCCATTT	2-2-2-11-2	TTtcCAtttatttccatTT	244_5	-20,70	15570
245	CTTTCCATTTATTTCCAT	3-12-3	CTTtccatttatttcCAT	245_1	-22,31	15572
246	TCTTTCCATTTATTTCCA	4-12-2	TCTTtccatttatttcCA	246_1	-22,74	15573
247	ATCTTTCCATTTATTTCC	3-12-3	ATCtttccatttattTCC	247_1	-22,85	15574
248	TTCCATGCAAACTTTA	4-10-2	TTCCatgcaaactttTA	248_1	-19,01	15722
249	CAGTTTAAATTCACAC	3-10-3	CAGtttaaattcaCAC	249_1	-16,68	16597
250	CTATTCCAGTTTAAAT	4-10-2	CTATtccagtttaaAT	250_1	-16,86	16603
251	TGCAAATACCTCTTCA	4-10-2	TGCAaatacctcttCA	251_1	-21,49	16730
252	CTAAATAGATTCCACT	2-10-4	CT aaatagattcCACT	252_1	-17,95	16849
253	TATTGATATTTACTCT	2-10-4	TAttgatatttaCTCT	253_1	-16,32	17089
254	CCTTAGTATTACAATT	4-10-2	CCTTagtattacaaTT	254_1	-17,43	17401
255	CTATTCAATAAACTAAACA	4-13-2	CTATtcaataaactaaaCA	255_1	-16,45	24290
256	CAGCTATTCAATAAAC	4-10-2	CAGCtattcaataaAC	256_1	-16,94	24296
257	TATAGACCCAAACTAT	3-10-3	TATagacccaaacTAT	257_1	-18,15	24811
258	TAATCCCATACATCTAT	2-11-4	TAatcccatacatCTAT	258_1	-20,45	25032
259	ATAATCCCATACATCTA	3-11-3	ATAatcccatacatCTA	259_1	-20,45	25033
260	ATCTCAACTACCATTT	4-10-2	ATCTcaactaccatTT	260_1	-18,14	25250
261	AATCTCAACTACCATT	4-10-2	AATCtcaactaccaTT	261_1	-16,76	25251
262	ACAACTTCTATCATAC	3-10-3	ACAacttctatcaTAC	262_1	-16,33	25718
263	GAACAACTTCTATCAT	2-10-4	GAacaacttctaTCAT	263_1	-16,94	25720
264	TGAACAACTTCTATCA	3-10-3	TGAacaacttctaTCA	264_1	-17,36	25721
265	TACACAAATACTTAAATCA	4-13-2	TACAcaaatacttaaatCA	265_1	-16,93	26331

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
266	TTAAGCTTTCACCTAT	2-10-4	TTaagctttcacCTAT	266_1	-19,36	27165
267	AAACTCTTGCATCTACT	2-13-2	AAactcttgcatctaCT	267_1	-16,65	27248
268	AAATTTCTCAACCTAAATTT	2-14-4	AAatttctcaacctaaATTT	268_1	-16,78	29330
269	CCAACATAGATCCTCT	2-10-4	CCaacatagatcCTCT	269_1	-22,49	29635
270	TCCAACATAGATCCTCT	2-11-4	TCcaacatagatcCTCT	270_1	-22,81	29635
271	CTCCAACATAGATCCTC	3-11-3	CTCcaacatagatcCTC	271_1	-22,81	29636
272	TCCAACATAGATCCTC	2-10-4	TCcaacatagatCCTC	272_1	-21,69	29636
273	CTCCAACATAGATCCT	3-10-3	CTCcaacatagatCCT	273_1	-22,68	29637
274	TCTCCAACATAGATCCT	4-11-2	TCTCcaacatagatcCT	274_1	-22,81	29637
275	ATTCTCAATTGCACTT	4-10-2	ATTCtcaattgcacTT	275_1	-17,90	29661
276	TATTCTCAATTGCACTT	4-11-2	TATTctcaattgcacTT	276_1	-18,54	29661
277	TCACCTAATAGCACCA	2-10-4	TCacctaatagcACCA	277_1	-21,99	29684
278	TTCACCTAATAGCACCA	2-11-4	TTcacctaatagcACCA	278_1	-22,53	29684
279	CATTATTATTTAACCTT	2-11-4	CAttattatttaaCCTT	279_1	-17,83	30455
280	ACATTATTATTTAACCT	3-11-3	ACAttattatttaaCCT	280_1	-18,05	30456
281	TACATTATTATTTAACC	4-11-2	TACAttattatttaaCC	281_1	-16,80	30457
282	CATTTACATTATTATTTAAC	2-14-4	CAtttacattattattTAAC	282_1	-16,44	30458
283	CTCATTTACATTATTATT	4-12-2	CTCAtttacattattaTT	283_1	-17,33	30462
284	TATCTCATTTACATTATT	4-12-2	TATCtcatttacattaTT	284_1	-17,62	30465
285	ATCATTCTCAACAATTA	4-11-2	ATCAttctcaacaatTA	285_1	-17,04	30601
285	ATCATTCTCAACAATTA	4-7-6	ATCAttctcaaCAATTA	285_2	-21,48	30601
285	ATCATTCTCAACAATTA	1-1-3-6-6	AtCATtctcaaCAATTA	285_3	-20,80	30601
285	ATCATTCTCAACAATTA	5-6-2-2-2	ATCATtctcaaCAatTA	285_4	-20,46	30601
285	ATCATTCTCAACAATTA	4-7-1-1-4	ATCAttctcaaCaATTA	285_5	-19,80	30601

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
285	ATCATTCTCAACAATTA	5-7-1-1-3	ATCATtctcaacAaTTA	285_6	-19,31	30601
285	ATCATTCTCAACAATTA	5-6-3-1-2	ATCATtctcaaCAAtTA	285_7	-20,97	30601
285	ATCATTCTCAACAATTA	4-7-2-1-3	ATCAttctcaaCAaTTA	285_8	-20,16	30601
285	ATCATTCTCAACAATTA	5-6-1-1-4	ATCATtctcaaCaATTA	285_9	-21,05	30601
285	ATCATTCTCAACAATTA	5-6-1-1-1-1-2	ATCATtctcaaCaAtTA	285_10	-19,29	30601
285	ATCATTCTCAACAATTA	1-1-3-7-5	AtCATtctcaacAATTA	285_11	-18,70	30601
286	AAGATCATTCTCAACA	4-10-2	AAGAtcattctcaaCA	286_1	-17,15	30605
287	TCTCAAAGATCATTCTC	3-11-3	TCTcaaagatcattCTC	287_1	-19,02	30609
288	TCTCAAAGATCATTCT	4-10-2	TCTCaaagatcattCT	288_1	-17,81	30610
289	ACTTAATTATACTTCC	4-10-2	ACTTaattatacttCC	289_1	-17,28	30667
290	TACACTTAATTATACTTC	2-12-4	TAcacttaattataCTTC	290_1	-16,87	30668
291	TTACACTTAATTATACTT	3-12-3	TTAcacttaattataCTT	291_1	-16,20	30669
292	TTTACACTTAATTATACT	2-12-4	TTtacacttaattaTACT	292_1	-16,23	30670
293	CTATTTAATTTACACTT	3-11-3	CTAtttaatttacaCTT	293_1	-16,26	30679
294	TATCTATTTAATTTACAC	3-12-3	TATctatttaatttaCAC	294_1	-16,06	30681
295	TTTATCTATTTAATTTACA	4-13-2	TTTAtctatttaatttaCA	295_1	-16,34	30682
296	CTCTGCTTATAACTTT	4-10-2	CTCTgcttataactTT	296_1	-18,51	30699
297	CCTCTGCTTATAACTT	3-10-3	CCTctgcttataaCTT	297_1	-21,29	30700
298	TCCTCTGCTTATAACTT	3-12-2	TCCtctgcttataacTT	298_1	-20,86	30700
299	TCCTCTGCTTATAACT	3-11-2	TCCtctgcttataaCT	299_1	-20,70	30701
300	TTCCTCTGCTTATAACT	3-12-2	TTCctctgcttataaCT	300_1	-20,03	30701
301	TTTCCTCTGCTTATAAC	4-11-2	TTTCctctgcttataAC	301_1	-19,20	30702
302	TACTATACTTTCCTCT	2-10-4	TActatactttcCTCT	302_1	-20,07	30711
303	TTCTACTATACTTTCC	4-10-2	TTCTactatactttCC	303_1	-19,55	30714

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
304	AGTTCTACTATACTTTC	4-11-2	AGTTctactatacttTC	304_1	-18,49	30715
304	AGTTCTACTATACTTTC	1-10-6	AgttctactatACTTTC	304_2	-18,76	30715
304	AGTTCTACTATACTTTC	1-1-2-7-1-1-4	AgTTctactatAcTTTC	304_3	-18,23	30715
304	AGTTCTACTATACTTTC	3-8-2-2-2	AGTtctactatACttTC	304_4	-19,19	30715
304	AGTTCTACTATACTTTC	2-2-1-6-1-1-4	AGttCtactatAcTTTC	304_5	-19,07	30715
304	AGTTCTACTATACTTTC	1-2-2-8-4	AgtTCtactatacTTTC	304_6	-18,46	30715
304	AGTTCTACTATACTTTC	3-10-1-1-2	AGTtctactatacTtTC	304_7	-18,12	30715
304	AGTTCTACTATACTTTC	3-11-3	AGTtctactatactTTC	304_8	-18,42	30715
304	AGTTCTACTATACTTTC	3-1-1-10-2	AGTtCtactatacttTC	304_9	-18,58	30715
304	AGTTCTACTATACTTTC	2-1-2-10-2	AGtTCtactatacttTC	304_10	-18,02	30715
304	AGTTCTACTATACTTTC	1-2-2-6-2-1-3	AgtTCtactatACtTTC	304_11	-19,02	30715
304	AGTTCTACTATACTTTC	2-1-2-6-1-3-2	AGtTCtactatActtTC	304_12	-18,22	30715
304	AGTTCTACTATACTTTC	2-2-1-7-2-1-2	AGttCtactataCTtTC	304_13	-19,22	30715
304	AGTTCTACTATACTTTC	3-1-1-7-1-1-3	AGTtCtactataCtTTC	304_14	-20,39	30715
304	AGTTCTACTATACTTTC	1-1-1-1-1-8-4	AgTtCtactatacTTTC	304_15	-18,13	30715
305	GTTCTACTATACTTTC	4-10-2	GTTCtactatacttTC	305_1	-17,48	30715
306	CATTATATTTAAACTATCA	4-13-2	CATTatatttaaactatCA	306_1	-16,93	31630
307	CACATTATATTTAAACTAT	2-13-4	CAcattatatttaaaCTAT	307_1	-17,11	31632
308	ACACATTATATTTAAACTA	3-13-3	ACAcattatatttaaaCTA	308_1	-17,09	31633
309	ACCACCTAAGACCTCAA	2-11-4	ACcacctaagaccTCAA	309_1	-22,49	32755
310	CCACCTAAGACCTCAA	2-10-4	CCacctaagaccTCAA	310_1	-22,63	32755
311	ACCACCTAAGACCTCA	2-11-3	ACcacctaagaccTCA	311_1	-21,74	32756
312	ACCTTAAGTAACATTT	4-10-2	ACCTtaagtaacatTT	312_1	-16,82	33366
313	CACCTTAAGTAACATT	4-10-2	CACCttaagtaacaTT	313_1	-18,05	33367

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
314	CCACCTTAAGTAACAT	3-10-3	CCAccttaagtaaCAT	314_1	-20,70	33368
315	ACCACCTTAAGTAACA	4-10-2	ACCAccttaagtaaCA	315_1	-20,68	33369
316	TTATTAACCACCTTAA	3-10-3	TTAttaaccacctTAA	316_1	-16,19	33375
317	CATTATTAACCACCTT	2-10-4	CAttattaaccaCCTT	317_1	-19,92	33377
318	ACATTATTAACCACCT	3-10-3	ACAttattaaccaCCT	318_1	-20,14	33378
319	ACCAATTATACTTACAA	3-11-3	ACCaattatacttaCAA	319_1	-17,16	36606
320	AACCAATTATACTTACA	4-11-2	AACCaattatacttaCA	320_1	-17,16	36607
321	CAAATACAGATTATCC	2-10-4	CAaatacagattATCC	321_1	-16,44	38092
322	TTTACATTCCCATCATC	2-11-4	TTtacattcccatCATC	322_1	-21,08	38297
323	CACACCTATTATATAAT	4-11-2	CACAcctattatataAT	323_1	-17,02	39173
324	TCACACCTATTATATAA	3-11-3	TCAcacctattataTAA	324_1	-17,02	39174
325	CTTCACACCTATTATATA	2-12-4	CTtcacacctattaTATA	325_1	-20,65	39175
326	ACTTCACACCTATTATAT	3-12-3	ACTtcacacctattaTAT	326_1	-20,46	39176
327	GCTCACACTAATTATT	2-10-4	GCtcacactaatTATT	327_1	-18,72	39228
328	ATGCTCACACTAATTA	4-10-2	ATGCtcacactaatTA	328_1	-19,38	39230
329	AATGCTCACACTAATT	4-10-2	AATGctcacactaaTT	329_1	-16,21	39231
330	AAACTGTACACCTACT	2-10-4	AAactgtacaccTACT	330_1	-17,99	39563
331	GTTTCCATCTACTATTA	2-11-4	GTttccatctactATTA	331_1	-19,78	39808
332	TTTCCATCTACTATTA	4-10-2	TTTCcatctactatTA	332_1	-17,25	39808
333	TGACATAACCATATAC	3-10-3	TGAcataaccataTAC	333_1	-16,63	39931
334	GCTCCCAAACAACTAA	2-12-2	GCtcccaaacaactAA	334_1	-17,55	41114
335	CCTCAATACTCTACTT	4-10-2	CCTCaatactctacTT	335_1	-20,30	41444
336	GACCTCAATACTCTACT	3-11-3	GACctcaatactctACT	336_1	-21,01	41445
337	GACCTCAATACTCTAC	4-10-2	GACCtcaatactctAC	337_1	-20,02	41446

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
338	TACTAAACATACACATA	4-11-2	TACTaaacatacacaTA	338_1	-16,12	41725
339	CTACTAAACATACACAT	3-11-3	CTActaaacatacaCAT	339_1	-17,31	41726
340	TTCTACTAAACATACAC	3-11-3	TTCtactaaacataCAC	340_1	-16,07	41728
341	TACCAATAGTTACCTT	2-10-4	TAccaatagttaCCTT	341_1	-20,03	42167
342	CTTACCAATAGTTACCT	3-11-3	CTTaccaatagttaCCT	342_1	-22,29	42168
343	TTACCAATAGTTACCT	3-10-3	TTAccaatagttaCCT	343_1	-20,03	42168
344	CTTACCAATAGTTACC	4-10-2	CTTAccaatagttaCC	344_1	-20,03	42169
345	TCTTACCAATAGTTACC	4-11-2	TCTTaccaatagttaCC	345_1	-21,30	42169
346	TCAAAGCACACCACCAC	2-12-3	TCaaagcacaccacCAC	346_1	-21,69	42287
347	ATTCAAAGCACACCACC	2-12-3	ATtcaaagcacaccACC	347_1	-21,00	42289
348	AGACTAATCCTCTTAA	3-10-3	AGActaatcctctTAA	348_1	-17,72	43452
349	TAGACTAATCCTCTTA	4-10-2	TAGActaatcctctTA	349_1	-19,20	43453
350	CCCATTTCTAACATTTAC	3-12-3	CCCatttctaacattTAC	350_1	-22,93	43562
351	ACCCATTTCTAACATT	4-10-2	ACCCatttctaacaTT	351_1	-20,64	43565
352	AACCCATTTCTAACAT	4-10-2	AACCcatttctaacAT	352_1	-18,25	43566
353	CCTCAACTTCACCAAT	2-10-4	CCtcaacttcacCAAT	353_1	-21,73	43634
354	ACTGATTTCCTTAAAC	4-10-2	ACTGatttccttaaAC	354_1	-16,67	44180
355	CACTGATTTCCTTAAAC	4-11-2	CACTgatttccttaaAC	355_1	-18,91	44180
356	CCACTGATTTCCTTAAA	4-11-2	CCACtgatttccttaAA	356_1	-20,91	44181
357	ACCACTGATTTCCTTA	2-10-4	ACcactgatttcCTTA	357_1	-20,98	44183
358	CACCACTGATTTCCTT	3-10-3	CACcactgatttcCTT	358_1	-22,04	44184
359	CTCTGCAATACACCAA	2-10-4	CTctgcaatacaCCAA	359_1	-20,90	44439
360	ACTCTGCAATACACCA	3-10-3	ACTctgcaatacaCCA	360_1	-22,19	44440
361	TACTCTGCAATACACCA	2-11-4	TActctgcaatacACCA	361_1	-22,32	44440

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
361	TACTCTGCAATACACCA	1-1-1-10-1-1-2	TaCtctgcaatacAcCA	361_2	-19,29	44440
361	TACTCTGCAATACACCA	1-3-1-8-1-1-2	TactCtgcaatacAcCA	361_3	-19,28	44440
361	TACTCTGCAATACACCA	1-10-1-3-2	TactctgcaatAcacCA	361_4	-18,35	44440
361	TACTCTGCAATACACCA	2-10-2-1-2	TActctgcaataCAcCA	361_5	-21,63	44440
361	TACTCTGCAATACACCA	1-13-3	TactctgcaatacaCCA	361_6	-20,54	44440
361	TACTCTGCAATACACCA	2-10-1-2-2	TActctgcaataCacCA	361_7	-20,06	44440
361	TACTCTGCAATACACCA	1-1-1-12-2	TaCtctgcaatacacCA	361_8	-19,14	44440
361	TACTCTGCAATACACCA	1-2-2-10-2	TacTCtgcaatacacCA	361_9	-20,33	44440
361	TACTCTGCAATACACCA	1-3-1-10-2	TactCtgcaatacacCA	361_10	-19,13	44440
362	TACTCTGCAATACACC	2-10-4	TActctgcaataCACC	362_1	-21,12	44441
362	TACTCTGCAATACACC	1-1-1-11-2	TaCtctgcaatacaCC	362_2	-18,23	44441
362	TACTCTGCAATACACC	1-1-1-10-3	TaCtctgcaatacACC	362_3	-18,78	44441
362	TACTCTGCAATACACC	1-3-1-7-4	TactCtgcaataCACC	362_4	-20,87	44441
362	TACTCTGCAATACACC	3-11-2	TACtctgcaatacaCC	362_5	-19,86	44441
362	TACTCTGCAATACACC	2-2-1-9-2	TActCtgcaatacaCC	362_6	-19,44	44441
362	TACTCTGCAATACACC	2-12-2	TActctgcaatacaCC	362_7	-18,47	44441
362	TACTCTGCAATACACC	1-2-2-9-2	TacTCtgcaatacaCC	362_8	-19,42	44441
362	TACTCTGCAATACACC	2-1-2-9-2	TAcTCtgcaatacaCC	362_9	-20,64	44441
362	TACTCTGCAATACACC	1-3-1-9-2	TactCtgcaatacaCC	362_10	-18,22	44441
363	TTACTCTGCAATACACC	2-11-4	TTactctgcaataCACC	363_1	-21,71	44441
364	TTACTCTGCAATACAC	3-10-3	TT ActctgcaataCAC	364_1	-17,75	44442
365	TTTACTCTGCAATACAC	3-11-3	TTTactctgcaataCAC	365_1	-18,34	44442
366	CTTTACTCTGCAATACA	2-11-4	CTttactctgcaaTACA	366_1	-20,23	44443
367	TTTACTCTGCAATACA	2-10-4	TTtactctgcaaTACA	367_1	-17,56	44443

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
368	GACCACACTTTCTACCA	2-13-2	GAccacactttctacCA	368_1	-21,72	44477
369	GACCACACTTTCTACC	2-12-2	GAccacactttctaCC	369_1	-20,81	44478
370	AAGAAACACCCTTCCA	2-10-4	AAgaaacaccctTCCA	370_1	-21,48	44776
371	ATCTGCTACATATTCTT	4-11-2	ATCTgctacatattcTT	371_1	-19,88	45216
372	ATCTGCTACATATTCT	4-10-2	ATCTgctacatattCT	372_1	-19,71	45217
373	CATCTGCTACATATTCT	4-11-2	CATCtgctacatattCT	373_1	-21,32	45217
374	CATCTGCTACATATTC	4-10-2	CATCtgctacatatTC	374_1	-18,82	45218
375	TTCAACCCTAATCACT	4-10-2	TTCAaccctaatcaCT	375_1	-19,99	45246
376	ATTCAACCCTAATCAC	2-10-4	ATtcaaccctaaTCAC	376_1	-18,67	45247
377	CATTCAACCCTAATCA	3-10-3	CATtcaaccctaaTCA	377_1	-19,93	45248
378	GCATTCAACCCTAATCA	3-12-2	GCAttcaaccctaatCA	378_1	-22,56	45248
379	AGCATTCAACCCTAATC	4-11-2	AGCAttcaaccctaaTC	379_1	-22,98	45249
380	GCATTCAACCCTAATC	4-10-2	GCATtcaaccctaaTC	380_1	-21,63	45249
381	AGCATTCAACCCTAAT	4-10-2	AGCAttcaaccctaAT	381_1	-21,62	45250
382	CAGCATTCAACCCTAAT	3-12-2	CAGcattcaaccctaAT	382_1	-21,12	45250
383	TTAAATCCAGCATTCA	3-10-3	TTAaatccagcatTCA	383_1	-18,08	45258
384	CTCCATATTTAAATCC	4-10-2	CTCCatatttaaatCC	384_1	-20,02	45266
385	GCTCCATATTTAAATCC	4-11-2	GCTCcatatttaaatCC	385_1	-22,84	45266
386	GCTCCATATTTAAATC	4-10-2	GCTCcatatttaaaTC	386_1	-18,78	45267
387	AGCTCCATATTTAAAT	4-10-2	AGCTccatatttaaAT	387_1	-18,62	45268
388	TAAGCTCCATATTTAA	3-10-3	TAAgctccatattTAA	388_1	-16,08	45270
389	CCTAAGCTCCATATTTA	3-11-3	CCTaagctccatatTTA	389_1	-22,65	45271
390	CTAAGCTCCATATTTA	4-10-2	CTAAgctccatattTA	390_1	-18,81	45271
391	CCTAAGCTCCATATTT	4-10-2	CCTAagctccatatTT	391_1	-21,57	45272

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
392	TCTACCCTAAATTCCC	2-11-3	TCtaccctaaattCCC	392_1	-23,00	45560
393	CACATCTTGTATACAA	3-10-3	CACatcttgtataCAA	393_1	-16,65	45627
394	ACACATCTTGTATACA	4-10-2	ACACatcttgtataCA	394_1	-17,95	45628
395	CTACACATCTTGTATAC	3-11-3	CTAcacatcttgtaTAC	395_1	-19,13	45629
396	TACACATCTTGTATAC	3-10-3	TACacatcttgtaTAC	396_1	-16,73	45629
397	CTTGACTACACATCTT	3-10-3	CTTgactacacatCTT	397_1	-18,89	45635
398	CTCTACAACAGTCCCA	3-11-2	CTCtacaacagtccCA	398_1	-22,06	45709
399	TCTCTACAACAGTCCCA	2-13-2	TCtctacaacagtccCA	399_1	-21,70	45709
400	ATAACATTACTCTTAACA	3-12-3	AT AacattactcttaACA	400_1	-17,03	46215
401	TTTGACATTCCATCTCC	2-12-3	TTtgacattccatcTCC	401_1	-21,62	46256
402	CTTTGACATTCCATCTC	2-11-4	CTttgacattccaTCTC	402_1	-21,88	46257
403	TCTTTGACATTCCATCTC	4-12-2	TCTTtgacattccatcTC	403_1	-22,41	46257
404	TTTGACATTCCATCTC	3-10-3	TTTgacattccatCTC	404_1	-19,40	46257
405	ATCTTTGACATTCCATC	2-11-4	ATctttgacattcCATC	405_1	-20,53	46259
406	TATCTTTGACATTCCAT	2-11-4	TAtctttgacattCCAT	406_1	-21,32	46260
407	TACTATCTTTGACATTC	4-11-2	TACTatctttgacatTC	407_1	-18,39	46263
408	TACTATCTTTGACATT	4-10-2	TACTatctttgacaTT	408_1	-16,84	46264
409	CTGTATACACCATCCC	2-12-2	CTgtatacaccatcCC	409_1	-21,84	46392
410	TCTGTATACACCATCC	4-10-2	TCTGtatacaccatCC	410_1	-22,73	46393
411	TTTCTGACTCCCTATCC	2-13-2	TTtctgactccctatCC	411_1	-22,48	46420
412	CCTATGTTAATACTTTC	4-11-2	CCTAtgttaatacttTC	412_1	-19,53	46505
413	CTATGTTAATACTTTC	4-10-2	CTATgttaatacttTC	413_1	-16,09	46505
414	CCTATGTTAATACTTT	4-10-2	CCTAtgttaatactTT	414_1	-17,85	46506
415	TCCTATGTTAATACTT	3-10-3	TCCtatgttaataCTT	415_1	-18,47	46507

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
416	ATCCTATGTTAATACT	4-10-2	ATCCtatgttaataCT	416_1	-18,71	46508
417	ATTTCATTAAGTCACCC	3-11-3	ATTtcattaagtcaCCC	417_1	-22,16	47364
418	ATTTCATTAAGTCACC	2-10-4	ATttcattaagtCACC	418_1	-18,79	47365
419	CTCTCCTCAAGATCAAC	3-11-3	CTCtcctcaagatcAAC	419_1	-20,29	48110
420	CTCTCCTCAAGATCAA	3-10-3	CTCtcctcaagatCAA	420_1	-20,33	48111
421	CCATACAGTATATACA	4-10-2	CCATacagtatataCA	421_1	-19,53	48186
422	CAACTATTATCTTCTT	2-10-4	CAactattatctTCTT	422_1	-16,38	48221
423	ACAACTATTATCTTCT	3-10-3	ACAactattatctTCT	423_1	-16,60	48222
424	TTGCTTCCAATTTATTT	4-11-2	TTGCttccaatttatTT	424_1	-19,93	50282
425	ATCTCATGACCACCTAA	3-11-3	ATCtcatgaccaccTAA	425_1	-21,74	51241
425	ATCTCATGACCACCTAA	1-1-1-9-2-1-2	AtCtcatgaccaCCtAA	425_2	-21,11	51241
425	ATCTCATGACCACCTAA	1-1-1-8-1-2-3	AtCtcatgaccAccTAA	425_3	-19,96	51241
425	ATCTCATGACCACCTAA	1-12-4	AtctcatgaccacCTAA	425_4	-20,40	51241
425	ATCTCATGACCACCTAA	3-10-1-1-2	ATCtcatgaccacCtAA	425_5	-20,66	51241
425	ATCTCATGACCACCTAA	1-1-1-10-1-1-2	AtCtcatgaccacCtAA	425_6	-18,72	51241
425	ATCTCATGACCACCTAA	1-1-1-9-1-1-3	AtCtcatgaccaCcTAA	425_7	-20,59	51241
425	ATCTCATGACCACCTAA	1-2-2-7-1-1-3	AtcTCatgaccaCcTAA	425_8	-21,48	51241
425	ATCTCATGACCACCTAA	1-3-1-8-4	AtctCatgaccacCTAA	425_9	-21,07	51241
425	ATCTCATGACCACCTAA	1-1-3-8-1-1-2	AtCTCatgaccacCtAA	425_10	-21,27	51241
426	TCTCATGACCACCTAA	2-10-4	TCtcatgaccacCTAA	426_1	-21,25	51241
427	ATCTCATGACCACCTA	3-10-3	ATCtcatgaccacCTA	427_1	-22,56	51242
428	TATCTCATGACCACCTA	2-12-3	T AtctcatgaccacCT A	428_1	-21,88	51242
429	TTTATCTCATGACCACC	2-11-4	TTtatctcatgacCACC	429_1	-22,37	51244
430	TTTATCTCATGACCAC	2-10-4	TTtatctcatgaCCAC	430_1	-19,56	51245

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
431	ATTCTTACCGTCTTTA	4-10-2	ATTCttaccgtcttTA	431_1	-19,52	51358
432	TATTCTTACCGTCTTTA	3-11-3	TATtcttaccgtctTTA	432_1	-20,10	51358
433	TATTCTTACCGTCTTT	2-10-4	TAttcttaccgtCTTT	433_1	-19,30	51359
434	TTATTCTTACCGTCTTT	2-11-4	TTattcttaccgtCTTT	434_1	-19,99	51359
435	ATCTGATCTCACACAT	3-10-3	ATCtgatctcacaCAT	435_1	-19,62	51438
436	CATCTGATCTCACACAT	4-11-2	CATCtgatctcacacAT	436_1	-20,82	51438
437	ACTTCCAGATTTCTACA	2-11-4	ACttccagatttcTACA	437_1	-21,44	51953
438	TTTATGTTTACTTCAT	3-10-3	TTTatgtttacttCAT	438_1	-16,05	52150
439	TAAAGATCCCATCACTC	3-11-3	TAAagatcccatcaCTC	439_1	-20,31	52549
440	TAAAGATCCCATCACT	4-10-2	TAAAgatcccatcaCT	440_1	-18,82	52550
441	CCTAAAGATCCCATCAC	2-12-3	CCtaaagatcccatCAC	441_1	-22,32	52551
442	ATCATCAGTTACATCA	4-10-2	ATCAtcagttacatCA	442_1	-18,64	52579
443	ACTCTCACTGTAACTTT	4-11-2	ACTCtcactgtaactTT	443_1	-19,76	53012
444	AACTCTCACTGTAACTT	3-11-3	AACtctcactgtaaCTT	444_1	-18,53	53013
445	ACTCTCACTGTAACTT	3-10-3	ACTctcactgtaaCTT	445_1	-19,04	53013
446	AACTCTCACTGTAACT	4-10-2	AACTctcactgtaaCT	446_1	-17,97	53014
447	CAACTCTCACTGTAACT	4-11-2	CAACtctcactgtaaCT	447_1	-20,01	53014
448	CCTTTCATTAACATTTA	3-11-3	CCTttcattaacatTTA	448_1	-19,03	54198
449	TTCCTTTCATTAACATTT	4-12-2	TTCCtttcattaacatTT	449_1	-19,92	54199
450	TAATCCTATTCCAACT	3-10-3	TAAtcctattccaACT	450_1	-18,05	54232
451	CTAATCCTATTCCAAC	2-10-4	CT aatcctattcCAAC	451_1	-18,65	54233
452	CTCTAATCCTATTCCA	3-10-3	CTCtaatcctattCCA	452_1	-22,58	54235
453	TCTCTAATCCTATTCC	4-10-2	TCTCtaatcctattCC	453_1	-21,78	54236
454	TTGTCTCTAATCCTATT	2-11-4	TTgtctctaatccTATT	454_1	-19,70	54238

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
455	TTGTCTCTAATCCTAT	2-10-4	TTgtctctaatcCTAT	455_1	-19,45	54239
456	TCTTTAAGCTTCCCAC	2-10-4	TCtttaagcttcCCAC	456_1	-22,96	54609
457	AAACTACCCTGCACAA	3-10-3	AAActaccctgcaCAA	457_1	-18,41	54924
458	CCATGCTACATAAACC	4-10-2	CCATgctacataaaCC	458_1	-22,25	55337
459	TCCATGCTACATAAAC	4-10-2	TCCAtgctacataaAC	459_1	-18,64	55338
460	ACTCCTAAGAATTACA	4-10-2	ACTCctaagaattaCA	460_1	-17,62	59565
461	GAAACTATTACTCCTA	2-10-4	GAaactattactCCTA	461_1	-19,06	59574
462	TGAAACTATTACTCCT	3-10-3	TGAaactattactCCT	462_1	-19,30	59575
463	ATGAAACTATTACTCC	2-10-4	ATgaaactattaCTCC	463_1	-17,96	59576
464	AACAACTCATGCCACA	2-10-4	AAcaactcatgcCACA	464_1	-19,72	60012
465	AAATATTGCCACCATT	2-10-4	AAatattgccacCATT	465_1	-17,78	60298
466	GTTACATATTCTTTCAC	3-11-3	GTTacatattctttCAC	466_1	-18,76	60448
467	TCATACTTGCTTTAAT	4-10-2	TCATacttgctttaAT	467_1	-17,29	60821
468	ATCCTGATAATTAACT	4-10-2	ATCCtgataattaaCT	468_1	-17,73	61925
469	CCTTAATCTGTATCAC	3-10-3	CCTtaatctgtatCAC	469_1	-19,92	62287
470	ATACACAGCACATATT	2-10-4	ATacacagcacaTATT	470_1	-17,58	62422
471	TCAGAATAATTCTCCT	3-10-3	TCAgaataattctCCT	471_1	-19,81	62443
472	TCTTCAGCTTTCTAAAT	4-11-2	TCTTcagctttctaaAT	472_1	-18,58	64113
473	AGTCCTTCCTTTAACCA	2-13-2	AGtccttcctttaacCA	473_1	-22,20	64461
474	TAGTCCTTCCTTTAACC	2-13-2	TAgtccttcctttaaCC	474_1	-22,12	64462
475	TTTAACCTTGCTTATA	2-10-4	TTtaaccttgctTATA	475_1	-17,50	65272
476	ATCCCTTTGTAATCAT	4-10-2	ATCCctttgtaatcAT	476_1	-20,31	66840
477	CTTGCATTTCTAATTAC	3-11-3	CTTgcatttctaatTAC	477_1	-18,09	67426
478	CTTGTCAAATCATTTCT	4-11-2	CTTGtcaaatcatttCT	478_1	-19,10	68194

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
479	CCATCTAATGATTATT	4-10-2	CCATctaatgattaTT	479_1	-17,28	68328
480	TATCAGTTATCCAATA	4-10-2	TATCagttatccaaTA	480_1	-17,39	68805
481	TCACTGCCATCAATAC	4-10-2	TCACtgccatcaatAC	481_1	-19,71	68921
482	TGTCATCTACAAATCA	4-10-2	TGTCatctacaaatCA	482_1	-18,01	70133
483	CTCTTTAGATTCATCC	4-10-2	CTCTttagattcatCC	483_1	-20,94	72377
484	ACTCTTTAGATTCATC	2-10-4	ACtctttagattCATC	484_1	-17,81	72378
485	CAACTCTATGACTACC	2-10-4	CAactctatgacTACC	485_1	-20,07	72826
486	ACCTGTAATACTTCTT	4-10-2	ACCTgtaatacttcTT	486_1	-19,67	72861
487	GAATTCTTTATTCCTCC	2-11-4	GAattctttattcCTCC	487_1	-22,53	72887
488	ATCTGAATCAAACCTT	2-10-4	ATctgaatcaaaCCTT	488_1	-17,97	73474
489	ACTTTACTGCCATAATC	3-11-3	ACTttactgccataATC	489_1	-19,60	73992
490	TTACTCTTAGCAACCT	4-10-2	TTACtcttagcaacCT	490_1	-20,19	74791
491	CACCAGTATTTCTTCTT	4-11-2	CACCagtatttcttcTT	491_1	-22,15	74851
492	TTCACCAGTATTTCTTC	4-11-2	TTCAccagtatttctTC	492_1	-20,43	74853
493	CCAAATAAGCAAACTC	3-10-3	CCAaataagcaaaCTC	493_1	-17,54	75840
494	CCCAAATAAGCAAACT	4-10-2	CCCAaataagcaaaCT	494_1	-20,23	75841
495	GACTACATTCTCAATA	3-10-3	GACtacattctcaATA	495_1	-17,49	76238
496	TTGTCAATCTTTATTCT	4-11-2	TTGTcaatctttattCT	496_1	-18,85	76254
497	AGCTTACCAAATATTC	4-10-2	AGCTtaccaaatatTC	497_1	-18,68	76811
498	TTACACATGTATATCC	3-10-3	TTAcacatgtataTCC	498_1	-18,23	77114
499	ATCCTGTTAATACCAT	2-10-4	ATcctgttaataCCAT	499_1	-20,41	80468
500	TTCTTAGTCACACACA	4-10-2	TTCTtagtcacacaCA	500_1	-19,37	81047
501	TTCTGTTTCCATTTACA	4-11-2	TTCTgtttccatttaCA	501_1	-21,31	82233
502	TCTATATCAAGTTCCTT	2-11-4	TCtatatcaagttCCTT	502_1	-20,95	84166

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
503	ATTCAGTTACCAACTA	3-10-3	ATTcagttaccaaCTA	503_1	-18,37	85392
504	GCTTCTACTTAAATAT	3-10-3	GCTtctacttaaaTAT	504_1	-17,58	86974
505	CCCTCAAAGTAATTTC	4-10-2	CCCTcaaagtaattTC	505_1	-20,53	87728
506	AACATGTAATTTCCAT	2-10-4	AAcatgtaatttCCAT	506_1	-17,21	87810
507	CCAGACTCCAATATTT	4-10-2	CCAGactccaatatTT	507_1	-20,78	88417
508	CTTAGACTTCACCTTTC	2-11-4	CTtagacttcaccTTTC	508_1	-20,56	88991
509	CTGCTTAATTATATCA	4-10-2	CTGCttaattatatCA	509_1	-18,85	90228
510	AAATTGTCTACCTTCCT	2-12-3	AAattgtctaccttCCT	510_1	-20,62	90474
511	CACTTAGAATATCCCT	2-10-4	CActtagaatatCCCT	511_1	-22,28	91625
512	ATCCAAAGTTTCTTTC	4-10-2	ATCCaaagtttcttTC	512_1	-18,64	91885
513	ATATTTGTCACCTAAC	4-10-2	ATATttgtcacctaAC	513_1	-17,12	92976
514	CTATTCTCAGTATTAT	3-10-3	CT AttctcagtatTAT	514_1	-17,42	94304
515	CCATTCAATGATCACT	2-10-4	CCattcaatgatCACT	515_1	-20,55	94528
516	CACTAGTACTCTTATT	4-10-2	CACTagtactcttaTT	516_1	-18,01	95653
517	GCCACAACATCTATTT	4-10-2	GCCAcaacatctatTT	517_1	-21,53	96751
518	AGCACATATACCATCA	4-10-2	AGCAcatataccatCA	518_1	-21,98	97636
519	GTCATCTAACTTCTTAC	3-11-3	GTCatctaacttctTAC	519_1	-19,25	98480
520	TGTCATCTAACTTCTTA	4-11-2	TGTCatctaacttctTA	520_1	-19,69	98481
521	CCCTTATAGTTATTAA	3-10-3	CCCttatagttatTAA	521_1	-19,32	99646
522	TCCATAGAATTCTTCA	4-10-2	TCCAtagaattcttCA	522_1	-19,92	100334
523	TTGATTCCACCATTAA	3-10-3	TTGattccaccatTAA	523_1	-18,05	101110
524	CAGCCATAAACTATAT	4-10-2	CAGCcataaactatAT	524_1	-18,60	101898
525	TATGACTTATTCCATA	2-10-4	TAtgacttattcCATA	525_1	-17,88	102558
526	GTTAACCTATATTTCA	4-10-2	GTT AacctatatttCA	526_1	-17,69	103589

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
527	TGTCTATTCTCTTCATT	4-11-2	TGTCtattctcttcaTT	527_1	-20,62	104309
528	TTACTCTTTGATTTCAT	3-11-3	TTActctttgatttCAT	528_1	-18,39	105686
529	GATAATTCCAAATCCC	2-10-4	GAtaattccaaaTCCC	529_1	-20,99	107972
530	TCTTATCCTTGAATTTC	4-11-2	TCTTatccttgaattTC	530_1	-18,85	108257
531	ATATCCCTTGATTATCC	3-11-3	ATAtcccttgattaTCC	531_1	-22,75	109407
532	TTAGTATACCCTTTAT	3-10-3	TTAgtataccctttTAT	532_1	-18,67	110210
533	CTCTTTGTCAAATACT	4-10-2	CTCTttgtcaaataCT	533_1	-18,16	110768
534	CCAAACTGTCTTCTAAT	2-11-4	CCaaactgtcttcTAAT	534_1	-19,87	111811
535	TCCAAACTGTCTTCTAA	3-12-2	TCCaaactgtcttctAA	535_1	-18,33	111812
536	CCAGCATATTATATAC	3-10-3	CCAgcatattataTAC	536_1	-18,96	112149
537	TCCAGCATATTATATA	4-10-2	TCCAgcatattataTA	537_1	-19,41	112150
538	TCATTGAACAACTCTTC	4-11-2	TCATtgaacaactctTC	538_1	-18,01	112945
539	CTGCCATCTTTATTTAT	4-11-2	CTGCcatctttatttAT	539_1	-21,89	113533
540	TGAAACATTCTTCCCAC	2-12-3	TGaaacattcttccCAC	540_1	-19,76	114274
541	TTTATTAGATTACTCC	2-10-4	TTtattagattaCTCC	541_1	-17,38	114495
542	TTCCAGCTTATTTACCT	3-12-2	TTCcagcttatttacCT	542_1	-21,28	114831
543	AGCATCATATAAACCT	3-10-3	AGCatcatataaaCCT	543_1	-20,62	115355
544	GTACTTACACATCTAT	2-10-4	GTacttacacatCTAT	544_1	-18,96	116105
545	TGTACTTACACATCTA	3-10-3	TGTacttacacatCTA	545_1	-19,38	116106
546	ATTTCTCTATGTCACAT	3-11-3	ATTtctctatgtcaCAT	546_1	-19,28	117096
547	CAAACCTACGTCTCTC	2-10-4	CAaacctacgtcTCTC	547_1	-20,87	117189
548	GTATTTACTCTTTACCT	3-11-3	GTAtttactctttaCCT	548_1	-22,15	117476
549	CTAATGCAATAACCCA	2-10-4	CTaatgcaataaCCCA	549_1	-21,79	118293
550	ACTAATGCAATAACCC	3-10-3	ACTaatgcaataaCCC	550_1	-20,53	118294

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
551	AGCTCTAAACCTTCAA	3-10-3	AGCtctaaaccttCAA	551_1	-20,51	118756
552	TATTTGTCACCAAACC	3-10-3	TATttgtcaccaaACC	552_1	-19,63	119621
553	CTCAGACATCTCAATA	4-10-2	CTCAgacatctcaaTA	553_1	-19,25	120655
554	TCTCAGCTTCTTCAAAT	2-12-3	TCtcagcttcttcaAAT	554_1	-18,33	123733
555	GCCAATACCCACAAAC	3-10-3	GCCaatacccacaAAC	555_1	-22,03	124163
556	CCTCTGACAACCATTA	4-10-2	CCTCtgacaaccatTA	556_1	-22,57	125512
557	CAGATAACTCTAAACC	4-10-2	CAGAtaactctaaaCC	557_1	-18,43	126882
558	CTAACTGTTTCTCAATT	3-11-3	CTAactgtttctcaATT	558_1	-18,10	127105
559	CCAAGATAATCATCAT	3-10-3	CCAagataatcatCAT	559_1	-18,37	127809
560	TACATATTGTACTTCT	4-10-2	TACAtattgtacttCT	560_1	-17,48	129020
561	TAGCCTACTTTAATAT	4-10-2	TAGCctactttaatAT	561_1	-18,67	129205
562	CATTTACAAGCACATA	2-10-4	CAtttacaagcaCATA	562_1	-17,81	129928
563	TTATTCTGACACACTT	3-10-3	TTAttctgacacaCTT	563_1	-17,49	130020
564	TACATTGACACCTAAT	4-10-2	TACAttgacacctaAT	564_1	-17,37	130884
565	TTTACATTGACACCTA	2-10-4	TTtacattgacaCCTA	565_1	-19,42	130886
566	TGTATATAACTATTCC	4-10-2	TGTAtataactattCC	566_1	-17,79	131404
567	GAATCTTCTAATTCCAC	2-11-4	GAatcttctaattCCAC	567_1	-20,40	132514
568	TGCTCACTAACTACAC	3-10-3	TGCtcactaactaCAC	568_1	-20,66	133367
569	TGCTACCATCATTACCT	2-13-2	TGctaccatcattacCT	569_1	-21,32	136198
570	TTTATCAATATCTTCTCACT	1-13-1-1-1-1-2	TttatcaatatcttCtCaCT	570_1	-19,69	5784
570	TTTATCAATATCTTCTCACT	1-2-1-10-1-2-3	TttAtcaatatcttCtcACT	570_2	-19,67	5784
570	TTTATCAATATCTTCTCACT	1-5-1-7-1-2-3	TttatcAatatcttCtcACT	570_3	-19,65	5784
570	TTTATCAATATCTTCTCACT	1-1-1-11-1-3-2	TtTatcaatatcttCtcaCT	570_4	-19,75	5784
570	TTTATCAATATCTTCTCACT	1-2-1-2-1-11-2	TttAtcAatatcttctcaCT	570_5	-18,21	5784

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
570	TTTATCAATATCTTCTCACT	1-4-1-8-1-3-2	TttatCaatatcttCtcaCT	570_6	-19,69	5784
570	TTTATCAATATCTTCTCACT	1-2-1-2-1-9-1-1-2	TttAtcAatatcttctCaCT	570_7	-18,88	5784
570	TTTATCAATATCTTCTCACT	1-2-1-1-1-11-3	TttAtCaatatcttctcACT	570_8	-19,36	5784
570	TTTATCAATATCTTCTCACT	1-4-1-10-1-1-2	TttatCaatatcttctCaCT	570_9	-19,38	5784
570	TTTATCAATATCTTCTCACT	2-1-1-10-1-1-1-1-2	TTtAtcaatatcttCtCaCT	570_10	-20,60	5784
570	TTTATCAATATCTTCTCACT	1-4-1-8-1-1-1-1-2	TttatCaatatcttCtCaCT	570_11	-20,36	5784
570	TTTATCAATATCTTCTCACT	1-2-1-1-1-8-1-2-3	TttAtCaatatcttCtcACT	570_12	-20,34	5784
570	TTTATCAATATCTTCTCACT	1-2-1-2-1-7-1-3-2	TttAtcAatatcttCtcaCT	570_13	-19,19	5784
570	TTTATCAATATCTTCTCACT	1-1-2-1-1-10-1-1-2	TtTAtCaatatcttctCaCT	570_14	-21,24	5784
571	TTTATCAATATCTTCTCAC	1-12-2-1-3	TttatcaatatctTCtCAC	571_1	-19,16	5785
571	TTTATCAATATCTTCTCAC	2-1-1-1-1-6-2-2-3	TTtAtCaatatcTTctCAC	571_2	-20,17	5785
571	TTTATCAATATCTTCTCAC	3-2-1-7-2-2-2	TTTatCaatatctTCtcAC	571_3	-19,79	5785
571	TTTATCAATATCTTCTCAC	1-2-3-8-1-2-2	TttATCaatatcttCtcAC	571_4	-18,78	5785
571	TTTATCAATATCTTCTCAC	1-4-1-9-4	TttatCaatatcttcTCAC	571_5	-19,06	5785
571	TTTATCAATATCTTCTCAC	2-1-1-1-1-8-1-1-3	TTtAtCaatatcttCtCAC	571_6	-19,75	5785
571	TTTATCAATATCTTCTCAC	1-1-1-2-1-6-1-3-3	TtTatCaatatcTtctCAC	571_7	-19,11	5785
571	TTTATCAATATCTTCTCAC	2-1-3-6-1-4-2	TTtATCaatatcTtctcAC	571_8	-19,13	5785
571	TTTATCAATATCTTCTCAC	4-12-3	TTTAtcaatatcttctCAC	571_9	-20,38	5785
571	TTTATCAATATCTTCTCAC	1-1-2-1-1-6-1-3-3	TtTAtCaatatcTtctCAC	571_10	-20,24	5785
571	TTTATCAATATCTTCTCAC	2-1-1-1-1-7-2-2-2	TTtAtCaatatctTCtcAC	571_11	-18,65	5785
571	TTTATCAATATCTTCTCAC	3-2-1-8-1-1-3	TTTatCaatatcttCtCAC	571_12	-20,89	5785
571	TTTATCAATATCTTCTCAC	1-3-2-8-1-1-3	TttaTCaatatcttCtCAC	571_13	-19,96	5785
571	TTTATCAATATCTTCTCAC	1-2-1-1-1-9-4	TttAtCaatatcttcTCAC	571_14	-19,16	5785
572	TTTATCAATATCTTCTCA	2-1-1-1-1-7-2-1-2	TTtAtCaatatctTCtCA	572_1	-18,69	5786

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
572	TTTATCAATATCTTCTCA	3-2-1-6-1-1-1-1-2	TTTatCaatatcTtCtCA	572_2	-19,36	5786
572	TTTATCAATATCTTCTCA	1-4-1-6-1-1-4	TttatCaatatcTtCTCA	572_3	-19,19	5786
572	TTTATCAATATCTTCTCA	1-2-3-6-1-2-3	TttATCaatatcTtcTCA	572_4	-19,56	5786
572	TTTATCAATATCTTCTCA	4-1-1-7-1-2-2	TTTAtCaatatctTctCA	572_5	-19,37	5786
572	TTTATCAATATCTTCTCA	1-2-3-8-1-1-2	TttATCaatatcttCtCA	572_6	-18,83	5786
572	TTTATCAATATCTTCTCA	3-2-1-9-3	TTTatCaatatcttcTCA	572_7	-19,07	5786
572	TTTATCAATATCTTCTCA	1-2-1-10-4	TttAtcaatatcttCTCA	572_8	-18,10	5786
572	TTTATCAATATCTTCTCA	4-10-1-1-2	TTTAtcaatatcttCtCA	572_9	-19,31	5786
572	TTTATCAATATCTTCTCA	2-1-3-6-1-1-1-1-2	TTtATCaatatcTtCtCA	572_10	-20,15	5786
572	TTTATCAATATCTTCTCA	3-2-1-6-1-2-3	TTTatCaatatcTtcTCA	572_11	-19,59	5786
572	TTTATCAATATCTTCTCA	1-1-2-1-1-7-2-1-2	TtTAtCaatatctTCtCA	572_12	-19,64	5786
572	TTTATCAATATCTTCTCA	4-9-1-1-3	TTTAtcaatatctTcTCA	572_13	-19,90	5786
572	TTTATCAATATCTTCTCA	1-3-2-8-4	TttaTCaatatcttCTCA	572_14	-19,80	5786
573	TATACCTTTCTTTAACCCTT	1-4-1-10-1-1-2	TatacCtttctttaacCcTT	573_1	-22,72	8116
573	TATACCTTTCTTTAACCCTT	2-4-1-11-2	TAtaccTttctttaacccTT	573_2	-22,80	8116
573	TATACCTTTCTTTAACCCTT	1-3-1-10-1-2-2	TataCctttctttaaCccTT	573_3	-22,72	8116
573	TATACCTTTCTTTAACCCTT	1-4-1-9-1-2-2	TatacCtttctttaaCccTT	573_4	-22,82	8116
573	TATACCTTTCTTTAACCCTT	1-5-1-9-1-1-2	TataccTttctttaacCcTT	573_5	-22,35	8116
573	TATACCTTTCTTTAACCCTT	1-15-1-1-2	TatacctttctttaacCcTT	573_6	-21,83	8116
573	TATACCTTTCTTTAACCCTT	1-2-1-1-1-10-1-1-2	TatAcCtttctttaacCcTT	573_7	-22,91	8116
573	TATACCTTTCTTTAACCCTT	2-2-1-1-1-11-2	TAtaCcTttctttaacccTT	573_8	-23,58	8116
573	TATACCTTTCTTTAACCCTT	2-3-1-12-2	TAtacCtttctttaacccTT	573_9	-23,17	8116
573	TATACCTTTCTTTAACCCTT	1-3-1-8-2-1-1-1-2	TataCctttctttAAcCcTT	573_10	-23,35	8116
573	TATACCTTTCTTTAACCCTT	2-2-1-1-1-7-1-1-1-1-2	TAtaCcTttctttaAcCcTT	573_11	-24,68	8116

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
573	TATACCTTTCTTTAACCCTT	2-4-1-8-2-1-2	TAtaccTttctttaaCCcTT	573_12	-25,86	8116
573	TATACCTTTCTTTAACCCTT	2-3-1-9-1-2-2	TAtacCtttctttaaCccTT	573_13	-23,96	8116
573	TATACCTTTCTTTAACCCTT	2-3-1-10-1-1-2	TAtacCtttctttaacCcTT	573_14	-23,85	8116
574	TTATACCTTTCTTTAACCCT	1-1-1-10-1-4-2	TtAtacctttcttTaaccCT	574_1	-22,31	8117
574	TTATACCTTTCTTTAACCCT	1-13-1-1-1-1-2	TtataccttcttttAaCcCT	574_2	-22,38	8117
574	TTATACCTTTCTTTAACCCT	1-1-1-3-1-11-2	TtAtacCtttctttaaccCT	574_3	-22,47	8117
574	TTATACCTTTCTTTAACCCT	1-3-1-1-1-7-1-3-2	TtatAcCtttctttAaccCT	574_4	-22,68	8117
574	TTATACCTTTCTTTAACCCT	1-4-1-8-1-3-2	TtataCctttctttAaccCT	574_5	-22,38	8117
574	TTATACCTTTCTTTAACCCT	1-1-1-13-1-1-2	TtAtacctttctttaaCcCT	574_6	-22,36	8117
574	TTATACCTTTCTTTAACCCT	1-3-1-11-1-1-2	TtatAcctttctttaaCcCT	574_7	-22,46	8117
574	TTATACCTTTCTTTAACCCT	1-1-1-2-1-12-2	TtAtaCctttctttaaccCT	574_8	-22,36	8117
574	TTATACCTTTCTTTAACCCT	1-5-1-11-2	TtatacCtttctttaaccCT	574_9	-22,37	8117
574	TTATACCTTTCTTTAACCCT	1-1-1-2-1-10-1-1-2	TtAtaCctttctttaaCcCT	574_10	-23,14	8117
574	TTATACCTTTCTTTAACCCT	1-1-1-3-1-9-1-1-2	TtAtacCtttctttaaCcCT	574_11	-23,25	8117
574	TTATACCTTTCTTTAACCCT	1-1-1-3-1-10-3	TtAtacCtttctttaacCCT	574_12	-24,75	8117
574	TTATACCTTTCTTTAACCCT	1-1-1-2-2-11-2	TtAtaCctttctttaaccCT	574_13	-24,85	8117
574	TTATACCTTTCTTTAACCCT	1-3-1-1-1-11-2	TtatAcCtttctttaaccCT	574_14	-22,56	8117
575	TTTATACCTTTCTTTAACCC	1-2-1-9-1-4-2	TttAtacctttctTtaacCC	575_1	-21,69	8118
575	TTTATACCTTTCTTTAACCC	1-12-1-4-2	TttatacctttctTtaacCC	575_2	-21,59	8118
575	TTTATACCTTTCTTTAACCC	1-12-1-1-1-2-2	TttatacctttctTtAacCC	575_3	-21,71	8118
575	TTTATACCTTTCTTTAACCC	1-4-1-10-1-1-2	TttatAcctttctttaAcCC	575_4	-21,90	8118
575	TTTATACCTTTCTTTAACCC	1-13-1-3-2	TttatacctttcttTaacCC	575_5	-22,01	8118
575	TTTATACCTTTCTTTAACCC	2-1-1-14-2	TTtAtacctttctttaacCC	575_6	-22,20	8118
575	TTTATACCTTTCTTTAACCC	1-14-2-1-2	TttatacctttctttAAcCC	575_7	-22,02	8118

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
575	TTTATACCTTTCTTTAACCC	1-14-1-2-2	TttatacctttctttAacCC	575_8	-21,41	8118
575	TTTATACCTTTCTTTAACCC	1-15-1-1-2	TttatacctttctttaAcCC	575_9	-21,71	8118
575	TTTATACCTTTCTTTAACCC	2-1-1-9-1-4-2	TTtAtacctttctTtaacCC	575_10	-22,50	8118
575	TTTATACCTTTCTTTAACCC	1-2-1-10-1-3-2	TttAtacctttcttTaacCC	575_11	-22,11	8118
575	TTTATACCTTTCTTTAACCC	1-4-2-8-2-1-2	TttatACctttctttAAcCC	575_12	-23,40	8118
575	TTTATACCTTTCTTTAACCC	1-2-1-2-1-9-1-1-2	TttAtaCctttctttaAcCC	575_13	-22,59	8118
575	TTTATACCTTTCTTTAACCC	1-1-2-14-2	TtTAtacctttctttaacCC	575_14	-23,15	8118
576	TTTTATACCTTTCTTTAACC	1-1-1-10-2-3-2	TtTtatacctttcTTtaaCC	576_1	-21,12	8119
576	TTTTATACCTTTCTTTAACC	1-3-1-8-1-4-2	TtttAtacctttcTttaaCC	576_2	-20,10	8119
576	TTTTATACCTTTCTTTAACC	1-1-1-10-1-2-4	TtTtatacctttcTttAACC	576_3	-21,45	8119
576	TTTTATACCTTTCTTTAACC	3-11-1-1-1-1-2	TTTtatacctttctTtAaCC	576_4	-21,54	8119
576	TTTTATACCTTTCTTTAACC	2-4-1-7-1-3-2	TTttatAcctttctTtaaCC	576_5	-20,80	8119
576	TTTTATACCTTTCTTTAACC	1-14-1-2-2	TtttatacctttcttTaaCC	576_6	-20,22	8119
576	TTTTATACCTTTCTTTAACC	1-15-1-1-2	TtttatacctttctttAaCC	576_7	-19,61	8119
576	TTTTATACCTTTCTTTAACC	1-5-1-10-3	TtttatAcctttctttaACC	576_8	-20,51	8119
576	TTTTATACCTTTCTTTAACC	1-1-2-14-2	TtTTatacctttctttaaCC	576_9	-21,03	8119
576	TTTTATACCTTTCTTTAACC	1-1-2-10-1-1-1-1-2	TtTTatacctttctTtAaCC	576_10	-21,46	8119
576	TTTTATACCTTTCTTTAACC	2-2-1-9-1-3-2	TTttAtacctttctTtaaCC	576_11	-20,70	8119
576	TTTTATACCTTTCTTTAACC	1-5-1-7-1-3-2	TtttatAcctttctTtaaCC	576_12	-19,99	8119
576	TTTTATACCTTTCTTTAACC	1-1-1-12-2-1-2	TtTtatacctttcttTAaCC	576_13	-21,68	8119
576	TTTTATACCTTTCTTTAACC	1-1-1-1-1-13-2	TtTtAtacctttctttaaCC	576_14	-19,89	8119
577	TTTTTATACCTTTCTTTAAC	1-12-1-2-4	TttttatacctttCttTAAC	577_1	-19,19	8120
577	TTTTTATACCTTTCTTTAAC	1-2-1-9-1-1-2-1-2	TttTtatacctttCtTTaAC	577_2	-18,96	8120
577	TTTTTATACCTTTCTTTAAC	2-12-3-1-2	TTtttatacctttcTTTaAC	577_3	-19,52	8120

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
577	TTTTTATACCTTTCTTTAAC	1-1-1-2-1-7-2-3-2	TtTttAtacctttCTttaAC	577_4	-18,71	8120
577	TTTTTATACCTTTCTTTAAC	4-9-1-1-1-2-2	TTTTtatacctttCtTtaAC	577_5	-19,85	8120
577	TTTTTATACCTTTCTTTAAC	3-1-1-8-1-1-1-1-3	TTTtTatacctttCtTtAAC	577_6	-20,08	8120
577	TTTTTATACCTTTCTTTAAC	2-1-2-8-2-2-3	TTtTTatacctttCTttAAC	577_7	-20,97	8120
577	TTTTTATACCTTTCTTTAAC	1-1-2-10-2-1-3	TtTTtatacctttcTTtAAC	577_8	-18,89	8120
577	TTTTTATACCTTTCTTTAAC	1-3-2-7-1-4-2	TtttTAtacctttCtttaAC	577_9	-18,97	8120
577	TTTTTATACCTTTCTTTAAC	1-2-1-9-2-1-1-1-2	TttTtatacctttCTtTaAC	577_10	-19,34	8120
577	TTTTTATACCTTTCTTTAAC	2-3-1-7-2-2-3	TTtttAtacctttCTttAAC	577_11	-19,53	8120
577	TTTTTATACCTTTCTTTAAC	1-1-2-9-1-1-1-1-3	TtTTtatacctttCtTtAAC	577_12	-18,84	8120
577	TTTTTATACCTTTCTTTAAC	1-3-2-7-1-1-1-2-2	TtttTAtacctttCtTtaAC	577_13	-19,27	8120
577	TTTTTATACCTTTCTTTAAC	3-1-1-8-1-2-1-1-2	TTTtTatacctttCttTaAC	577_14	-20,20	8120
578	TTTTTTCTTACTATCTTCAA	1-5-1-7-2-2-2	TtitttCttactatCTtcAA	578_1	-19,02	8584
578	TTTTTTCTTACTATCTTCAA	2-2-1-1-1-7-1-1-1-1-2	TTttTtCttactatCtTcAA	578_2	-19,31	8584
578	TTTTTTCTTACTATCTTCAA	1-2-2-9-1-2-3	TttTTtcttactatCttCAA	578_3	-20,05	8584
578	TTTTTTCTTACTATCTTCAA	1-1-1-1-1-1-1-7-1-3-2	TtTtTtCttactatCttcAA	578_4	-18,43	8584
578	TTTTTTCTTACTATCTTCAA	3-3-1-8-1-2-2	TTTtttCttactatcTtcAA	578_5	-18,99	8584
578	TTTTTTCTTACTATCTTCAA	2-1-2-1-1-8-1-2-2	TTtTTtCttactatcTtcAA	578_6	-19,29	8584
578	TTTTTTCTTACTATCTTCAA	1-1-3-1-1-9-1-1-2	TtTTTtCttactatctTcAA	578_7	-19,15	8584
578	TTTTTTCTTACTATCTTCAA	2-1-1-11-1-1-3	TTtTttcttactatcTtCAA	578_8	-19,58	8584
578	TTTTTTCTTACTATCTTCAA	1-4-1-10-4	TttttTcttactatctTCAA	578_9	-19,31	8584
579	TTTTTTTCTTACTATCTTCA	1-12-1-1-1-2-2	TttttttcttactAtCttCA	579_1	-19,29	8585
579	TTTTTTTCTTACTATCTTCA	2-1-1-9-1-4-2	TTtTtttcttactAtcttCA	579_2	-19,42	8585
579	TTTTTTTCTTACTATCTTCA	1-1-1-2-1-7-1-4-2	TtTttTtcttactAtcttCA	579_3	-18,91	8585
579	TTTTTTTCTTACTATCTTCA	1-1-2-9-1-2-1-1-2	TtTTtttcftactAtcTtCA	579_4	-19,94	8585

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
579	TTTTTTTCTTACTATCTTCA	1-3-2-10-1-1-2	TtttTTtcttactatcTtCA	579_5	-19,84	8585
579	TTTTTTTCTTACTATCTTCA	2-3-1-12-2	TTtttTtcttactatcttCA	579_6	-19,33	8585
579	TTTTTTTCTTACTATCTTCA	3-15-2	TTTttttcttactatcttCA	579_7	-19,84	8585
579	TTTTTTTCTTACTATCTTCA	1-2-2-13-2	TttTTttcttactatcttCA	579_8	-19,33	8585
579	TTTTTTTCTTACTATCTTCA	1-14-1-2-2	TttttttcttactatCttCA	579_9	-19,19	8585
580	ATTTTTTTCTTACTATCTTC	1-4-1-8-1-1-1-1-2	AttttTttcttactAtCtTC	580_1	-18,09	8586
580	ATTTTTTTCTTACTATCTTC	2-1-1-10-1-2-3	ATtTttttcttactAtcTTC	580_2	-19,39	8586
580	ATTTTTTTCTTACTATCTTC	1-3-2-8-1-2-3	AtttTTttcttactAtcTTC	580_3	-18,95	8586
580	ATTTTTTTCTTACTATCTTC	1-5-1-6-1-3-3	AtttttTtcttacTatcTTC	580_4	-18,98	8586
580	ATTTTTTTCTTACTATCTTC	2-2-1-1-1-7-1-3-2	ATttTtTtcttactAtctTC	580_5	-18,66	8586
580	ATTTTTTTCTTACTATCTTC	1-1-3-8-1-4-2	AtTTTtttcttacTatctTC	580_6	-19,58	8586
580	ATTTTTTTCTTACTATCTTC	2-1-1-12-1-1-2	ATtTttttcttactatCtTC	580_7	-19,24	8586
580	ATTTTTTTCTTACTATCTTC	1-1-1-2-1-11-3	AtTttTttcttactatcTTC	580_8	-18,34	8586
580	ATTTTTTTCTTACTATCTTC	1-1-2-1-2-11-2	AtTTtTTtcttactatctTC	580_9	-18,94	8586
581	AAIIIIIIICTTACTATCTT	1-4-1-7-1-1-1-1-3	AatttTtttcttaCtAtCTT	581_1	-18,53	8587
581	AAIIIIIIICTTACTATCTT	1-3-1-1-1-6-2-3-2	AattTtTttcttaCTatcTT	581_2	-18,69	8587
581	AAIIIIIIICTTACTATCTT	1-1-2-10-2-2-2	AaTTtttttcttacTAtcTT	581_3	-18,80	8587
581	AAIIIIIIICTTACTATCTT	2-1-1-1-1-8-1-2-3	AAtTtTtttcttacTatCTT	581_4	-19,20	8587
581	AAIIIIIIICTTACTATCTT	4-2-1-7-1-3-2	AATTttTttcttacT atcTT	581_5	-19,30	8587
581	AAIIIIIIICTTACTATCTT	2-2-2-7-1-1-2-1-2	AAttTTtttcttaCtATcTT	581_6	-19,52	8587
581	AAIIIIIIICTTACTATCTT	1-12-1-2-4	AattttttttcttaCtaTCTT	581_7	-19,25	8587
581	AAIIIIIIICTTACTATCTT	1-1-4-7-1-4-2	AaTTTTtttcttaCtatcTT	581_8	-19,35	8587
581	AAIIIIIIICTTACTATCTT	2-1-3-9-1-1-3	AAtTTTtttcttactAtCTT	581_9	-19,68	8587
582	GTTTATACCCTTTCCAAT	1-1-1-1-1-7-2-2-2	GtTtAtaccctttTCcaAT	582_1	-21,48	9209

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
582	GTTTATACCCTTTCCAAT	1-12-2-1-2	GtttataccctttCCaAT	582_2	-22,28	9209
582	GTTTATACCCTTTCCAAT	1-3-1-8-1-1-3	GtttAtaccctttCcAAT	582_3	-20,46	9209
582	GTTTATACCCTTTCCAAT	1-1-1-1-1-9-1-1-2	GtTtAtaccctttcCaAT	582_4	-20,30	9209
582	GTTTATACCCTTTCCAAT	2-11-1-2-2	GTttataccctttCcaAT	582_5	-21,64	9209
582	GTTTATACCCTTTCCAAT	1-1-2-9-1-1-3	GtTTataccctttCcAAT	582_6	-21,90	9209
582	GTTTATACCCTTTCCAAT	1-1-1-13-2	GtTtataccctttccaAT	582_7	-19,63	9209
582	GTTTATACCCTTTCCAAT	1-2-1-12-2	GttTataccctttccaAT	582_8	-20,05	9209
582	GTTTATACCCTTTCCAAT	1-13-4	GtttataccctttcCAAT	582_9	-21,59	9209
583	TGTTTATACCCTTTCCAA	2-1-1-10-1-1-2	TGtTtataccctttCcAA	583_1	-21,08	9210
583	TGTTTATACCCTTTCCAA	1-4-1-6-1-1-1-1-2	TgtttAtaccctTtCcAA	583_2	-19,97	9210
583	TGTTTATACCCTTTCCAA	1-3-1-9-1-1-2	T gttT ataccctttCcAA	583_3	-20,30	9210
583	TGTTTATACCCTTTCCAA	2-1-1-1-1-6-1-3-2	TGtTtAtaccctTtccAA	583_4	-20,71	9210
583	TGTTTATACCCTTTCCAA	1-2-1-8-1-2-3	TgtTtataccctTtcCAA	583_5	-21,40	9210
583	TGTTTATACCCTTTCCAA	1-4-1-9-3	TgtttAtaccctttcCAA	583_6	-20,89	9210
583	TGTTTATACCCTTTCCAA	1-1-2-12-2	TgTTtataccctttccAA	583_7	-20,27	9210
583	TGTTTATACCCTTTCCAA	1-12-2-1-2	TgtttatacccttTCcAA	583_8	-20,56	9210
583	TGTTTATACCCTTTCCAA	2-2-1-11-2	TGttTataccctttccAA	583_9	-20,74	9210
584	CTGTTTATACCCTTTCCA	1-1-1-10-1-2-2	CtGtttatacccTtcCA	584_1	-22,45	9211
584	CTGTTTATACCCTTTCCA	1-12-1-2-2	CtgtttatacccTtcCA	584_2	-22,14	9211
584	CTGTTTATACCCTTTCCA	1-1-1-1-1-11-2	CtGtTtataccctttcCA	584_3	-22,45	9211
584	CTGTTTATACCCTTTCCA	1-1-1-13-2	CtGtttataccctttcCA	584_4	-22,15	9211
584	CTGTTTATACCCTTTCCA	1-2-1-12-2	CtgTttataccctttcCA	584_5	-22,50	9211
584	CTGTTTATACCCTTTCCA	1-3-1-11-2	CtgtTtataccctttcCA	584_6	-22,14	9211
584	CTGTTTATACCCTTTCCA	1-4-1-10-2	Ctgtt T ata ccctttcCA	584_7	-22,57	9211

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
584	CTGTTTATACCCTTTCCA	1-15-2	CtgtttataccctttcCA	584_8	-21,84	9211
585	AATTATTTATACACCATCAT	2-1-1-1-8-3-1-2	AAtTaTttatacacCATcAT	585_1	-20,76	11511
585	AATTATTTATACACCATCAT	3-2-2-6-1-1-2-1-2	AATtaTTtatacaCcATcAT	585_2	-20,88	11511
585	AATTATTTATACACCATCAT	1-4-1-7-2-1-1-1-2	AattaTttatacaCCaT cAT	585_3	-19,62	11511
585	AATTATTTATACACCATCAT	1-3-1-1-1-6-1-3-3	AattAtTtatacaCcatCAT	585_4	-18,98	11511
585	AATTATTTATACACCATCAT	1-2-3-7-1-1-1-2-2	AatTATttatacaCcAtcAT	585_5	-19,65	11511
585	AATTATTTATACACCATCAT	1-1-2-11-1-1-3	AaTTatttatacaccAtCAT	585_6	-19,53	11511
585	AATTATTTATACACCATCAT	2-2-1-9-1-1-4	AAttAtttatacacCaTCAT	585_7	-20,11	11511
585	AATTATTTATACACCATCAT	3-1-2-8-1-2-3	AATtATttatacacCatCAT	585_8	-21,48	11511
585	AATTATTTATACACCATCAT	4-2-1-7-1-3-2	AATTatTtatacacCatcAT	585_9	-19,60	11511
585	AATTATTTATACACCATCAT	2-1-1-2-1-6-3-2-2	AAtTatTtatacaCCAtcAT	585_10	-21,69	11511
585	AATTATTTATACACCATCAT	1-3-2-7-1-1-1-1-3	AattATttatacaCcAtCAT	585_11	-19,97	11511
585	AATTATTTATACACCATCAT	2-1-3-8-1-1-1-1-2	AAtTATttatacacCaTcAT	585_12	-20,42	11511
585	AATTATTTATACACCATCAT	1-1-2-1-1-8-1-2-3	AaTTaTttatacacCatCAT	585_13	-20,49	11511
585	AATTATTTATACACCATCAT	2-1-1-2-1-9-4	AAtTatTtatacaccaTCAT	585_14	-20,47	11511
586	AAATTATTTATACACCATCA	1-12-3-1-3	AaattatttatacACCaTCA	586_1	-20,58	11512
586	AAATTATTTATACACCATCA	1-1-1-2-1-7-1-1-2-1-2	AaAttAtttatacAcCAtCA	586_2	-18,56	11512
586	AAATTATTTATACACCATCA	3-2-2-6-2-3-2	AAAttATttatacACcatCA	586_3	-19,68	11512
586	AAATTATTTATACACCATCA	4-10-1-2-3	AAATtatttatacaCcaTCA	586_4	-20,15	11512
586	AAATTATTTATACACCATCA	1-1-4-8-1-1-1-1-2	AaATTAtttatacaCcAtCA	586_5	-20,72	11512
586	AAATTATTTATACACCATCA	2-1-2-1-1-7-1-3-2	AAaTTaTttatacaCcatCA	586_6	-19,39	11512
586	AAATTATTTATACACCATCA	1-3-2-7-1-1-1-1-3	AaatTAtttatacAcCaTCA	586_7	-19,65	11512
586	AAATTATTTATACACCATCA	1-1-3-8-1-2-4	AaATTatttatacAccATCA	586_8	-20,88	11512
586	AAATTATTTATACACCATCA	2-2-1-1-1-9-4	AAatTaTttatacaccATCA	586_9	-19,63	11512

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
586	AAATTATTTATACACCATCA	1-1-1-1-1-1-6-3-2-2	AaAtTaTttatacACCatCA	586_10	-20,95	11512
586	AAATTATTTATACACCATCA	1-3-2-7-1-1-2-1-2	AaatTAtttatacAcCAtCA	586_11	-20,00	11512
586	AAATTATTTATACACCATCA	2-1-2-1-1-7-1-1-1-1-2	AAaTTaTttatacaCcAtCA	586_12	-19,44	11512
586	AAATTATTTATACACCATCA	3-2-1-8-1-2-3	AAAttAtttatacaCcaTCA	586_13	-19,00	11512
586	AAATTATTTATACACCATCA	1-1-4-9-1-1-3	AaATTAtttatacacCaTCA	586_14	-21,59	11512
587	AAAATTATTTATACACCATC	2-3-1-7-1-1-5	AAaatTatttataCaCCATC	587_1	-21,17	11513
587	AAAATTATTTATACACCATC	1-2-2-9-6	AaaATtatttatacACCATC	587_2	-21,34	11513
587	AAAATTATTTATACACCATC	2-3-2-6-3-1-3	AAaatTAtttataCACcATC	587_3	-20,67	11513
587	AAAATTATTTATACACCATC	3-1-1-1-1-7-3-1-2	AAAaTtAtttatacACCaTC	587_4	-19,11	11513
587	AAAATTATTTATACACCATC	7-6-1-1-1-2-2	AAAATTAtttataCaCcaTC	587_5	-20,66	11513
587	AAAATTATTTATACACCATC	1-1-1-1-2-8-2-1-3	AaAaTTatttatacACcATC	587_6	-18,20	11513
587	AAAATTATTTATACACCATC	1-1-5-6-2-3-2	AaAATTAtttataCAccaTC	587_7	-20,71	11513
587	AAAATTATTTATACACCATC	2-1-3-7-1-2-4	AAaATTatttataCacCATC	587_8	-20,87	11513
587	AAAATTATTTATACACCATC	4-1-1-8-1-1-4	AAAAtTatttatacAcCATC	587_9	-19,30	11513
587	AAAATTATTTATACACCATC	1-1-2-1-2-6-3-2-2	AaAAtTAtttataCACcaTC	587_10	-20,13	11513
587	AAAATTATTTATACACCATC	1-2-3-7-1-1-2-1-2	AaaATTatttataCaCCaTC	587_11	-20,44	11513
587	AAAATTATTTATACACCATC	3-1-2-7-1-2-4	AAAaTTatttataCacCATC	587_12	-20,27	11513
587	AAAATTATTTATACACCATC	3-2-1-8-3-1-2	AAAatTatttatacACCaTC	587_13	-19,30	11513
587	AAAATTATTTATACACCATC	2-1-3-8-2-1-3	AAaATTatttatacACcATC	587_14	-19,52	11513
588	TAAAATTATTTATACACCAT	2-3-1-7-1-1-5	TAaaaTtatttatAcACCAT	588_1	-20,14	11514
588	TAAAATTATTTATACACCAT	1-2-1-2-1-6-2-1-4	TaaAatTatttatACaCCAT	588_2	-20,15	11514
588	TAAAATTATTTATACACCAT	1-1-1-1-2-8-1-1-4	TaAaATtatttataCaCCAT	588_3	-20,40	11514
588	TAAAATTATTTATACACCAT	4-1-2-6-4-1-2	TAAAaTTatttatACACcAT	588_4	-21,36	11514
588	TAAAATTATTTATACACCAT	1-3-3-6-3-1-3	TaaaATTatttatACAcCAT	588_5	-21,07	11514

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
588	TAAAATTATTTATACACCAT	2-1-4-7-3-1-2	TAaAATTatttataCACcAT	588_6	-21,36	11514
588	TAAAATTATTTATACACCAT	3-1-1-1-1-7-2-1-3	TAAaAtTatttataCAcCAT	588_7	-20,41	11514
588	TAAAATTATTTATACACCAT	7-6-1-3-3	TAAAATTatttatAcacCAT	588_8	-20,85	11514
588	TAAAATTATTTATACACCAT	2-1-2-11-4	TAaAAttatttatacaCCAT	588_9	-19,82	11514
588	TAAAATTATTTATACACCAT	2-2-3-6-4-1-2	TAaaATTatttatACACcAT	588_10	-21,41	11514
588	TAAAATTATTTATACACCAT	1-1-1-1-3-6-1-2-4	TaAaATTatttatAcaCCAT	588_11	-21,15	11514
588	TAAAATTATTTATACACCAT	2-1-2-1-1-7-2-1-3	TAaAAtTatttataCAcCAT	588_12	-20,41	11514
588	TAAAATTATTTATACACCAT	3-2-2-7-1-1-4	TAAaaTTatttataCaCCAT	588_13	-21,86	11514
588	TAAAATTATTTATACACCAT	1-1-2-1-1-9-5	TaAAaTtatttatacACCAT	588_14	-19,68	11514
589	TAAAATTATTTATACACCA	1-1-2-1-1-7-6	TaAAaTtatttatACACCA	589_1	-20,31	11515
589	TAAAATTATTTATACACCA	1-2-3-6-1-1-5	TaaAATtatttaTaCACCA	589_2	-21,36	11515
589	TAAAATTATTTATACACCA	2-3-1-7-6	TAaaaTtatttatACACCA	589_3	-20,58	11515
589	TAAAATTATTTATACACCA	3-1-2-6-4-1-2	TAAaATtatttaTACAcCA	589_4	-21,36	11515
589	TAAAATTATTTATACACCA	4-1-1-6-2-2-3	TAAAaTtatttaTAcaCCA	589_5	-20,51	11515
589	TAAAATTATTTATACACCA	2-1-2-7-1-1-1-1-3	TAaAAttatttaTaCaCCA	589_6	-19,30	11515
589	TAAAATTATTTATACACCA	1-3-2-6-2-2-3	TaaaATtatttaTAcaCCA	589_7	-19,40	11515
589	TAAAATTATTTATACACCA	5-8-2-1-3	TAAAAttatttatACaCCA	589_8	-19,77	11515
589	TAAAATTATTTATACACCA	3-1-2-9-4	TAAaATtatttatacACCA	589_9	-19,55	11515
589	TAAAATTATTTATACACCA	2-1-3-6-4-1-2	TAaAATtatttaTACAcCA	589_10	-21,36	11515
589	TAAAATTATTTATACACCA	3-1-2-6-3-1-3	TAAaATtatttaTACaCCA	589_11	-22,18	11515
589	TAAAATTATTTATACACCA	1-1-3-7-2-1-4	TaAAAttatttaTAcACCA	589_12	-19,78	11515
589	TAAAATTATTTATACACCA	2-2-1-7-1-1-1-1-3	TAaaAttatttaTaCaCCA	589_13	-18,76	11515
589	TAAAATTATTTATACACCA	4-1-1-8-5	TAAAaTtatttataCACCA	589_14	-21,06	11515
590	ATATTGATTCAATTCCC	2-9-2-1-3	ATattgattcaATtCCC	590_1	-21,84	13226

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
590	ATATTGATTCAATTCCC	1-2-1-7-6	AtaTtgattcaATTCCC	590_2	-22,10	13226
590	ATATTGATTCAATTCCC	2-9-1-1-1-1-2	ATattgattcaAtTcCC	590_3	-18,59	13226
590	ATATTGATTCAATTCCC	1-1-2-8-5	AtATtgattcaaTTCCC	590_4	-21,87	13226
590	ATATTGATTCAATTCCC	1-2-2-7-2-1-2	AtaTTgattcaaTTcCC	590_5	-19,29	13226
590	ATATTGATTCAATTCCC	1-3-1-6-2-2-2	AtatTgattcaATtcCC	590_6	-18,59	13226
590	ATATTGATTCAATTCCC	1-2-2-6-1-2-3	AtaTTgattcaAttCCC	590_7	-20,66	13226
590	ATATTGATTCAATTCCC	1-1-1-1-1-7-1-1-3	AtAtTgattcaaTtCCC	590_8	-19,92	13226
590	ATATTGATTCAATTCCC	1-1-1-8-1-2-3	AtAttgattcaAttCCC	590_9	-19,01	13226
590	ATATTGATTCAATTCCC	4-7-1-3-2	ATATtgattcaAttcCC	590_10	-20,60	13226
590	ATATTGATTCAATTCCC	3-1-1-7-1-2-2	ATAtTgattcaaTtcCC	590_11	-20,26	13226
590	ATATTGATTCAATTCCC	1-3-1-8-4	AtatTgattcaatTCCC	590_12	-20,37	13226
590	ATATTGATTCAATTCCC	2-1-1-10-3	ATaTtgattcaattCCC	590_13	-20,71	13226
590	ATATTGATTCAATTCCC	2-2-1-9-3	ATatTgattcaattCCC	590_14	-21,06	13226
590	ATATTGATTCAATTCCC	1-1-3-10-2	AtATTgattcaattcCC	590_15	-18,87	13226
590	ATATTGATTCAATTCCC	2-2-1-6-2-2-2	ATatTgattcaATtcCC	590_16	-20,26	13226
590	ATATTGATTCAATTCCC	3-8-1-1-4	ATAttgattcaAtTCCC	590_17	-22,71	13226
590	ATATTGATTCAATTCCC	1-1-3-6-1-2-3	AtATTgattcaAttCCC	590_18	-21,57	13226
590	ATATTGATTCAATTCCC	1-1-1-1-1-7-5	AtAtTgattcaaTTCCC	590_19	-21,42	13226
590	ATATTGATTCAATTCCC	2-1-1-8-1-1-3	ATaTtgattcaaTtCCC	590_20	-21,15	13226
591	GCACATTCTTTCTATACCT	1-1-1-1-1-12-2	GcAcAttctttctatacCT	591_1	-21,27	15113
591	GCACATTCTTTCTATACCT	1-3-1-12-2	GcacAttctttctatacCT	591_2	-21,12	15113
592	GCACATTCTTTCTATACC	1-12-1-2-2	GcacattctttctAtaCC	592_1	-20,07	15114
592	GCACATTCTTTCTATACC	1-1-1-1-1-11-2	GcAcAttctttctataCC	592_2	-20,17	15114
592	GCACATTCTTTCTATACC	1-3-1-11-2	GcacAttctttctataCC	592_3	-20,02	15114

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
592	GCACATTCTTTCTATACC	1-1-2-11-3	GcACattctttctatACC	592_4	-21,80	15114
592	GCACATTCTTTCTATACC	1-1-1-1-2-7-1-1-3	GcAcATtctttctAtACC	592_5	-22,11	15114
592	GCACATTCTTTCTATACC	1-1-1-1-2-7-1-2-2	GcAcATtctttctAtaCC	592_6	-21,51	15114
592	GCACATTCTTTCTATACC	1-15-2	GcacattctttctataCC	592_7	-19,97	15114
592	GCACATTCTTTCTATACC	1-4-1-9-3	GcacaTtctttctatACC	592_8	-21,01	15114
592	GCACATTCTTTCTATACC	1-4-1-10-2	GcacaTtctttctataCC	592_9	-20,41	15114
592	GCACATTCTTTCTATACC	2-11-1-2-2	GCacattctttctAtaCC	592_10	-22,39	15114
592	GCACATTCTTTCTATACC	1-1-1-1-1-8-1-2-2	GcAcAttctttctAtaCC	592_11	-20,27	15114
592	GCACATTCTTTCTATACC	1-3-1-9-1-1-2	GcacAttctttctaTaCC	592_12	-20,89	15114
592	GCACATTCTTTCTATACC	1-1-1-1-1-10-3	GcAcAttctttctatACC	592_13	-20,77	15114
592	GCACATTCTTTCTATACC	1-1-1-2-1-10-2	GcAcaTtctttctataCC	592_14	-20,56	15114
593	TTATTTCCATTTATTTTCA	1-1-1-1-1-8-3-1-2	TtAtTtccatttaTTTtCA	593_1	-19,10	15563
593	TTATTTCCATTTATTTTCA	1-2-2-7-1-1-1-1-3	TtaTTtccatttAtTtTCA	593_2	-19,27	15563
593	TTATTTCCATTTATTTTCA	2-2-1-8-1-1-1-1-2	TTatTtccatttaTtTtCA	593_3	-18,92	15563
593	TTATTTCCATTTATTTTCA	1-1-2-9-1-2-3	TtATttccatttaTttTCA	593_4	-19,41	15563
594	TTTATTTCCATTTATTTTCA	1-1-1-11-1-2-3	TtTatttccatttaTftTCA	594_1	-19,80	15563
594	TTTATTTCCATTTATTTTCA	1-4-1-7-1-1-1-2-2	TttatTtccatttAtTttCA	594_2	-18,34	15563
594	TTTATTTCCATTTATTTTCA	1-3-2-9-2-1-2	TttaTTtccatttatTTtCA	594_3	-20,01	15563
594	TTTATTTCCATTTATTTTCA	2-1-1-1-1-8-1-1-1-1-2	TTtAtTtccatttaTtTtCA	594_4	-19,60	15563
595	ATTTATTTCCATTTATTTTC	1-1-1-2-1-8-3-1-2	AtTtaTttccatttATTtTC	595_1	-19,05	15564
595	ATTTATTTCCATTTATTTTC	1-3-2-7-1-3-3	AtttATttccattTattTTC	595_2	-19,03	15564
595	ATTTATTTCCATTTATTTTC	1-1-2-10-1-2-3	AtTTatttccatttAttTTC	595_3	-18,60	15564
595	ATTTATTTCCATTTATTTTC	2-1-1-1-1-8-1-1-1-1-2	ATtTaTttccatttAtTtTC	595_4	-18,96	15564
596	TTTATTTCCATTTATTTTC	1-1-1-1-1-8-2-1-3	TtTaTttccatttATtTTC	596_1	-18,66	15564

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
596	TTTATTTCCATTTATTTTC	3-2-1-7-3-1-2	TTTatTtccatttATTtTC	596_2	-19,84	15564
596	TTTATTTCCATTTATTTTC	2-2-2-7-1-1-4	TTtaTTtccatttAtTTTC	596_3	-19,12	15564
596	TTTATTTCCATTTATTTTC	5-7-1-3-3	TTTATttccattTattTTC	596_4	-21,30	15564
597	CCATTTATTTCCATTTATTT	1-1-1-11-2-2-2	CcAtttatttccatTTatTT	597_1	-19,89	15566
597	CCATTTATTTCCATTTATTT	1-3-1-9-1-1-1-1-2	CcatTtatttccatTtAtTT	597_2	-19,00	15566
597	CCATTTATTTCCATTTATTT	1-1-1-2-1-8-1-2-3	CcAttTatttccatTtaTTT	597_3	-20,33	15566
597	CCATTTATTTCCATTTATTT	1-2-2-1-1-11-2	CcaTTtAtttccatttatTT	597_4	-19,64	15566
598	TCCATTTATTTCCATTTATT	2-11-2-3-2	TCcatttatttccATttaTT	598_1	-21,22	15567
598	TCCATTTATTTCCATTTATT	2-2-1-8-1-1-1-2-2	TCcaTttatttccAtTtaTT	598_2	-20,71	15567
598	TCCATTTATTTCCATTTATT	1-1-2-9-1-4-2	TcCAtttatttccAtttaTT	598_3	-20,63	15567
598	TCCATTTATTTCCATTTATT	2-1-1-1-1-11-3	TCcAtTtatttccatttATT	598_4	-21,18	15567
599	TCCATTTATTTCCATTTAT	2-11-2-2-2	TCcatttatttccATttAT	599_1	-20,30	15568
599	TCCATTTATTTCCATTTAT	2-2-1-8-1-1-1-1-2	TCcaTttatttccAtTtAT	599_2	-19,80	15568
599	TCCATTTATTTCCATTTAT	1-1-2-9-1-3-2	TcCAtttatttccAtttAT	599_3	-19,72	15568
599	TCCATTTATTTCCATTTAT	1-1-1-1-2-7-1-3-2	TcCaTTtatttccAtttAT	599_4	-19,50	15568
600	TTCCATTTATTTCCATTTAT	1-1-1-2-1-8-1-1-1-1-2	TtCcaTttatttccAtTtAT	600_1	-20,12	15568
600	TTCCATTTATTTCCATTTAT	1-3-1-10-2-1-2	TtccAtttatttccaTTtAT	600_2	-19,86	15568
600	TTCCATTTATTTCCATTTAT	1-1-1-3-1-7-1-3-2	TtCcatTtatttccAtttAT	600_3	-19,68	15568
600	TTCCATTTATTTCCATTTAT	1-1-1-1-2-8-1-3-2	TtCcATttatttccAtttAT	600_4	-20,68	15568
601	TTTCCATTTATTTCCATTTA	1-4-1-7-1-2-1-1-2	TttccAtttatttCcaTtTA	601_1	-20,53	15569
601	TTTCCATTTATTTCCATTTA	2-2-1-12-3	TTtcCatttatttccatTTA	601_2	-21,47	15569
601	TTTCCATTTATTTCCATTTA	1-2-1-2-1-8-1-2-2	TttCcaTttatttccAttTA	601_3	-20,53	15569
601	TTTCCATTTATTTCCATTTA	1-4-1-9-1-2-2	TttccAtttatttccAttTA	601_4	-19,37	15569
602	CTTTCCATTTATTTCCATT	1-11-1-1-1-1-3	CtttccatttatTtCcATT	602_1	-21,20	15571

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
602	CTTTCCATTTATTTCCATT	2-2-1-9-1-2-2	CTttCcatttatttCcaTT	602_2	-22,00	15571
602	CTTTCCATTTATTTCCATT	1-4-1-9-1-1-2	CtttcCatttatttcCaTT	602_3	-20,42	15571
602	CTTTCCATTTATTTCCATT	1-3-1-11-3	CtttCcatttatttccATT	602_4	-20,89	15571
603	ATCTTTCCATTTATTTCCAT	1-2-1-12-1-1-2	AtcTttccatttatttCcAT	603_1	-21,24	15572
603	ATCTTTCCATTTATTTCCAT	1-3-1-1-1-7-1-3-2	AtctTtCcatttatTtccAT	603_2	-21,33	15572
603	ATCTTTCCATTTATTTCCAT	1-5-1-6-1-4-2	AtctttCcatttaTttccAT	603_3	-21,16	15572
603	ATCTTTCCATTTATTTCCAT	1-16-3	AtctttccatttatttcCAT	603_4	-21,95	15572
604	TCTTTCCATTTATTTCCAT	2-13-1-1-2	TCtttccatttatttCcAT	604_1	-21,57	15572
604	TCTTTCCATTTATTTCCAT	1-2-1-1-1-7-1-1-1-1-2	TctTtCcatttatTtCcAT	604_2	-21,35	15572
604	TCTTTCCATTTATTTCCAT	2-14-3	TCtttccatttatttcCAT	604_3	-22,80	15572
604	TCTTTCCATTTATTTCCAT	2-3-1-11-2	TCtttCcatttatttccAT	604_4	-21,57	15572
605	ATCTTTCCATTTATTTCCA	1-2-1-10-1-2-2	AtcTttccatttatTtcCA	605_1	-20,70	15573
605	ATCTTTCCATTTATTTCCA	1-3-1-8-1-3-2	AtctTtccatttaTttcCA	605_2	-20,63	15573
605	ATCTTTCCATTTATTTCCA	1-1-1-14-2	AtCtttccatttatttcCA	605_3	-20,86	15573
605	ATCTTTCCATTTATTTCCA	1-4-1-9-1-1-2	AtcttTccatttattTcCA	605_4	-20,63	15573
606	TATCTTTCCATTTATTTCCA	1-4-1-8-2-2-2	TatctTtccatttaTTtcCA	606_1	-22,54	15573
606	TATCTTTCCATTTATTTCCA	2-16-2	TAtctttccatttatttcCA	606_2	-22,12	15573
606	TATCTTTCCATTTATTTCCA	1-2-1-14-2	TatctttccatttatttcCA	606_3	-21,97	15573
606	TATCTTTCCATTTATTTCCA	1-17-2	TatctttccatttatttcCA	606_4	-20,99	15573
607	TATCTTTCCATTTATTTCC	2-12-1-2-2	TAtctttccatttaTttCC	607_1	-21,63	15574
607	TATCTTTCCATTTATTTCC	1-2-1-13-2	TatCtttccatttatttCC	607_2	-21,04	15574
607	TATCTTTCCATTTATTTCC	1-2-2-12-2	TatCTttccatttatttCC	607_3	-22,23	15574
607	TATCTTTCCATTTATTTCC	1-4-1-9-1-1-2	TatctTtccatttatTtCC	607_4	-20,66	15574
608	AAATCTCAACTACCATTTTT	1-1-1-3-1-7-3-1-2	AaAtctCaactaccATTtTT	608_1	-19,53	25248

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
608	AAATCTCAACTACCATTTTT	3-1-1-9-2-1-3	AAAtCtcaactaccATtTTT	608_2	-20,58	25248
608	AAATCTCAACTACCATTTTT	1-3-1-8-1-1-5	AaatCtcaactacCaTTTTT	608_3	-20,56	25248
608	AAATCTCAACTACCATTTTT	1-1-1-2-1-7-2-2-3	AaAtcT caactacCAttTTT	608_4	-20,20	25248
608	AAATCTCAACTACCATTTTT	1-3-1-1-1-6-1-1-1-2-2	AaatCtCaactacCaTttTT	608_5	-19,10	25248
608	AAATCTCAACTACCATTTTT	2-3-2-6-1-2-4	AAatcTCaactacCatTTTT	608_6	-21,04	25248
608	AAATCTCAACTACCATTTTT	2-1-2-1-1-7-1-3-2	AAaTCtCaactaccAtttTT	608_7	-19,79	25248
608	AAATCTCAACTACCATTTTT	1-1-3-11-1-1-2	AaATCtcaactaccatTtTT	608_8	-19,97	25248
608	AAATCTCAACTACCATTTTT	3-1-1-1-1-10-3	AAAtCtCaactaccattTTT	608_9	-19,95	25248
609	AAAATCTCAACTACCATTTT	1-12-4-1-2	AaaatctcaactaCCATtTT	609_1	-21,31	25249
609	AAAATCTCAACTACCATTTT	3-11-2-1-3	AAAatctcaactacCAtTTT	609_2	-19,57	25249
609	AAAATCTCAACTACCATTTT	2-1-1-1-1-8-2-1-3	AAaAtCtcaactacCAtTTT	609_3	-20,33	25249
609	AAAATCTCAACTACCATTTT	1-1-4-9-1-2-2	AaAATCtcaactaccAttTT	609_4	-19,46	25249
609	AAAATCTCAACTACCATTTT	1-1-2-2-1-7-2-2-2	AaAAtcTcaactacCAttTT	609_5	-19,13	25249
609	AAAATCTCAACTACCATTTT	4-1-1-7-1-2-4	AAAAtCtcaactaCcaTTTT	609_6	-20,75	25249
609	AAAATCTCAACTACCATTTT	1-1-1-2-1-8-1-1-4	AaAatCtcaactacCaTTTT	609_7	-19,30	25249
609	AAAATCTCAACTACCATTTT	1-2-3-7-1-1-1-1-3	AaaATCtcaactaCcAtTTT	609_8	-20,51	25249
609	AAAATCTCAACTACCATTTT	2-2-2-10-1-1-2	AAaaTCtcaactaccaTtTT	609_9	-18,72	25249
610	AAAATCTCAACTACCATTT	1-4-1-6-4-1-2	AaaatCtcaactACCAtTT	610_1	-20,63	25250
610	AAAATCTCAACTACCATTT	3-10-6	AAAatctcaactaCCATTT	610_2	-21,90	25250
610	AAAATCTCAACTACCATTT	6-6-2-2-3	AAAATCtcaactACcaTTT	610_3	-21,46	25250
610	AAAATCTCAACTACCATTT	2-2-2-7-2-1-3	AAaaTCtcaactaCCaTTT	610_4	-21,18	25250
610	AAAATCTCAACTACCATTT	6-7-2-2-2	AAAATCtcaactaCCatTT	610_5	-22,10	25250
610	AAAATCTCAACTACCATTT	2-1-1-1-1-8-5	AAaAtCtcaactacCATTT	610_6	-20,27	25250
610	AAAATCTCAACTACCATTT	1-1-1-1-2-8-5	AaAaTCtcaactacCATTT	610_7	-20,88	25250

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
610	AAAATCTCAACTACCATTT	1-1-2-1-1-8-2-1-2	AaAAtCtcaactacCAtTT	610_8	-18,51	25250
610	AAAATCTCAACTACCATTT	6-9-4	AAAATCtcaactaccATTT	610_9	-20,94	25250
611	GAAAATCTCAACTACCATT	1-1-3-7-1-2-4	GaAAAtctcaacTacCATT	611_1	-20,48	25251
611	GAAAATCTCAACTACCATT	1-1-2-8-1-1-1-1-3	GaAAatctcaacTaCcATT	611_2	-18,75	25251
611	GAAAATCTCAACTACCATT	3-1-1-10-4	GAAaAtctcaactacCATT	611_3	-20,73	25251
611	GAAAATCTCAACTACCATT	2-1-2-10-4	GAaAAtctcaactacCATT	611_4	-20,73	25251
611	GAAAATCTCAACTACCATT	2-2-1-7-1-4-2	GAaaAtctcaacTaccaTT	611_5	-18,28	25251
611	GAAAATCTCAACTACCATT	2-12-5	GAaaatctcaactaCCATT	611_6	-22,25	25251
611	GAAAATCTCAACTACCATT	4-10-2-1-2	GAAAatctcaactaCCaTT	611_7	-21,06	25251
611	GAAAATCTCAACTACCATT	4-10-1-1-3	GAAAatctcaactaCcATT	611_8	-19,73	25251
611	GAAAATCTCAACTACCATT	5-12-2	GAAAAtctcaactaccaTT	611_9	-18,61	25251
612	TGAAAATCTCAACTACCAT	1-4-1-6-1-1-2-1-2	TgaaaAtctcaaCtACcAT	612_1	-18,43	25252
612	TGAAAATCTCAACTACCAT	2-1-2-7-1-2-1-1-2	TGaAAatctcaaCtaCcAT	612_2	-19,46	25252
612	TGAAAATCTCAACTACCAT	1-1-2-8-1-2-1-1-2	TgAAaatctcaaCtaCcAT	612_3	-18,58	25252
612	TGAAAATCTCAACTACCAT	1-2-1-1-1-6-1-3-3	TgaAaAtctcaaCtacCAT	612_4	-19,40	25252
612	TGAAAATCTCAACTACCAT	1-3-2-10-3	TgaaAAtctcaactacCAT	612_5	-18,60	25252
612	TGAAAATCTCAACTACCAT	1-11-1-2-4	TgaaaatctcaaCtaCCAT	612_6	-21,11	25252
612	TGAAAATCTCAACTACCAT	3-1-2-6-1-4-2	TGAaAAtctcaaCtaccAT	612_7	-20,39	25252
612	TGAAAATCTCAACTACCAT	1-1-1-1-1-7-1-3-3	TgAaAatctcaaCtacCAT	612_8	-19,60	25252
612	TGAAAATCTCAACTACCAT	4-12-3	TGAAaatctcaactacCAT	612_9	-21,07	25252
613	ATCATTCTCAACAATTAAA	4-8-7	A TCAttctcaacAA TT AAA	613_1	-20,89	30599
613	ATCATTCTCAACAATTAAA	1-1-4-6-7	AtCATTctcaacAATTAAA	613_2	-21,09	30599
613	ATCATTCTCAACAATTAAA	5-7-2-1-1-1-2	ATCATtctcaacAAtTaAA	613_3	-19,03	30599
613	ATCATTCTCAACAATTAAA	5-8-2-2-2	ATCATtctcaacaATtaAA	613_4	-19,28	30599

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
613	ATCATTCTCAACAATTAAA	4-1-1-8-5	ATCAtTctcaacaaTTAAA	613_5	-19,86	30599
613	ATCATTCTCAACAATTAAA	5-7-4-1-2	ATCATtctcaacAATTaAA	613_6	-20,79	30599
613	ATCATTCTCAACAATTAAA	4-8-1-1-5	ATCAttctcaacAaTTAAA	613_7	-19,56	30599
613	ATCATTCTCAACAATTAAA	1-1-4-6-1-1-5	AtCATTctcaacAaTTAAA	613_8	-19,76	30599
613	ATCATTCTCAACAATTAAA	4-1-1-7-3-1-2	ATCAtTctcaacaATTaAA	613_9	-19,64	30599
613	ATCATTCTCAACAATTAAA	5-8-1-1-4	ATCATtctcaacaAtTAAA	613_10	-20,11	30599
614	ATCATTCTCAACAATTAA	4-8-6	ATCAttctcaacAATTAA	614_1	-20,14	30600
614	ATCATTCTCAACAATTAA	1-1-4-6-6	AtCATTctcaacAATTAA	614_2	-20,34	30600
614	ATCATTCTCAACAATTAA	5-8-1-1-3	ATCATtctcaacaAtTAA	614_3	-19,36	30600
614	ATCATTCTCAACAATTAA	4-8-1-1-4	ATCAttctcaacAaTTAA	614_4	-18,81	30600
614	ATCATTCTCAACAATTAA	5-8-5	ATCATtctcaacaATTAA	614_5	-21,12	30600
614	ATCATTCTCAACAATTAA	5-7-1-2-3	ATCATtctcaacAatTAA	614_6	-19,11	30600
614	ATCATTCTCAACAATTAA	3-10-5	ATCattctcaacaATTAA	614_7	-18,40	30600
614	ATCATTCTCAACAATTAA	4-9-1-1-3	ATCAttctcaacaAtTAA	614_8	-18,11	30600
614	ATCATTCTCAACAATTAA	4-1-1-8-4	ATCAtTctcaacaaTTAA	614_9	-19,11	30600
614	ATCATTCTCAACAATTAA	1-1-3-9-4	AtCA Ttctcaacaa TT AA	614_10	-18,05	30600
615	GATCATTCTCAACAATTAA	2-3-1-6-2-1-4	GAtcaTtctcaaCAaTTAA	615_1	-20,54	30600
615	GATCATTCTCAACAATTAA	1-2-2-7-1-2-4	GatCAttctcaaCaaTTAA	615_2	-19,04	30600
615	GATCATTCTCAACAATTAA	2-1-3-6-3-2-2	GAtCATtctcaaCAAttAA	615_3	-21,29	30600
615	GATCATTCTCAACAATTAA	2-1-2-8-2-1-3	GAtCAttctcaacAAtTAA	615_4	-19,70	30600
615	GATCATTCTCAACAATTAA	5-8-1-1-1-1-2	GATCAttctcaacAaTtAA	615_5	-19,79	30600
615	GATCATTCTCAACAATTAA	4-8-3-2-2	GATCattctcaaCAAttAA	615_6	-20,50	30600
615	GATCATTCTCAACAATTAA	1-2-3-6-2-2-3	GatCATtctcaaCAatTAA	615_7	-20,82	30600
615	GATCATTCTCAACAATTAA	2-2-2-6-1-1-5	GAtcATtctcaaCaATTAA	615_8	-21,04	30600

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
615	GATCATTCTCAACAATTAA	2-1-1-8-1-2-4	GAtCattctcaaCaaTTAA	615_9	-19,28	30600
615	GATCATTCTCAACAATTAA	1-1-3-9-1-1-3	GaTCAttctcaacaAtTAA	615_10	-18,85	30600
616	AGATCATTCTCAACAATTA	1-1-1-2-1-7-3-1-2	AgAtcAttctcaaCAAtTA	616_1	-19,10	30601
616	AGATCATTCTCAACAATTA	1-3-1-8-2-1-3	AgatCattctcaaCAaTTA	616_2	-19,65	30601
616	AGATCATTCTCAACAATTA	1-3-2-6-1-1-1-2-2	AgatCAttctcaAcAatTA	616_3	-18,49	30601
616	AGATCATTCTCAACAATTA	1-1-1-1-2-11-2	AgAtC AttctcaacaatT A	616_4	-18,49	30601
616	AGATCATTCTCAACAATTA	1-1-1-2-1-9-4	AgAtcAttctcaacaATTA	616_5	-18,49	30601
616	AGATCATTCTCAACAATTA	1-3-2-6-1-1-5	AgatCAttctcaAcAATTA	616_6	-20,76	30601
616	AGATCATTCTCAACAATTA	2-2-1-8-3-1-2	AGatCattctcaaCAAtTA	616_7	-20,47	30601
616	AGATCATTCTCAACAATTA	3-2-1-7-1-2-3	AGAtcAttctcaaCaaTTA	616_8	-20,51	30601
616	AGATCATTCTCAACAATTA	1-2-3-7-1-3-2	AgaTCAttctcaaCaatTA	616_9	-19,80	30601
616	AGATCATTCTCAACAATTA	1-1-1-1-2-8-2-1-2	AgAtCAttctcaacAAtTA	616_10	-19,08	30601
617	GATCATTCTCAACAATTA	2-3-1-6-6	GAtcaTtctcaaCAATTA	617_1	-21,11	30601
617	GATCATTCTCAACAATTA	2-1-2-8-5	GAtCAttctcaacAATTA	617_2	-20,71	30601
617	GATCATTCTCAACAATTA	2-2-2-6-2-2-2	GAtcATtctcaaCAatTA	617_3	-19,70	30601
617	GATCATTCTCAACAATTA	1-1-3-7-1-1-1-1-2	GaTCAttctcaaCaAtTA	617_4	-18,78	30601
617	GATCATTCTCAACAATTA	2-1-2-10-3	GAtCAttctcaacaaTTA	617_5	-19,31	30601
617	GATCATTCTCAACAATTA	2-1-1-1-1-6-3-1-2	GAtCaTtctcaaCAAtTA	617_6	-20,02	30601
617	GATCATTCTCAACAATTA	2-1-2-7-2-2-2	GAtCAttctcaaCAatTA	617_7	-20,53	30601
617	GATCATTCTCAACAATTA	2-1-3-6-1-2-3	GAtCATtctcaaCaaTTA	617_8	-21,24	30601
617	GATCATTCTCAACAATTA	2-2-1-8-5	GAtcAttctcaacAATTA	617_9	-18,63	30601
617	GATCATTCTCAACAATTA	1-1-3-9-1-1-2	GaTCAttctcaacaAtTA	617_10	-18,10	30601
618	AGATCATTCTCAACAATT	1-3-2-6-6	AgatCAttctcaACAATT	618_1	-21,03	30602
618	AGATCATTCTCAACAATT	1-1-1-1-2-7-5	AgAtCAttctcaaCAATT	618_2	-20,70	30602

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
618	AGATCATTCTCAACAATT	1-1-4-6-1-3-2	AgATCAttctcaAcaaTT	618_3	-19,56	30602
618	AGATCATTCTCAACAATT	3-1-1-9-4	AGAtCattctcaacAATT	618_4	-19,61	30602
618	AGATCATTCTCAACAATT	2-1-3-10-2	AGaTCAttctcaacaaTT	618_5	-19,09	30602
618	AGATCATTCTCAACAATT	1-2-3-6-1-3-2	AgaTCAttctcaAcaaTT	618_6	-18,25	30602
618	AGATCATTCTCAACAATT	2-2-2-7-2-1-2	AGatCAttctcaaCAaTT	618_7	-20,14	30602
618	AGATCATTCTCAACAATT	1-1-1-1-2-7-1-1-3	AgAtCAttctcaaCaATT	618_8	-19,02	30602
618	AGATCATTCTCAACAATT	1-2-3-8-4	AgaTCAttctcaacAATT	618_9	-19,23	30602
618	AGATCATTCTCAACAATT	3-1-1-10-3	AGAtCattctcaacaATT	618_10	-19,34	30602
619	GATCATTCTCAACAATT	2-1-2-6-6	GAtCAttctcaACAATT	619_1	-21,40	30602
619	GATCATTCTCAACAATT	1-1-3-7-5	GaTCAttctcaaCAATT	619_2	-19,99	30602
619	GATCATTCTCAACAATT	5-7-1-2-2	GATCAttctcaaCaaTT	619_3	-19,69	30602
619	GATCATTCTCAACAATT	5-6-1-1-4	GATCAttctcaAcAATT	619_4	-20,83	30602
619	GATCATTCTCAACAATT	2-1-2-7-5	GAtCAttctcaaCAATT	619_5	-20,57	30602
619	GATCATTCTCAACAATT	5-6-1-3-2	GATCAttctcaAcaaTT	619_6	-19,43	30602
619	GATCATTCTCAACAATT	4-8-5	GATCattctcaaCAATT	619_7	-21,04	30602
619	GATCATTCTCAACAATT	1-1-3-7-2-1-2	GaTCAttctcaaCAaTT	619_8	-18,67	30602
619	GATCATTCTCAACAATT	5-7-1-1-3	GATCAttctcaaCaATT	619_9	-20,82	30602
619	GATCATTCTCAACAATT	2-1-2-8-4	GAtCAttctcaacAATT	619_10	-18,48	30602
620	AAGATCATTCTCAACAAT	4-1-1-6-1-1-4	AAGAtCattctcAaCAAT	620_1	-20,71	30603
620	AAGATCATTCTCAACAAT	4-9-5	AAGAtcattctcaACAAT	620_2	-20,79	30603
620	AAGATCATTCTCAACAAT	2-2-2-6-6	AAgaTCattctcAACAAT	620_3	-19,88	30603
620	AAGATCATTCTCAACAAT	4-1-1-7-2-1-2	AAGAtCattctcaACaAT	620_4	-19,77	30603
620	AAGATCATTCTCAACAAT	2-1-3-8-4	AAgATCattctcaaCAAT	620_5	-20,10	30603
620	AAGATCATTCTCAACAAT	4-1-1-6-2-2-2	AAGAtCattctcAAcaAT	620_6	-18,96	30603

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
620	AAGATCATTCTCAACAAT	3-1-2-6-1-1-4	AAGaTCattctcAaCAAT	620_7	-20,12	30603
620	AAGATCATTCTCAACAAT	2-1-3-6-1-1-4	AAgATCattctcAaCAAT	620_8	-20,17	30603
620	AAGATCATTCTCAACAAT	1-1-1-2-1-7-5	AaGatCattctcaACAAT	620_9	-18,21	30603
620	AAGATCATTCTCAACAAT	4-1-1-8-4	AAGAtCattctcaaCAAT	620_10	-20,63	30603
621	AAAGATCATTCTCAACAA	1-1-1-9-6	AaAgatcattctCAACAA	621_1	-18,13	30604
621	AAAGATCATTCTCAACAA	1-1-3-7-2-1-3	AaAGAtcattctCAaCAA	621_2	-20,08	30604
621	AAAGATCATTCTCAACAA	1-3-2-6-2-1-3	AaagATcattctCAaCAA	621_3	-18,11	30604
621	AAAGATCATTCTCAACAA	1-2-2-7-1-1-4	AaaGAtcattctCaACAA	621_4	-18,07	30604
621	AAAGATCATTCTCAACAA	5-10-3	AAAGAtcattctcaaCAA	621_5	-18,65	30604
621	AAAGATCATTCTCAACAA	1-1-3-7-3-1-2	AaAGAtcattctCAAcAA	621_6	-18,59	30604
621	AAAGATCATTCTCAACAA	4-8-2-1-3	AAAGatcattctCAaCAA	621_7	-19,10	30604
621	AAAGATCATTCTCAACAA	3-1-1-7-2-1-3	AAAgAtcattctCAaCAA	621_8	-18,35	30604
621	AAAGATCATTCTCAACAA	1-1-2-8-2-1-3	AaAGatcattctCAaCAA	621_9	-18,37	30604
621	AAAGATCATTCTCAACAA	1-2-2-7-2-1-3	AaaGAtcattctCAaCAA	621_10	-18,74	30604
621	AAAGATCATTCTCAACAA	5-7-1-2-3	AAAGAtcattctcaaCAA	621_11	-19,32	30604
622	CAAAGATCATTCTCAACA	1-1-2-8-6	CaAAgatcattcTCAACA	622_1	-20,93	30605
622	CAAAGATCATTCTCAACA	2-1-1-9-5	CAaAgatcattctCAACA	622_2	-20,68	30605
622	CAAAGATCATTCTCAACA	1-4-1-7-5	CaaagAtcattctCAACA	622_3	-18,86	30605
622	CAAAGATCATTCTCAACA	4-1-1-7-1-2-2	CAAAgAtcattctCaaCA	622_4	-19,40	30605
622	CAAAGATCATTCTCAACA	3-1-2-10-2	CAAaGAtcattctcaaCA	622_5	-19,67	30605
622	CAAAGATCATTCTCAACA	4-8-2-2-2	CAAAgatcattcTCaaCA	622_6	-20,10	30605
622	CAAAGATCATTCTCAACA	1-1-2-1-1-7-5	CaAAgAtcattctCAACA	622_7	-20,23	30605
622	CAAAGATCATTCTCAACA	2-1-1-9-2-1-2	CAaAgatcattctCAaCA	622_8	-19,66	30605
622	CAAAGATCATTCTCAACA	3-2-1-7-1-1-3	CAAagAtcattctCaACA	622_9	-19,21	30605

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
622	CAAAGATCATTCTCAACA	1-3-2-7-1-2-2	CaaaGAtcattctCaaCA	622_10	-18,30	30605
623	CAAAGATCATTCTCAAC	3-8-6	CAAagatcattCTCAAC	623_1	-19,95	30606
623	CAAAGATCATTCTCAAC	2-1-1-7-6	CAaAgatcattCTCAAC	623_2	-20,23	30606
623	CAAAGATCATTCTCAAC	2-2-1-6-6	CAaaGatcattCTCAAC	623_3	-20,15	30606
623	CAAAGATCATTCTCAAC	1-2-2-6-6	CaaAGatcattCTCAAC	623_4	-20,00	30606
623	CAAAGATCATTCTCAAC	5-6-1-1-4	CAAAGatcattCtCAAC	623_5	-20,35	30606
623	CAAAGATCATTCTCAAC	4-7-3-1-2	CAAAgatcattCTCaAC	623_6	-19,28	30606
623	CAAAGATCATTCTCAAC	3-1-1-6-1-1-4	CAAaGatcattCtCAAC	623_7	-18,81	30606
623	CAAAGATCATTCTCAAC	2-1-1-7-1-1-4	CAaAgatcattCtCAAC	623_8	-18,36	30606
623	CAAAGATCATTCTCAAC	1-2-2-6-1-1-4	CaaAGatcattCtCAAC	623_9	-18,12	30606
623	CAAAGATCATTCTCAAC	4-8-5	CAAAgatcattcTCAAC	623_10	-19,31	30606
624	CTCAAAGATCATTCTCA	1-2-1-7-6	CtcAaagatcaTTCTCA	624_1	-20,57	30608
624	CTCAAAGATCATTCTCA	1-1-1-1-1-7-2-1-2	CtCaAagatcatTCtCA	624_2	-18,69	30608
624	CTCAAAGATCATTCTCA	1-1-2-7-1-2-3	CtCAaagatcaTtcTCA	624_3	-19,51	30608
624	CTCAAAGATCATTCTCA	3-10-1-1-2	CTCaaagatcattCtCA	624_4	-19,23	30608
624	CTCAAAGATCATTCTCA	1-1-3-8-4	CtCAAagatcattCTCA	624_5	-21,26	30608
624	CTCAAAGATCATTCTCA	1-1-3-6-1-1-1-1-2	CtCAAagatcaTtCtCA	624_6	-19,82	30608
624	CTCAAAGATCATTCTCA	4-7-1-3-2	CTCAaagatcaTtctCA	624_7	-20,18	30608
624	CTCAAAGATCATTCTCA	1-2-2-7-5	CtcAAagatcatTCTCA	624_8	-20,16	30608
624	CTCAAAGATCATTCTCA	1-1-2-8-2-1-2	CtCAaagatcatTCtCA	624_9	-19,83	30608
624	CTCAAAGATCATTCTCA	3-10-4	CTCaaagatcattCTCA	624_10	-21,11	30608
625	TACACTTAATTATACTTCCA	1-2-1-1-1-7-2-3-2	TacAcTtaattatACttcCA	625_1	-20,33	30666
625	TACACTTAATTATACTTCCA	1-2-1-2-1-6-1-4-2	TacActTaattatActtcCA	625_2	-19,15	30666
625	TACACTTAATTATACTTCCA	1-4-1-7-1-1-1-2-2	TacacTtaattatAcTtcCA	625_3	-19,30	30666

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Seq ID NO	Motif	Design	Compound	CMP ID NO	∆G°	Start SEQ ID NO 1
625	TACACTTAATTATACTTCCA	1-1-1-2-2-6-1-4-2	TaCacTTaattatActtcCA	625_4	-20,71	30666
625	TACACTTAATTATACTTCCA	1-1-1-3-1-8-1-2-2	TaCactTaattatacTtcCA	625_5	-20,00	30666
625	TACACTTAATTATACTTCCA	1-2-1-1-2-8-1-2-2	TacAcTTaattatacTtcCA	625_6	-20,50	30666
625	TACACTTAATTATACTTCCA	1-2-1-13-3	TacActtaattatacttCCA	625_7	-20,60	30666
625	TACACTTAATTATACTTCCA	1-4-1-11-3	TacacTtaattatacttCCA	625_8	-20,96	30666
625	TACACTTAATTATACTTCCA	2-1-1-1-1-12-2	TAcAcTtaattatacttcCA	625_9	-19,97	30666
625	TACACTTAATTATACTTCCA	1-1-1-2-1-7-2-3-2	TaCacTtaattatACttcCA	625_10	-20,87	30666
625	TACACTTAATTATACTTCCA	1-2-1-1-2-6-1-1-1-2-2	TacAcTTaattatAcTtcCA	625_11	-20,69	30666
625	TACACTTAATTATACTTCCA	1-2-1-1-1-9-1-1-3	TacAcTtaattatacTtCCA	625_12	-21,63	30666
625	TACACTTAATTATACTTCCA	1-1-1-3-1-10-3	TaCactTaattatacttCCA	625_13	-21,86	30666
625	TACACTTAATTATACTTCCA	2-1-2-1-1-11-2	TAcACtTaattatacttcCA	625_14	-21,58	30666
626	TTACACTTAATTATACTTCC	1-3-1-1-1-7-2-2-2	TtacAcTtaattatACttCC	626_1	-19,98	30667
626	TTACACTTAATTATACTTCC	1-5-1-7-1-1-1-1-2	TtacacTtaattatAcTtCC	626_2	-18,96	30667
626	TTACACTTAATTATACTTCC	2-4-1-11-2	TTacacTtaattatacttCC	626_3	-19,49	30667
626	TTACACTTAATTATACTTCC	1-5-1-9-4	TtacacTtaattatacTTCC	626_4	-20,26	30667
626	TTACACTTAATTATACTTCC	1-1-1-3-1-8-1-2-2	TtAcacTtaattataCttCC	626_5	-19,43	30667
626	TTACACTTAATTATACTTCC	1-1-2-2-1-7-1-3-2	TtACacTtaattatActtCC	626_6	-19,72	30667
626	TTACACTTAATTATACTTCC	3-1-1-12-3	TTAcActtaattatactTCC	626_7	-21,33	30667
626	TTACACTTAATTATACTTCC	1-1-1-1-1-1-1-9-1-1-2	TtAcAcTtaattatacTtCC	626_8	-19,10	30667
626	TTACACTTAATTATACTTCC	1-2-2-1-1-11-2	TtaCAcTtaattatacttCC	626_9	-20,49	30667
626	TTACACTTAATTATACTTCC	1-5-1-7-2-1-3	TtacacTtaattatACtTCC	626_10	-20,82	30667
626	TTACACTTAATTATACTTCC	4-2-1-7-1-3-2	TTACacTtaattatActtCC	626_11	-21,99	30667
626	TTACACTTAATTATACTTCC	1-1-1-1-3-8-1-2-2	TtAcACTtaattataCttCC	626_12	-21,65	30667
626	TTACACTTAATTATACTTCC	2-1-2-11-4	TTaCActtaattatacTTCC	626_13	-23,23	30667

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
626	TTACACTTAATTATACTTCC	2-2-1-1-1-9-1-1-2	TTacAcTtaattatacTtCC	626_14	-20,15	30667
627	TTTACACTTAATTATACTTC	2-1-2-8-1-1-5	TTtACacttaattAtACTTC	627_1	-20,02	30668
627	TTTACACTTAATTATACTTC	2-3-1-7-4-1-2	TTtacActtaattATACtTC	627_2	-19,89	30668
627	TTTACACTTAATTATACTTC	1-2-1-1-1-7-2-1-4	TttAcActtaattATaCTTC	627_3	-19,35	30668
627	TTTACACTTAATTATACTTC	1-1-3-8-3-2-2	TtTACacttaattATActTC	627_4	-20,58	30668
627	TTTACACTTAATTATACTTC	3-2-1-7-3-1-3	TTTacActtaattATAcTTC	627_5	-20,76	30668
627	TTTACACTTAATTATACTTC	1-3-2-7-2-2-3	TttaCActtaattATacTTC	627_6	-19,58	30668
627	TTTACACTTAATTATACTTC	3-2-1-7-2-1-4	TTTacActtaattATaCTTC	627_7	-21,21	30668
627	TTTACACTTAATTATACTTC	3-1-1-8-1-2-4	TTTaCacttaattAtaCTTC	627_8	-20,07	30668
627	TTTACACTTAATTATACTTC	6-7-1-4-2	TTTACActtaattAtactTC	627_9	-20,56	30668
627	TTTACACTTAATTATACTTC	4-1-1-7-4-1-2	TTTAcActtaattATACtTC	627_10	-22,36	30668
627	TTTACACTTAATTATACTTC	3-1-1-1-1-6-3-1-3	TTTaCaCttaattATAcTTC	627_11	-22,29	30668
627	TTTACACTTAATTATACTTC	2-1-3-7-3-2-2	TTtACActtaattATActTC	627_12	-21,19	30668
627	TTTACACTTAATTATACTTC	3-1-2-7-2-1-4	TTTaCActtaattATaCTTC	627_13	-23,30	30668
627	TTTACACTTAATTATACTTC	1-1-4-7-1-2-4	TtTACActtaattAtaCTTC	627_14	-21,94	30668
628	ATTTACACTTAATTATACTT	2-1-1-2-1-6-3-1-3	ATtTacActtaatTATaCTT	628_1	-21,21	30669
628	ATTTACACTTAATTATACTT	3-1-1-8-2-1-4	ATTtAcacttaatTAtACTT	628_2	-20,27	30669
628	ATTTACACTTAATTATACTT	1-1-2-2-1-6-4-1-2	AtTTacActtaatTATAcTT	628_3	-20,33	30669
628	ATTTACACTTAATTATACTT	1-3-1-1-1-7-6	AtttAcActtaattATACTT	628_4	-19,30	30669
628	ATTTACACTTAATTATACTT	2-2-2-7-3-2-2	ATttACacttaatTATacTT	628_5	-19,94	30669
628	ATTTACACTTAATTATACTT	4-1-2-6-2-3-2	ATTTaCActtaatTAtacTT	628_6	-21,29	30669
628	ATTTACACTTAATTATACTT	1-1-4-7-1-1-1-2-2	AtTTACacttaatTaTacTT	628_7	-19,33	30669
628	ATTTACACTTAATTATACTT	2-2-3-6-1-2-4	ATttACActtaatTatACTT	628_8	-20,97	30669
628	ATTTACACTTAATTATACTT	4-2-1-6-1-3-3	ATTTacActtaatTataCTT	628_9	-19,73	30669

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
628	ATTTACACTTAATTATACTT	1-1-2-1-2-6-4-1-2	AtTTaCActtaatTATAcTT	628_10	-22,43	30669
628	ATTTACACTTAATTATACTT	3-2-2-6-2-2-3	ATTtaCActtaatTAtaCTT	628_11	-21,72	30669
628	ATTTACACTTAATTATACTT	1-2-4-6-2-2-3	AttTACActtaatTAtaCTT	628_12	-22,02	30669
628	ATTTACACTTAATTATACTT	2-1-1-1-2-6-1-1-5	ATtTaCActtaatTaTACTT	628_13	-23,00	30669
628	ATTTACACTTAATTATACTT	5-8-1-1-1-1-3	ATTTAcacttaatTaTaCTT	628_14	-21,68	30669
629	TTCTACTATACTTTCCTCT	1-3-1-7-1-1-1-2-2	TtctActatactTtCctCT	629_1	-21,04	30711
629	TTCTACTATACTTTCCTCT	1-11-1-1-1-2-2	TtctactatactTtCctCT	629_2	-20,85	30711
629	TTCTACTATACTTTCCTCT	1-11-1-2-1-1-2	TtctactatactTtcCtCT	629_3	-20,97	30711
629	TTCTACTATACTTTCCTCT	1-1-1-9-1-4-2	TtCtactatactTtcctCT	629_4	-21,06	30711
629	TTCTACTATACTTTCCTCT	1-1-1-11-1-2-2	TtCtactatactttCctCT	629_5	-21,53	30711
629	TTCTACTATACTTTCCTCT	1-3-1-9-1-2-2	TtctActatactttCctCT	629_6	-20,74	30711
629	TTCTACTATACTTTCCTCT	1-4-1-8-1-2-2	TtctaCtatactttCctCT	629_7	-21,54	30711
629	TTCTACTATACTTTCCTCT	1-13-1-2-2	TtCtactatactttCctCT	629_8	-20,55	30711
629	TTCTACTATACTTTCCTCT	1-1-1-12-1-1-2	TtCtactatactttcCtCT	629_9	-21,65	30711
629	TTCTACTATACTTTCCTCT	1-3-1-10-1-1-2	TtctActatactttcCtCT	629_10	-20,86	30711
629	TTCTACTATACTTTCCTCT	1-14-1-1-2	TtctactatactttcCtCT	629_11	-20,67	30711
629	TTCTACTATACTTTCCTCT	1-1-1-1-1-7-1-1-1-2-2	TtCtActatactTtCctCT	629_12	-22,02	30711
629	TTCTACTATACTTTCCTCT	1-1-1-2-1-8-1-2-2	TtCta Ctata ctttCctCT	629_13	-22,52	30711
629	TTCTACTATACTTTCCTCT	1-3-2-8-1-2-2	TtctACtatactttCctCT	629_14	-22,14	30711
629	TTCTACTATACTTTCCTCT	1-1-1-1-1-10-1-1-2	TtCtActatactttcCtCT	629_15	-21,84	30711
629	TTCTACTATACTTTCCTCT	1-1-1-2-1-9-1-1-2	TtCtaCtatactttcCtCT	629_16	-22,64	30711
630	GTTCTACTATACTTTCCTC	1-12-1-1-1-1-2	GttctactatactTtCcTC	630_1	-20,78	30712
630	GTTCTACTATACTTTCCTC	1-4-1-9-1-1-2	GttctActatactttCcTC	630_2	-20,67	30712
630	GTTCTACTATACTTTCCTC	1-14-1-1-2	GttctactatactttCcTC	630_3	-20,48	30712

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
631	GTTCTACTATACTTTCCT	1-2-1-1-1-7-1-2-2	GttCtActatactTtcCT	631_1	-20,25	30713
631	GTTCTACTATACTTTCCT	1-2-1-9-1-2-2	GttCtactatactTtcCT	631_2	-20,06	30713
631	GTTCTACTATACTTTCCT	1-2-1-11-3	GttCtactatactttCCT	631_3	-22,13	30713
631	GTTCTACTATACTTTCCT	1-4-1-9-3	GttctActatactttCCT	631_4	-21,34	30713
631	GTTCTACTATACTTTCCT	1-14-3	GttctactatactttCCT	631_5	-21,15	30713
631	GTTCTACTATACTTTCCT	2-1-1-1-1-10-2	GTtCtActatactttcCT	631_6	-21,50	30713
631	GTTCTACTATACTTTCCT	2-1-1-12-2	GTtCtactatactttcCT	631_7	-21,30	30713
631	GTTCTACTATACTTTCCT	1-2-1-1-1-10-2	GttCtActatactttcCT	631_8	-19,95	30713
631	GTTCTACTATACTTTCCT	1-2-1-12-2	GttCtactatactttcCT	631_9	-19,76	30713
631	GTTCTACTATACTTTCCT	1-15-2	GttctactatactttcCT	631_10	-18,78	30713
631	GTTCTACTATACTTTCCT	1-2-1-9-1-1-3	GttCtactatactTtCCT	631_11	-22,43	30713
631	GTTCTACTATACTTTCCT	2-1-1-1-1-7-1-2-2	GTtCtActatactTtcCT	631_12	-21,80	30713
631	GTTCTACTATACTTTCCT	1-2-2-8-1-2-2	GttCTactatactTtcCT	631_13	-21,68	30713
631	GTTCTACTATACTTTCCT	1-2-1-1-1-9-3	GttCtActatactttCCT	631_14	-22,32	30713
631	GTTCTACTATACTTTCCT	1-2-3-10-2	GttCTActatactttcCT	631_15	-22,60	30713
632	AGTTCTACTATACTTTCC	1-12-1-2-2	AgttctactatacTttCC	632_1	-19,37	30714
632	AGTTCTACTATACTTTCC	1-13-1-1-2	AgttctactatactTtCC	632_2	-19,16	30714
632	AGTTCTACTATACTTTCC	1-1-1-13-2	AgTtctactatactttCC	632_3	-19,51	30714
632	AGTTCTACTATACTTTCC	1-15-2	AgttctactatactttCC	632_4	-18,86	30714
632	AGTTCTACTATACTTTCC	1-1-1-10-1-2-2	AgTtctactatacTttCC	632_5	-20,03	30714
632	AGTTCTACTATACTTTCC	1-4-1-7-1-2-2	AgttcTactatacTttCC	632_6	-20,31	30714
632	AGTTCTACTATACTTTCC	2-14-2	AGttctactatactttCC	632_7	-20,26	30714
632	AGTTCTACTATACTTTCC	1-2-1-12-2	AgtTctactatactttCC	632_8	-19,23	30714
632	AGTTCTACTATACTTTCC	1-4-1-10-2	AgttcTactatactttCC	632_9	-19,80	30714

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
632	AGTTCTACTATACTTTCC	2-10-1-3-2	AGttctactataCtttCC	632_10	-21,25	30714
632	AGTTCTACTATACTTTCC	1-4-1-6-1-3-2	AgttcTactataCtttCC	632_11	-20,79	30714
632	AGTTCTACTATACTTTCC	1-4-1-7-2-1-2	AgttcTactatacTTtCC	632_12	-21,13	30714
632	AGTTCTACTATACTTTCC	1-1-1-11-1-1-2	AgTtctactatactTtCC	632_13	-19,82	30714
632	AGTTCTACTATACTTTCC	1-3-1-11-2	AgttCtactatactttCC	632_14	-19,83	30714
633	CAACATTATTAACCACCTTA	1-13-3-1-2	CaacattattaaccACCtTA	633_1	-22,44	33376
633	CAACATTATTAACCACCTTA	4-10-1-2-3	CAACattattaaccAccTTA	633_2	-22,98	33376
633	CAACATTATTAACCACCTTA	2-2-1-10-1-1-3	CAacAttattaaccaCcTTA	633_3	-21,97	33376
633	CAACATTATTAACCACCTTA	1-4-2-8-1-2-2	CaacaTTattaaccaCctTA	633_4	-21,08	33376
633	CAACATTATTAACCACCTTA	1-1-2-11-1-2-2	CaACattattaaccaCctTA	633_5	-20,90	33376
633	CAACATTATTAACCACCTTA	1-2-2-13-2	CaaCAttattaaccacctTA	633_6	-20,76	33376
633	CAACATTATTAACCACCTTA	1-1-1-1-1-11-1-1-2	CaAcAttattaaccacCtTA	633_7	-19,97	33376
633	CAACATTATTAACCACCTTA	1-15-4	CaacattattaaccacCTTA	633_8	-21,21	33376
633	CAACATTATTAACCACCTTA	2-4-1-11-2	CAacatTattaaccacctTA	633_9	-20,83	33376
634	CAACATTATTAACCACCTT	2-10-2-3-2	CAacattattaaCCaccTT	634_1	-21,86	33377
634	CAACATTATTAACCACCTT	1-14-4	CaacattattaaccaCCTT	634_2	-21,36	33377
634	CAACATTATTAACCACCTT	1-1-1-11-1-1-3	CaAcattattaaccAcCTT	634_3	-19,54	33377
634	CAACATTATTAACCACCTT	3-1-1-11-3	CAAcAttattaaccacCTT	634_4	-21,13	33377
634	CAACATTATTAACCACCTT	3-11-2-1-2	CAAcattattaaccACcTT	634_5	-20,84	33377
634	CAACATTATTAACCACCTT	2-1-2-9-1-1-3	CAaCAttattaaccAcCTT	634_6	-22,76	33377
634	CAACATTATTAACCACCTT	2-1-2-10-1-1-2	CAaCAttattaaccaCcTT	634_7	-21,83	33377
634	CAACATTATTAACCACCTT	1-1-2-11-1-1-2	CaACattattaaccaCcTT	634_8	-19,70	33377
634	CAACATTATTAACCACCTT	1-2-1-12-3	CaaCattattaaccacCTT	634_9	-19,66	33377
635	GCAACATTATTAACCACCT	1-1-1-2-1-6-2-3-2	GcAacAttattaACcacCT	635_1	-21,56	33378

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
635	GCAACATTATTAACCACCT	1-1-2-1-1-6-1-2-1-1-2	GcAAcAttattaAccAcCT	635_2	-21,14	33378
635	GCAACATTATTAACCACCT	1-11-2-1-1-1-2	GcaacattattaACcAcCT	635_3	-21,59	33378
635	GCAACATTATTAACCACCT	1-4-1-6-1-3-3	GcaacAttattaAccaCCT	635_4	-22,69	33378
635	GCAACATTATTAACCACCT	1-1-1-1-1-7-1-4-2	GcAaCattattaAccacCT	635_5	-21,01	33378
635	GCAACATTATTAACCACCT	1-11-1-1-1-2-2	GcaacattattaAcCacCT	635_6	-20,83	33378
635	GCAACATTATTAACCACCT	2-3-1-6-1-4-2	GCaacAttattaAccacCT	635_7	-22,63	33378
635	GCAACATTATTAACCACCT	1-1-1-12-1-1-2	GcAacattattaaccAcCT	635_8	-20,05	33378
635	GCAACATTATTAACCACCT	1-2-1-1-1-11-2	GcaAcAttattaaccacCT	635_9	-20,30	33378
636	AGCAACATTATTAACCACC	1-2-1-9-2-1-3	AgcAacattattaACcACC	636_1	-22,13	33379
636	AGCAACATTATTAACCACC	1-11-1-1-1-2-2	AgcaacattattAaCcaCC	636_2	-20,80	33379
636	AGCAACATTATTAACCACC	1-4-1-6-2-3-2	AgcaaCattattAAccaCC	636_3	-21,32	33379
636	AGCAACATTATTAACCACC	1-2-2-7-1-2-1-1-2	AgcAAcattattAacCaCC	636_4	-21,29	33379
636	AGCAACATTATTAACCACC	2-11-1-3-2	AGcaacattattaAccaCC	636_5	-21,75	33379
636	AGCAACATTATTAACCACC	1-1-1-1-1-8-1-2-3	AgCaAcattattaAccACC	636_6	-22,16	33379
636	AGCAACATTATTAACCACC	1-2-1-1-1-6-1-3-3	AgcAaCattattAaccACC	636_7	-21,33	33379
636	AGCAACATTATTAACCACC	2-1-2-12-2	AGcAAcattattaaccaCC	636_8	-22,02	33379
636	AGCAACATTATTAACCACC	1-15-3	AgcaacattattaaccACC	636_9	-20,45	33379
637	AGCAACATTATTAACCAC	2-1-1-9-5	AGcAacattattaACCAC	637_1	-21,97	33380
637	AGCAACATTATTAACCAC	1-3-1-7-6	AgcaAcattattAACCAC	637_2	-21,20	33380
637	AGCAACATTATTAACCAC	2-10-2-1-3	AGcaacattattAAcCAC	637_3	-19,42	33380
637	AGCAACATTATTAACCAC	1-2-1-8-1-1-4	AgcAacattattAaCCAC	637_4	-19,84	33380
637	AGCAACATTATTAACCAC	3-9-3-1-2	AGCaacattattAACcAC	637_5	-20,94	33380
637	AGCAACATTATTAACCAC	1-1-3-7-3-1-2	AgCAAcattattAACcAC	637_6	-20,15	33380
637	AGCAACATTATTAACCAC	1-1-3-7-2-1-3	AgCAAcattattAAcCAC	637_7	-20,96	33380

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
637	AGCAACATTATTAACCAC	5-7-1-3-2	AGCAAcattattAaccAC	637_8	-21,24	33380
637	AGCAACATTATTAACCAC	3-1-1-8-1-2-2	AGCaAcattattaAccAC	637_9	-19,86	33380
638	GTTTCCATCTACTATTAAT	1-3-1-7-1-1-1-1-3	GtttCcatctacTaTtAAT	638_1	-19,59	39806
638	GTTTCCATCTACTATTAAT	1-1-1-9-2-3-2	GtTtccatctacTAttaAT	638_2	-19,50	39806
638	GTTTCCATCTACTATTAAT	1-4-1-6-2-2-3	GtttcCatctacTAttAAT	638_3	-20,09	39806
638	GTTTCCATCTACTATTAAT	1-3-1-8-1-2-3	GtttCcatctactAttAAT	638_4	-18,30	39806
638	GTTTCCATCTACTATTAAT	3-1-1-8-1-3-2	GTTtCcatctactAttaAT	638_5	-20,35	39806
638	GTTTCCATCTACTATTAAT	1-2-2-12-2	GttTCcatctactattaAT	638_6	-18,88	39806
638	GTTTCCATCTACTATTAAT	1-1-1-11-1-1-3	GtTtccatctactaTtAAT	638_7	-18,18	39806
638	GTTTCCATCTACTATTAAT	2-2-1-10-1-1-2	GTttCcatctactatTaAT	638_8	-20,16	39806
638	GTTTCCATCTACTATTAAT	1-1-1-1-2-10-3	GtTtCCatctactattAAT	638_9	-20,69	39806
638	GTTTCCATCTACTATTAAT	2-2-1-7-1-3-3	GTttCcatctacT attAAT	638_10	-20,69	39806
638	GTTTCCATCTACTATTAAT	1-1-1-10-2-1-3	GtTtccatctactATtAAT	638_11	-19,08	39806
638	GTTTCCATCTACTATTAAT	1-3-1-8-1-1-1-1-2	GtttCcatctactAtTaAT	638_12	-18,72	39806
638	GTTTCCATCTACTATTAAT	1-2-3-7-1-2-3	GttTCCatctactAttAAT	638_13	-21,47	39806
638	GTTTCCATCTACTATTAAT	1-1-1-1-2-11-2	GtTtCCatctactattaAT	638_14	-20,37	39806
639	GTTTCCATCTACTATTAA	1-11-2-1-3	GtttccatctacTAtTAA	639_1	-19,21	39807
639	GTTTCCATCTACTATTAA	1-3-1-7-1-1-4	GtttCcatctacTaTTAA	639_2	-19,80	39807
639	GTTTCCATCTACTATTAA	3-1-1-7-2-2-2	GTTtCcatctacTAttAA	639_3	-20,57	39807
639	GTTTCCATCTACTATTAA	2-2-1-7-1-1-1-1-2	GTttCcatctacTaTtAA	639_4	-19,07	39807
639	GTTTCCATCTACTATTAA	1-3-2-7-2-1-2	GtttCCatctactATtAA	639_5	-19,67	39807
639	GTTTCCATCTACTATTAA	3-2-1-6-1-3-2	GTTtcCatctacTattAA	639_6	-19,25	39807
639	GTTTCCATCTACTATTAA	1-1-3-8-1-2-2	GtTTCcatctactAttAA	639_7	-18,04	39807
639	GTTTCCATCTACTATTAA	1-1-1-1-2-10-2	GtTtCCatctactattAA	639_8	-18,62	39807

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
639	GTTTCCATCTACTATTAA	3-1-1-9-4	GTTtCcatctactaTTAA	639_9	-21,21	39807
639	GTTTCCATCTACTATTAA	1-3-2-6-2-2-2	GtttCCatctacTAttAA	639_10	-20,39	39807
639	GTTTCCATCTACTATTAA	1-1-3-7-1-1-1-1-2	GtTTCcatctacTaTtAA	639_11	-19,32	39807
639	GTTTCCATCTACTATTAA	2-2-1-7-1-2-3	GTttCcatctacTatTAA	639_12	-20,39	39807
639	GTTTCCATCTACTATTAA	2-2-1-8-2-1-2	GTttCcatctactATtAA	639_13	-19,03	39807
639	GTTTCCATCTACTATTAA	1-1-1-1-2-8-4	GtTtCCatctactaTTAA	639_14	-21,34	39807
640	TGTTTCCATCTACTATTA	1-1-1-11-1-1-2	TgTttccatctactAtTA	640_1	-18,41	39808
640	TGTTTCCATCTACTATTA	1-2-1-9-2-1-2	TgtTtccatctacTAtTA	640_2	-20,03	39808
640	TGTTTCCATCTACTATTA	1-4-1-7-1-2-2	TgtttCcatctacTatTA	640_3	-19,37	39808
640	TGTTTCCATCTACTATTA	1-4-1-8-4	TgtttCcatctactATTA	640_4	-20,28	39808
640	TGTTTCCATCTACTATTA	1-4-1-8-1-1-2	TgtttCcatctactAtTA	640_5	-18,52	39808
640	TGTTTCCATCTACTATTA	1-1-2-1-1-10-2	TgTTtCcatctactatTA	640_6	-19,89	39808
640	TGTTTCCATCTACTATTA	1-4-1-9-3	TgtttCcatctactaTTA	640_7	-19,37	39808
640	TGTTTCCATCTACTATTA	1-2-1-1-1-10-2	TgtTtCcatctactatTA	640_8	-18,73	39808
640	TGTTTCCATCTACTATTA	1-4-1-10-2	TgtttCcatctactatTA	640_9	-18,42	39808
640	TGTTTCCATCTACTATTA	1-4-1-6-1-1-4	TgtttCcatctaCtATTA	640_10	-21,27	39808
640	TGTTTCCATCTACTATTA	2-1-1-9-2-1-2	TGtTtccatctacTAtTA	640_11	-21,24	39808
640	TGTTTCCATCTACTATTA	1-3-2-8-1-1-2	TgttTCcatctactAtTA	640_12	-19,51	39808
640	TGTTTCCATCTACTATTA	2-1-1-1-1-10-2	TGtTtCcatctactatTA	640_13	-19,94	39808
640	TGTTTCCATCTACTATTA	1-1-1-2-1-10-2	TgTttCcatctactatTA	640_14	-19,08	39808
641	ACTCTGCAATACACCAA	2-1-1-8-2-1-2	ACtCtgcaatacACcAA	641_1	-19,61	44439
641	ACTCTGCAATACACCAA	2-2-1-6-1-1-1-1-2	ACtcTgcaataCaCcAA	641_2	-19,77	44439
641	ACTCTGCAATACACCAA	1-2-1-7-1-1-1-1-2	ActCtgcaataCaCcAA	641_3	-18,35	44439
641	ACTCTGCAATACACCAA	2-1-2-6-2-2-2	ACtCTgcaataCAccAA	641_4	-22,21	44439

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
641	ACTCTGCAATACACCAA	1-3-1-7-1-1-3	ActcTgcaatacAcCAA	641_5	-19,05	44439
641	ACTCTGCAATACACCAA	4-8-1-2-2	ACTCtgcaatacAccAA	641_6	-20,30	44439
641	ACTCTGCAATACACCAA	2-1-2-9-3	ACtCTgcaatacacCAA	641_7	-21,96	44439
641	ACTCTGCAATACACCAA	2-11-4	ACtctgcaatacaCCAA	641_8	-21,68	44439
641	ACTCTGCAATACACCAA	1-1-2-10-3	AcTCtgcaatacacCAA	641_9	-20,07	44439
642	CTGTATACACCATCCCA	1-10-1-1-1-1-2	CtgtatacaccAtCcCA	642_1	-21,99	46391
642	CTGTATACACCATCCCA	1-10-1-3-2	CtgtatacaccAtccCA	642_2	-21,22	46391
642	CTGTATACACCATCCCA	1-1-1-8-1-3-2	CtGtatacaccAtccCA	642_3	-21,53	46391
642	CTGTATACACCATCCCA	1-2-1-7-1-3-2	CtgTatacaccAtccCA	642_4	-22,31	46391
642	CTGTATACACCATCCCA	1-3-1-6-1-3-2	CtgtAtacaccAtccCA	642_5	-21,32	46391
642	CTGTATACACCATCCCA	1-11-2-1-2	CtgtatacaccaTCcCA	642_6	-23,06	46391
642	CTGTATACACCATCCCA	1-1-1-1-1-8-1-1-2	CtGtAtacaccatCcCA	642_7	-22,35	46391
642	CTGTATACACCATCCCA	1-1-1-10-1-1-2	CtGtatacaccatCcCA	642_8	-22,25	46391
642	CTGTATACACCATCCCA	1-2-1-9-1-1-2	CtgTatacaccatCcCA	642_9	-23,02	46391
642	CTGTATACACCATCCCA	1-3-1-8-1-1-2	CtgtAtacaccatCcCA	642_10	-22,04	46391
642	CTGTATACACCATCCCA	1-12-1-1-2	CtgtatacaccatCcCA	642_11	-21,94	46391
642	CTGTATACACCATCCCA	2-2-1-10-2	CTgtAtacaccatccCA	642_12	-22,95	46391
642	CTGTATACACCATCCCA	1-1-1-1-1-10-2	CtGtAtacaccatccCA	642_13	-21,58	46391
642	CTGTATACACCATCCCA	1-1-1-12-2	CtGtatacaccatccCA	642_14	-21,48	46391
642	CTGTATACACCATCCCA	1-2-2-10-2	CtgTAtacaccatccCA	642_15	-23,39	46391
642	CTGTATACACCATCCCA	1-3-1-10-2	CtgtAtacaccatccCA	642_16	-21,27	46391
642	CTGTATACACCATCCCA	1-14-2	CtgtatacaccatccCA	642_17	-21,17	46391
642	CTGTATACACCATCCCA	1-3-1-6-3-1-2	CtgtAtacaccATCcCA	642_18	-24,02	46391
642	CTGTATACACCATCCCA	1-1-1-8-1-1-1-1-2	CtGtatacaccAtCcCA	642_19	-22,30	46391

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
642	CTGTATACACCATCCCA	1-1-3-6-1-3-2	CtGTAtacaccAtccCA	642_20	-24,64	46391
642	CTGTATACACCATCCCA	2-2-1-8-1-1-2	CTgtAtacaccatCcCA	642_21	-23,72	46391
642	CTGTATACACCATCCCA	1-3-1-9-3	CtgtAtacaccatcCCA	642_22	-23,55	46391
643	TCTGTATACACCATCCCA	1-4-1-8-1-1-2	TctgtAtacaccatCcCA	643_1	-22,94	46391
644	TCTGTATACACCATCCC	2-10-1-2-2	TCtgtatacaccAtcCC	644_1	-22,70	46392
644	TCTGTATACACCATCCC	1-11-1-2-2	TctgtatacaccAtcCC	644_2	-21,11	46392
644	TCTGTATACACCATCCC	2-1-1-11-2	TCtGtatacaccatcCC	644_3	-22,96	46392
644	TCTGTATACACCATCCC	2-13-2	TCtgtatacaccatcCC	644_4	-22,65	46392
644	TCTGTATACACCATCCC	3-9-1-2-2	TCTgtatacaccAtcCC	644_5	-24,39	46392
644	TCTGTATACACCATCCC	2-1-1-8-1-2-2	TCtGtatacaccAtcCC	644_6	-23,01	46392
645	TTCTGTATACACCATCCC	1-11-1-3-2	TtctgtatacacCatcCC	645_1	-22,57	46392
645	TTCTGTATACACCATCCC	1-1-1-10-1-2-2	TtCtgtatacaccAtcCC	645_2	-23,02	46392
645	TTCTGTATACACCATCCC	1-3-1-8-1-2-2	TtctGtatacaccAtcCC	645_3	-22,36	46392
645	TTCTGTATACACCATCCC	1-12-1-2-2	TtctgtatacaccAtcCC	645_4	-22,05	46392
645	TTCTGTATACACCATCCC	1-15-2	TtctgtatacaccatcCC	645_5	-22,00	46392
645	TTCTGTATACACCATCCC	1-4-1-6-2-2-2	TtctgTatacacCAtcCC	645_6	-25,12	46392
645	TTCTGTATACACCATCCC	1-3-1-8-1-1-3	TtctGtatacaccAtCCC	645_7	-24,73	46392
645	TTCTGTATACACCATCCC	3-10-1-2-2	TTCtgtatacaccAtcCC	645_8	-24,52	46392
645	TTCTGTATACACCATCCC	1-1-2-9-1-2-2	TtCTgtatacaccAtcCC	645_9	-24,71	46392
645	TTCTGTATACACCATCCC	1-1-1-1-1-8-1-2-2	TtCtGtatacaccAtcCC	645_10	-23,34	46392
646	TTCTGTATACACCATCC	1-10-1-3-2	TtctgtatacaCcatCC	646_1	-19,96	46393
646	TTCTGTATACACCATCC	1-12-4	TtctgtatacaccATCC	646_2	-21,16	46393
646	TTCTGTATACACCATCC	2-11-1-1-2	TTctgtatacaccAtCC	646_3	-20,11	46393
646	TTCTGTATACACCATCC	1-2-1-9-1-1-2	TtcTgtatacaccAtCC	646_4	-20,24	46393

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
646	TTCTGTATACACCATCC	1-3-1-8-1-1-2	TtctGtatacaccAtCC	646_5	-19,54	46393
646	TTCTGTATACACCATCC	1-2-1-8-1-2-2	TtcTgtatacacCatCC	646_6	-20,77	46393
646	TTCTGTATACACCATCC	1-12-1-1-2	TtctgtatacaccAtCC	646_7	-19,23	46393
646	TTCTGTATACACCATCC	1-3-1-7-1-1-3	TtctGtatacacCaTCC	646_8	-21,19	46393
646	TTCTGTATACACCATCC	1-1-1-1-1-10-2	TtCtGtatacaccatCC	646_9	-20,47	46393
646	TTCTGTATACACCATCC	1-1-1-12-2	TtCtgtatacaccatCC	646_10	-20,16	46393
646	TTCTGTATACACCATCC	1-1-1-11-3	TtCtgtatacaccaTCC	646_11	-21,28	46393
646	TTCTGTATACACCATCC	1-3-1-9-3	TtctGtatacaccaTCC	646_12	-20,61	46393
646	TTCTGTATACACCATCC	1-13-3	TtctgtatacaccaTCC	646_13	-20,30	46393
646	TTCTGTATACACCATCC	3-1-1-10-2	TTCtGtatacaccatCC	646_14	-21,96	46393
646	TTCTGTATACACCATCC	3-12-2	TTCtgtatacaccatCC	646_15	-21,65	46393
646	TTCTGTATACACCATCC	1-1-2-11-2	TtCTgtatacaccatCC	646_16	-21,84	46393
646	TTCTGTATACACCATCC	1-2-1-11-2	TtcTgtatacaccatCC	646_17	-20,19	46393
646	TTCTGTATACACCATCC	1-3-1-10-2	TtctGtatacaccatCC	646_18	-19,49	46393
646	TTCTGTATACACCATCC	1-14-2	TtctgtatacaccatCC	646_19	-19,18	46393
646	TTCTGTATACACCATCC	3-8-1-3-2	TTCtgtatacaCcatCC	646_20	-22,44	46393
646	TTCTGTATACACCATCC	1-3-1-6-1-3-2	TtctGtatacaCcatCC	646_21	-20,27	46393
646	TTCTGTATACACCATCC	1-3-1-7-2-1-2	TtctGtatacacCAtCC	646_22	-21,53	46393
646	TTCTGTATACACCATCC	1-1-1-9-1-2-2	TtCtgtatacacCatCC	646_23	-20,74	46393
646	TTCTGTATACACCATCC	1-1-1-10-1-1-2	TtCtgtatacaccAtCC	646_24	-20,21	46393
647	AGCTTTTAACCAGAGT	2-10-4	AGcttttaaccaGAGT	647_1	-21,73	EX-EX
648	AGCTTTTAACCAGAGTG	2-11-4	AGcttttaaccagAGTG	648_1	-22,27	EX-EX
649	AGCTTTTAACCAGAGTGG	1-14-3	AgcttttaaccagagTGG	649_1	-21,63	EX-EX
650	AGCTTTTAACCAGAGTGGC	1-16-2	AgcttttaaccagagtgGC	650_1	-23,20	EX-EX

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
651	AGCTTTTAACCAGAGTGGCA	1-17-2	AgcttttaaccagagtggCA	651_1	-24,11	EX-EX
652	CAGCTTTTAACCAGAGT	2-12-3	CAgcttttaaccagAGT	652_1	-21,65	EX-EX
653	CAGCTTTTAACCAGAGTG	3-13-2	CAGcttttaaccagagTG	653_1	-22,27	EX-EX
654	CAGCTTTTAACCAGAGTGG	1-15-3	CagcttttaaccagagTGG	654_1	-22,97	EX-EX
655	CAGCTTTTAACCAGAGTGGC	1-17-2	CagcttttaaccagagtgGC	655_1	-24,53	EX-EX
656	CTTTTAACCAGAGTG	4-7-4	CTTTtaaccagAGTG	656_1	-20,12	EX-EX
657	CTTTTAACCAGAGTGG	4-9-3	CTTTtaaccagagTGG	657_1	-20,92	EX-EX
658	CTTTTAACCAGAGTGGC	4-11-2	CTTTtaaccagagtgGC	658_1	-22,48	EX-EX
659	CTTTTAACCAGAGTGGCA	1-14-3	CttttaaccagagtgGCA	659_1	-22,96	EX-EX
660	CTTTTAACCAGAGTGGCAT	3-13-3	CTTttaaccagagtggCAT	660_1	-24,65	EX-EX
661	CTTTTAACCAGAGTGGCATC	2-16-2	CTtttaaccagagtggcaTC	661_1	-23,19	EX-EX
662	GCTTTTAACCAGAGT	3-9-3	GCTtttaaccagAGT	662_1	-21,02	EX-EX
663	GCTTTTAACCAGAGTG	4-10-2	GCTTttaaccagagTG	663_1	-21,02	EX-EX
664	GCTTTTAACCAGAGTGG	1-12-4	GcttttaaccagaGTGG	664_1	-22,24	EX-EX
665	GCTTTTAACCAGAGTGGC	1-14-3	GcttttaaccagagtGGC	665_1	-23,42	EX-EX
666	GCTTTTAACCAGAGTGGCA	1-16-2	GcttttaaccagagtggCA	666_1	-22,94	EX-EX
667	GCTTTTAACCAGAGTGGCAT	1-16-3	GcttttaaccagagtggCAT	667_1	-25,01	EX-EX
668	TCAGCTTTTAACCAGAGT	2-13-3	TCagcttttaaccagAGT	668_1	-22,18	EX-EX
669	TCAGCTTTTAACCAGAGTG	2-14-3	TCagcttttaaccagaGTG	669_1	-23,15	EX-EX
670	TCAGCTTTTAACCAGAGTGG	2-16-2	TCagcttttaaccagagtGG	670_1	-23,41	EX-EX
671	TTCAGCTTTTAACCAGAGT	2-14-3	TTcagcttttaaccagAGT	671_1	-22,72	EX-EX
672	TTCAGCTTTTAACCAGAGTG	2-15-3	TTcagcttttaaccagaGTG	672_1	-23,69	EX-EX
673	TTTCAGCTTTTAACCAGAGT	2-15-3	TTtcagcttttaaccagAGT	673_1	-23,66	EX-EX
674	TTTTAACCAGAGTGGC	1-11-4	TtttaaccagagTGGC	674_1	-20,81	EX-EX

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Seq ID NO	Motif	Design	Compound	CMP ID NO	∆G°	Start SEQ ID NO 1
675	TTTTAACCAGAGTGGCA	3-11-3	TTTtaaccagagtgGCA	675_1	-22,30	EX-EX
676	TTTTAACCAGAGTGGCAT	4-11-3	TTTTaaccagagtggCAT	676_1	-23,21	EX-EX
677	TTTTAACCAGAGTGGCATC	4-13-2	TTTTaaccagagtggcaTC	677_1	-22,57	EX-EX
678	TTTTAACCAGAGTGGCATCC	2-16-2	TTttaaccagagtggcatCC	678_1	-24,58	EX-EX
679	ATCAATATCTTCTCACT	1-1-2-7-1-1-1-1-2	AtCAatatcttCtCaCT	679_1	-19,16	5782
679	ATCAATATCTTCTCACT	5-6-1-2-3	ATCAAtatcttCtcACT	679_2	-21,49	5782
679	ATCAATATCTTCTCACT	1-1-1-1-1-7-5	AtCaAtatcttcTCACT	679_3	-20,18	5782
679	ATCAATATCTTCTCACT	1-1-3-8-4	AtCAAtatcttctCACT	679_4	-20,66	5782
679	ATCAATATCTTCTCACT	3-10-1-1-2	ATCaatatcttctCaCT	679_5	-18,62	5782
680	TATCAATATCTTCTCACT	2-2-1-7-1-1-1-1-2	TAtcAatatcttCtCaCT	680_1	-19,31	5782
680	TATCAATATCTTCTCACT	1-1-2-8-1-1-1-1-2	TaTCaatatcttCtCaCT	680_2	-19,89	5782
680	TATCAATATCTTCTCACT	1-2-3-6-1-2-3	TatCAAtatcttCtcACT	680_3	-20,66	5782
680	TATCAATATCTTCTCACT	1-2-3-7-2-1-2	TatCAAtatcttcTCaCT	680_4	-20,99	5782
680	TATCAATATCTTCTCACT	2-1-1-10-4	TAtCaatatcttctCACT	680_5	-20,89	5782
681	TATCAATATCTTCTCAC	4-7-2-1-3	TATCaatatctTCtCAC	681_1	-21,30	5783
681	TATCAATATCTTCTCAC	1-2-2-6-2-1-3	TatCAatatctTCtCAC	681_2	-19,73	5783
681	TATCAATATCTTCTCAC	2-1-1-8-5	TAtCaatatcttCTCAC	681_3	-20,26	5783
681	TATCAATATCTTCTCAC	1-1-3-7-5	TaTCAatatcttCTCAC	681_4	-21,74	5783
681	TATCAATATCTTCTCAC	5-9-3	TATCAatatcttctCAC	681_5	-20,83	5783
682	TTATCAATATCTTCTCAC	1-1-1-1-2-6-2-2-2	TtAtCAatatctTCtcAC	682_1	-18,32	5783
682	TTATCAATATCTTCTCAC	1-3-1-8-5	TtatCaatatcttCTCAC	682_2	-19,71	5783
682	TTATCAATATCTTCTCAC	3-10-1-1-3	TTAtcaatatcttCtCAC	682_3	-19,53	5783
682	TTATCAATATCTTCTCAC	2-1-2-8-1-1-3	TTaTCaatatcttCtCAC	682_4	-20,20	5783
682	TTATCAATATCTTCTCAC	1-2-3-9-3	TtaTCAatatcttctCAC	682_5	-19,47	5783

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
683	TTATCAATATCTTCTCACT	1-1-1-1-1-8-1-1-1-1-2	TtAtCaatatcttCtCaCT	683_1	-19,45	5782
683	TTATCAATATCTTCTCACT	1-3-1-8-1-1-1-1-2	TtatCaatatcttCtCaCT	683_2	-19,35	5782
683	TTATCAATATCTTCTCACT	1-1-1-1-1-8-1-2-3	TtAtCaatatcttCtcACT	683_3	-19,33	5782
683	TTATCAATATCTTCTCACT	1-1-1-2-1-7-1-3-2	TtAtcAatatcttCtcaCT	683_4	-18,18	5782
683	TTATCAATATCTTCTCACT	1-1-1-2-1-9-4	TtAtcAatatcttctCACT	683_5	-19,84	5782
684	ACCTTTCTTTAACCCTTT	2-1-1-8-2-1-3	ACcTttctttaaCCcTTT	684_1	-25,24	8113
684	ACCTTTCTTTAACCCTTT	2-10-1-1-1-1-2	ACctttctttaaCcCtTT	684_2	-22,31	8113
684	ACCTTTCTTTAACCCTTT	1-1-1-9-1-1-1-1-2	AcCtttctttaaCcCtTT	684_3	-22,01	8113
684	ACCTTTCTTTAACCCTTT	1-1-1-1-1-9-1-1-2	AcCtTtctttaaccCtTT	684_4	-21,53	8113
684	ACCTTTCTTTAACCCTTT	1-1-1-11-1-1-2	AcCtttctttaaccCtTT	684_5	-21,23	8113
685	TACCTTTCTTTAACCCTTT	1-2-1-8-1-1-1-2-2	TacCtttctttaAcCctTT	685_1	-22,44	8113
685	TACCTTTCTTTAACCCTTT	1-2-1-1-1-7-1-1-1-1-2	TacCtTtctttaaCcCtTT	685_2	-23,32	8113
685	TACCTTTCTTTAACCCTTT	2-1-1-10-1-1-3	TAcCtttctttaacCcTTT	685_3	-24,28	8113
685	TACCTTTCTTTAACCCTTT	1-1-1-12-1-1-2	TaCctttctttaaccCtTT	685_4	-22,13	8113
685	TACCTTTCTTTAACCCTTT	1-2-1-11-1-1-2	TacCtttctttaaccCtTT	685_5	-22,23	8113
686	ATACCTTTCTTTAACCC	1-2-1-7-1-1-1-1-2	AtaCctttcttTaAcCC	686_1	-20,53	8116
686	ATACCTTTCTTTAACCC	1-3-1-6-1-3-2	AtacCtttcttTaacCC	686_2	-20,21	8116
686	ATACCTTTCTTTAACCC	2-2-1-7-2-1-2	ATacCtttctttAAcCC	686_3	-21,89	8116
686	ATACCTTTCTTTAACCC	1-1-1-1-1-8-1-1-2	AtAcCtttctttaAcCC	686_4	-20,10	8116
686	ATACCTTTCTTTAACCC	1-2-1-10-3	AtaCctttctttaaCCC	686_5	-21,76	8116
687	ATACCTTTCTTTAACCCTT	1-3-2-6-1-2-4	AtacCTttctttAacCCTT	687_1	-26,10	8114
687	ATACCTTTCTTTAACCCTT	1-1-1-1-1-8-1-1-1-1-2	AtAcCtttctttaAcCcTT	687_2	-22,23	8114
687	ATACCTTTCTTTAACCCTT	1-2-1-9-1-1-1-1-2	AtaCctttctttaAcCcTT	687_3	-21,93	8114
687	ATACCTTTCTTTAACCCTT	1-2-1-1-1-8-2-1-2	AtaCcTttctttaaCCcTT	687_4	-24,41	8114

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
687	ATACCTTTCTTTAACCCTT	1-3-1-11-3	AtacCtttctttaaccCTT	687_5	-22,51	8114
688	ATACCTTTCTTTAACCCTTT	1-3-1-8-1-1-1-2-2	AtacCtttctttaAcCctTT	688_1	-22,83	8113
688	ATACCTTTCTTTAACCCTTT	1-3-1-9-1-1-1-1-2	AtacCtttctttaaCcCtTT	688_2	-23,41	8113
688	ATACCTTTCTTTAACCCTTT	1-4-2-7-1-2-3	AtaccTTtctttaaCccTTT	688_3	-23,98	8113
688	ATACCTTTCTTTAACCCTTT	1-1-1-1-1-10-1-1-3	AtAcCtttctttaacCcTTT	688_4	-23,63	8113
688	ATACCTTTCTTTAACCCTTT	1-2-1-12-1-1-2	AtaCctttctttaaccCtTT	688_5	-22,52	8113
689	ATACCTTTCTTTAACCCT	1-3-2-6-2-2-2	AtacCTttctttAAccCT	689_1	-22,61	8115
689	ATACCTTTCTTTAACCCT	1-1-1-1-2-8-1-1-2	AtAcCTttctttaaCcCT	689_2	-22,85	8115
689	ATACCTTTCTTTAACCCT	1-2-1-10-1-1-2	AtaCctttctttaaCcCT	689_3	-21,36	8115
689	ATACCTTTCTTTAACCCT	1-2-3-10-2	AtaCCTttctttaaccCT	689_4	-24,26	8115
689	ATACCTTTCTTTAACCCT	1-3-1-11-2	AtacCtttctttaaccCT	689_5	-20,69	8115
690	TATACCTTTCTTTAACCCT	2-2-1-10-1-1-2	TAtaCctttctttaaCcCT	690_1	-23,60	8115
690	TATACCTTTCTTTAACCCT	1-4-1-9-1-1-2	TatacCtttctttaaCcCT	690_2	-22,57	8115
690	TATACCTTTCTTTAACCCT	2-3-1-11-2	TAtacCtttctttaaccCT	690_3	-22,92	8115
690	TATACCTTTCTTTAACCCT	1-3-1-12-2	TataCctttctttaaccCT	690_4	-21,68	8115
690	TATACCTTTCTTTAACCCT	1-4-1-11-2	TatacCtttctttaaccCT	690_5	-21,79	8115
691	TTATACCTTTCTTTAAC	4-7-2-2-2	TTATacctttcTTtaAC	691_1	-18,49	8118
691	TTATACCTTTCTTTAAC	3-8-1-1-4	TTAtacctttcTtTAAC	691_2	-18,07	8118
692	TTATACCTTTCTTTAACCC	2-10-1-1-1-2-2	TTataccttttctTtAacCC	692_1	-21,94	8116
692	TTATACCTTTCTTTAACCC	1-1-1-9-1-4-2	TtAtacctttctTtaacCC	692_2	-20,68	8116
692	TTATACCTTTCTTTAACCC	1-4-1-7-1-3-2	TtataCctttcttTaacCC	692_3	-21,79	8116
692	TTATACCTTTCTTTAACCC	1-3-2-8-2-1-2	TtatACctttctttAAcCC	692_4	-22,39	8116
692	TTATACCTTTCTTTAACCC	1-1-1-2-1-9-1-1-2	TtAtaCctttctttaAcCC	692_5	-21,58	8116
693	TTATACCTTTCTTTAACC	2-3-1-6-1-3-2	TTataCctttctTtaaCC	693_1	-19,80	8117

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
693	TTATACCTTTCTTTAACC	1-1-1-1-2-6-1-3-2	TtAtACctttctTtaaCC	693_2	-19,25	8117
693	TTATACCTTTCTTTAACC	1-3-2-7-2-1-2	TtatACctttcttTAaCC	693_3	-20,74	8117
693	TTATACCTTTCTTTAACC	1-1-1-2-1-7-1-2-2	TtAtaCctttcttTaaCC	693_4	-19,08	8117
693	TTATACCTTTCTTTAACC	1-2-1-1-1-8-4	TtaTaCctttctttAACC	693_5	-20,26	8117
694	TTTATACCTTTCTTTAACC	2-1-1-8-2-3-2	TTtAtacctttcTTtaaCC	694_1	-20,72	8117
694	TTTATACCTTTCTTTAACC	1-4-1-6-1-2-4	TttatAcctttcTttAACC	694_2	-20,33	8117
694	TTTATACCTTTCTTTAACC	2-11-1-1-1-1-2	TTtatacctttctTtAaCC	694_3	-19,72	8117
694	TTTATACCTTTCTTTAACC	1-1-2-9-1-3-2	TtTAtacctttctTtaaCC	694_4	-20,65	8117
694	TTTATACCTTTCTTTAACC	1-3-2-7-1-3-2	TttaTAcctttctTtaaCC	694_5	-20,88	8117
695	TTTATACCTTTCTTTAAC	3-9-3-1-2	TTTatacctttcTTTaAC	695_1	-18,74	8118
695	TTTATACCTTTCTTTAAC	5-7-2-2-2	TTTATacctttcTTtaAC	695_2	-20,31	8118
695	TTTATACCTTTCTTTAAC	1-1-3-7-2-2-2	TtTATacctttcTTtaAC	695_3	-18,98	8118
695	TTTATACCTTTCTTTAAC	4-8-1-1-4	TTTAtacctttcTtTAAC	695_4	-19,89	8118
695	TTTATACCTTTCTTTAAC	2-3-1-7-5	TTtatAcctttctTTAAC	695_5	-18,02	8118
696	TTTTATACCTTTCTTTAAC	2-3-1-6-3-2-2	TTttaTacctttCTTtaAC	696_1	-19,79	8118
696	TTTTATACCTTTCTTTAAC	1-1-2-8-2-1-1-1-2	TtTTatacctttCTtTaAC	696_2	-19,57	8118
696	TTTTATACCTTTCTTTAAC	2-1-2-7-2-2-3	TTtTAtacctttCTttAAC	696_3	-20,28	8118
696	TTTTATACCTTTCTTTAAC	3-9-1-1-5	TTTtatacctttCtTTAAC	696_4	-20,62	8118
696	TTTTATACCTTTCTTTAAC	1-1-3-7-1-1-1-2-2	TtTTAtacctttCtTtaAC	696_5	-19,08	8118
697	TGTACTTTCCTTTACCA	2-9-1-3-2	TGtactttcctTtacCA	697_1	-20,68	11462
697	TGTACTTTCCTTTACCA	1-2-1-7-1-3-2	TgtActttcctTtacCA	697_2	-19,66	11462
697	TGTACTTTCCTTTACCA	1-3-1-6-1-3-2	TgtaCtttcctTtacCA	697_3	-20,46	11462
697	TGTACTTTCCTTTACCA	2-2-1-8-1-1-2	TGtaCtttcctttAcCA	697_4	-21,56	11462
697	TGTACTTTCCTTTACCA	1-3-1-9-3	TgtaCtttcctttaCCA	697_5	-22,54	11462

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
698	TTATACACCATCATTAT	4-7-3-1-2	TTATacaccatCATtAT	698_1	-21,13	11506
698	TTATACACCATCATTAT	4-7-2-1-3	TTATacaccatCAtTAT	698_2	-21,64	11506
698	TTATACACCATCATTAT	3-8-1-1-4	TTAtacaccatCaTTAT	698_3	-19,45	11506
698	TTATACACCATCATTAT	2-1-2-7-5	TTaTAcaccatcATTAT	698_4	-20,61	11506
698	TTATACACCATCATTAT	5-9-3	TT AT AcaccatcatT AT	698_5	-20,74	11506
699	TTATACACCATCATTATA	3-2-1-6-2-2-2	TTAtaCaccatcATtaTA	699_1	-19,38	11505
699	TTATACACCATCATTATA	1-2-3-6-1-1-4	TtaTACaccatcAtTATA	699_2	-20,93	11505
699	TTATACACCATCATTATA	4-1-1-7-2-1-2	TTATaCaccatcaTTaTA	699_3	-21,44	11505
699	TTATACACCATCATTATA	2-1-2-8-1-1-3	TTaTAcaccatcaTtATA	699_4	-19,71	11505
699	TTATACACCATCATTATA	3-2-1-8-4	TTAtaCaccatcatTATA	699_5	-20,75	11505
700	TTTATACACCATCATTAT	2-1-2-7-3-1-2	TTtATacaccatCATtAT	700_1	-20,67	11506
700	TTTATACACCATCATTAT	3-1-1-7-2-1-3	TTTaTacaccatCAtTAT	700_2	-21,52	11506
700	TTTATACACCATCATTAT	1-3-2-6-2-1-3	TttaTAcaccatCAtTAT	700_3	-20,70	11506
700	TTTATACACCATCATTAT	1-1-3-8-1-1-3	TtTATacaccatcAtTAT	700_4	-20,05	11506
700	TTTATACACCATCATTAT	3-1-1-9-4	TTTaTacaccatcaTTAT	700_5	-20,34	11506
701	TTTATACACCATCATTATA	4-8-1-1-2-1-2	TTTAtacaccatCaTTaTA	701_1	-21,57	11505
701	TTTATACACCATCATTATA	2-2-1-7-1-2-4	TTtaTacaccatCatTATA	701_2	-21,05	11505
701	TTTATACACCATCATTATA	1-1-1-1-1-8-2-1-3	TtTaTacaccatcATtATA	701_3	-19,83	11505
701	TTTATACACCATCATTATA	2-2-2-7-2-2-2	TTtaTAcaccatcATtaTA	701_4	-20,24	11505
701	TTTATACACCATCATTATA	1-1-3-10-1-1-2	TtTATacaccatcatTaTA	701_5	-20,30	11505
702	ATTTATACACCATCATTAT	1-1-1-2-1-7-3-1-2	AtTtaTacaccatCATtAT	702_1	-20,07	11506
702	ATTTATACACCATCATTAT	1-1-2-1-1-7-2-2-2	AtTTaTacaccatCAttAT	702_2	-20,07	11506
702	ATTTATACACCATCATTAT	2-1-2-8-1-1-1-1-2	ATtTAtacaccatCaTtAT	702_3	-19,74	11506
702	ATTTATACACCATCATTAT	2-3-1-7-1-2-3	ATttaTacaccatCatTAT	702_4	-20,07	11506

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
702	ATTTATACACCATCATTAT	1-1-1-1-1-10-4	AtTtAtacaccatcaTTAT	702_5	-18,64	11506
703	ATTTATACACCATCATTATA	1-4-1-7-1-2-4	AtttaTacaccatCatTATA	703_1	-21,05	11505
703	ATTTATACACCATCATTATA	2-1-1-2-1-7-2-2-2	ATtTatAcaccatcATtaTA	703_2	-20,32	11505
703	ATTTATACACCATCATTATA	1-1-1-2-1-8-1-1-1-1-2	AtTtaTacaccatcAtTaTA	703_3	-18,80	11505
703	ATTTATACACCATCATTATA	1-2-3-8-1-1-1-1-2	AttTATacaccatcAtTaTA	703_4	-21,17	11505
703	ATTTATACACCATCATTATA	3-1-1-9-1-2-3	ATTtAtacaccatcAttATA	703_5	-19,97	11505
704	TATTTATACACCATCATTA	1-2-3-6-2-3-2	TatTTAtacaccATcatTA	704_1	-20,37	11507
704	TATTTATACACCATCATTA	4-8-1-1-2-1-2	TATTtatacaccAtCAtTA	704_2	-21,70	11507
704	TATTTATACACCATCATTA	1-1-1-1-1-7-1-1-1-1-3	TaTtTatacaccAtCaTTA	704_3	-19,16 11507	
704	TATTTATACACCATCATTA	2-2-1-8-2-2-2	TAttTatacaccaTCatTA	704_4	-19,98	11507
704	TATTTATACACCATCATTA	2-2-1-10-4	TAttTatacaccatcATTA	704_5	-19,99	11507
705	TATTTATACACCATCATTAT	2-2-1-1-1-7-2-2-2	TAttTaTacaccatCAttAT	705_1	-21,49	11506
705	TATTTATACACCATCATTAT	2-1-1-10-1-1-4	TAtTtatacaccatCaTTAT	705_2	-21,44	11506
705	TATTTATACACCATCATTAT	1-1-1-2-1-8-1-1-1-1-2	TaTttAtacaccatCaTtAT	705_3	-18,27	11506
705	TATTTATACACCATCATTAT	2-1-2-9-1-3-2	TAtTTatacaccatCattAT	705_4	-19,97	11506
705	TATTTATACACCATCATTAT	1-2-3-9-1-1-3	TatTTAtacaccatcAtTAT	705_5	-21,11	11506
706	TTATTTATACACCATCATTA	2-3-1-7-1-1-1-1-3	TTattTatacaccAtCaTTA	706_1	-20,54	11507
706	TTATTTATACACCATCATTA	1-1-2-1-1-7-1-2-4	TtATtTatacaccAtcATTA	706_2	-20,84	11507
706	TTATTTATACACCATCATTA	1-1-1-2-1-8-2-2-2	TtAttTatacaccaTCatTA	706_3	-19,52	11507
706	TTATTTATACACCATCATTA	1-2-3-8-1-1-1-1-2	TtaTTTatacaccaTcAtTA	706_4	-19,96	11507
706	TTATTTATACACCATCATTA	3-1-1-11-1-1-2	TTAtTtatacaccatcAtTA	706_5	-19,63	11507
707	ATTATTTATACACCATCAT	2-2-2-6-3-2-2	ATtaTTtatacaCCAtcAT	707_1	-22,41	11509
707	ATTATTTATACACCATCAT	2-3-1-6-1-2-4	ATtatTtatacaCcaTCAT	707_2	-21,02	11509
707	ATTATTTATACACCATCAT	1-1-1-1-1-8-3-1-2	AtTaTttatacacCATcAT	707_3	-20,01	11509

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
707	ATTATTTATACACCATCAT	1-1-2-1-1-7-1-2-3	AtTAtTtatacacCatCAT	707_4	-20,30	11509
707	ATTATTTATACACCATCAT	2-1-2-9-1-1-3	ATtATttatacaccAtCAT	707_5	-20,20	11509
708	ATTATTTATACACCATCA	2-2-2-6-2-2-2	ATtaTTtatacaCCatCA	708_1	-20,96	11510
708	ATTATTTATACACCATCA	3-1-1-7-1-1-4	ATTaTttatacaCcATCA	708_2	-21,19	11510
708	ATTATTTATACACCATCA	1-1-3-7-1-3-2	AtTATttatacaCcatCA	708_3	-19,39	11510
708	ATTATTTATACACCATCA	1-1-1-2-1-7-2-1-2	AtTatTtatacacCAtCA	708_4	-18,57	11510
708	ATTATTTATACACCATCA	2-1-2-8-1-1-3	ATtATttatacacCaTCA	708_5	-19,79	11510
709	ATTATTTATACACCATCATT	1-2-3-7-1-1-2-1-2	AttATTtatacacCaTCaTT	709_1	-20,97	11508
709	ATTATTTATACACCATCATT	1-1-1-2-2-6-1-4-2	AtTatTTatacacCatcaTT	709_2	-19,29	11508
709	ATTATTTATACACCATCATT	1-1-1-2-1-8-2-1-3	AtTatTtatacaccATcATT	709_3	-19,70	11508
709	ATTATTTATACACCATCATT	3-1-1-9-1-1-1-1-2	ATTaTttatacaccAtCaTT	709_4	-20,09	11508
709	ATTATTTATACACCATCATT	2-1-2-1-1-7-1-2-3	ATtATtTatacaccAtcATT	709_5	-20,67	11508
710	ATTATTTATACACCATC	5-6-3-1-2	ATTATttatacACCaTC	710_1	-21,70	11511
710	ATTATTTATACACCATC	5-6-2-1-3	ATTATttatacACcATC	710_2	-20,38	11511
710	ATTATTTATACACCATC	2-2-1-7-5	ATtaTttatacaCCATC	710_3	-20,25	11511
710	ATTATTTATACACCATC	1-1-2-8-5	AtTAtttatacaCCATC	710_4	-20,42	11511
710	ATTATTTATACACCATC	5-8-4	ATTATttatacacCATC	710_5	-21,04	11511
711	AATTATTTATACACCATC	2-2-2-6-3-1-2	AAttATttatacACCaTC	711_1	-18,93	11511
711	AATTATTTATACACCATC	2-1-3-6-1-1-4	AAtTATttatacAcCATC	711_2	-20,18	11511
711	AATTATTTATACACCATC	4-1-1-7-5	AATTaTttatacaCCATC	711_3	-22,24	11511
711	AATTATTTATACACCATC	2-1-2-8-5	AAtTAtttatacaCCATC	711_4	-21,17	11511
711	AATTATTTATACACCATC	1-1-4-7-2-1-2	AaTTATttatacaCCaTC	711_5	-20,58	11511
712	AATTATTTATACACCATCA	1-2-1-1-1-6-3-2-2	AatTaTttatacACCatCA	712_1	-20,42	11510
712	AATTATTTATACACCATCA	2-2-1-7-1-1-2-1-2	AAttAtttatacAcCAtCA	712_2	-18,54	11510

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
712	AATTATTTATACACCATCA	1-1-3-7-1-2-4	AaTTAtttatacAccATCA	712_3	-20,67	11510
712	AATTATTTATACACCATCA	2-1-2-8-2-1-3	AAtTAtttatacaCCaTCA	712_4	-22,20	11510
712	AATTATTTATACACCATCA	3-1-1-8-1-2-3	AATtAtttatacaCcaTCA	712_5	-19,50	11510
713	AAATTATTTATACACCATC	3-2-1-6-3-1-3	AAAttAtttataCACcATC	713_1	-19,21	11511
713	AAATTATTTATACACCATC	1-2-3-6-3-2-2	AaaTTAtttataCACcaTC	713_2	-20,01	11511
713	AAATTATTTATACACCATC	1-1-3-7-2-1-4	AaATTatttataCAcCATC	713_3	-21,68	11511
713	AAATTATTTATACACCATC	2-1-2-7-1-1-2-1-2	AAaTTatttataCaCCaTC	713_4	-19,63	11511
713	AAATTATTTATACACCATC	1-1-2-1-1-8-5	AaATtAtttatacaCCATC	713_5	-20,67	11511
714	AAATTATTTATACACCAT	1-1-4-6-2-1-3	AaATTAtttataCAcCAT	714_1	-20,31	11512
714	AAATTATTTATACACCAT	2-2-2-6-1-1-4	AAatTAtttataCaCCAT	714_2	-19,59	11512
714	AAATTATTTATACACCAT	1-1-3-7-1-1-4	AaATTatttataCaCCAT	714_3	-20,00	11512
714	AAATTATTTATACACCAT	4-9-5	AAATtatttatacACCAT	714_4	-19,36	11512
714	AAATTATTTATACACCAT	3-1-2-7-5	AAAtTAtttatacACCAT	714_5	-19,98	11512
715	AAAATTATTTATACACCAT	2-1-2-7-3-1-3	AAaATtatttatACAcCAT	715_1	-19,29	11512
715	AAAATTATTTATACACCAT	1-3-2-6-2-1-4	AaaaTTatttatACaCCAT	715_2	-19,68	11512
715	AAAATTATTTATACACCAT	3-2-1-6-1-1-5	AAAatTatttatAcACCAT	715_3	-19,27	11512
715	AAAATTATTTATACACCAT	1-1-4-7-1-1-4	AaAATTatttataCaCCAT	715_4	-20,75	11512
715	AAAATTATTTATACACCAT	2-1-2-9-5	AAaATtatttatacACCAT	715_5	-19,38	11512
716	TAAAATTATTTATACACC	2-1-3-6-3-1-2	TAaAATtatttaTACaCC	716_1	-18,88	11514
716	TAAAATTATTTATACACC	3-1-2-7-5	TAAaATtatttatACACC	716_2	-18,95	11514
716	TAAAATTATTTATACACC	1-1-4-7-5	TaAAATtatttatACACC	716_3	-18,33	11514
716	TAAAATTATTTATACACC	3-1-2-8-4	TAAaATtatttataCACC	716_4	-18,35	11514
716	TAAAATTATTTATACACC	2-1-3-8-4	TAaAATtatttataCACC	716_5	-18,35	11514
717	GTAAAATTATTTATACACC	2-1-3-6-4-1-2	GTaAAAttatttATACaCC	717_1	-21,68	11514

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
717	GTAAAATTATTTATACACC	3-2-1-6-2-2-3	GTAaaAttatttATacACC	717_2	-20,00	11514
717	GTAAAATTATTTATACACC	3-1-2-7-2-1-3	GTAaAAttatttaTAcACC	717_3	-20,86	11514
717	GTAAAATTATTTATACACC	2-1-3-7-1-1-4	GTaAAAttatttaTaCACC	717_4	-21,11	11514
717	GTAAAATTATTTATACACC	4-1-1-8-5	GTAAaAttatttatACACC	717_5	-21,46	11514
718	GTAAAATTATTTATACAC	4-1-1-7-5	GTAAaAttatttaTACAC	718_1	-18,17	11515
718	GTAAAATTATTTATACAC	3-1-2-7-5	GTAaAAttatttaTACAC	718_2	-18,17	11515
719	GAGTATATTACCTCCA	3-10-3	GAGtatattacctCCA	719_1	-22,56	15162
719	GAGTATATTACCTCCA	2-1-1-9-3	GAgTatattacctCCA	719_2	-22,24	15162
719	GAGTATATTACCTCCA	2-11-3	GAgtatattacctCCA	719_3	-21,15	15162
719	GAGTATATTACCTCCA	1-1-3-8-3	GaGTAtattacctCCA	719_4	-22,93	15162
719	GAGTATATTACCTCCA	5-9-2	GAGTAtattacctcCA	719_5	-23,29	15162
720	CTTTTCTATAATCTCAC	2-2-1-6-3-1-2	CTttTctataaTCTcAC	720_1	-18,54	30553
720	CTTTTCTATAATCTCAC	3-8-2-1-3	CTTttctataaTCtCAC	720_2	-19,80	30553
720	CTTTTCTATAATCTCAC	1-1-3-6-1-1-4	CtTTTctataaTcTCAC	720_3	-19,40	30553
720	CTTTTCTATAATCTCAC	4-8-5	CTTTtctataatCTCAC	720_4	-21,37	30553
720	CTTTTCTATAATCTCAC	1-3-1-7-5	CtttTctataatCTCAC	720_5	-18,92	30553
721	CTTTTCTATAATCTCACA	2-3-1-6-1-1-1-1-2	CTtttCtataatCtCaCA	721_1	-20,17	30552
721	CTTTTCTATAATCTCACA	1-1-1-1-2-6-1-2-3	CtTtTCtataatCtcACA	721_2	-20,15	30552
721	CTTTTCTATAATCTCACA	1-2-1-1-1-7-2-1-2	CttTtCtataatcTCaCA	721_3	-19,50	30552
721	CTTTTCTATAATCTCACA	1-1-3-8-1-1-3	CtTTTctataatcTcACA	721_4	-19,49	30552
721	CTTTTCTATAATCTCACA	3-2-1-8-4	CTTttCtataatctCACA	721_5	-21,97	30552
722	TCTTTTCTATAATCTCACA	1-1-3-7-1-1-1-1-3	TcTTTtctataaTcTcACA	722_1	-21,04	30552
722	TCTTTTCTATAATCTCACA	1-4-1-6-1-2-1-1-2	TctttTctataaTctCaCA	722_2	-18,81	30552
722	TCTTTTCTATAATCTCACA	2-2-1-8-1-2-3	TCttTtctataatCtcACA	722_3	-20,68	30552

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
722	TCTTTTCTATAATCTCACA	2-1-1-9-1-3-2	TCtTttctataatCtcaCA	722_4	-20,13	30552
722	TCTTTTCTATAATCTCACA	2-13-1-1-2	TCttttctataatctCaCA	722_5	-19,52	30552
723	TCTTTTCTATAATCTCAC	2-1-1-8-2-2-2	TCtTttctataaTCtcAC	723_1	-18,51	30553
723	TCTTTTCTATAATCTCAC	3-10-1-1-3	TCTtttctataatCtCAC	723_2	-20,36	30553
723	TCTTTTCTATAATCTCAC	1-2-3-7-1-1-3	TctTTTctataatCtCAC	723_3	-19,57	30553
723	TCTTTTCTATAATCTCAC	2-2-2-8-4	TCttTTctataatcTCAC	723_4	-20,57	30553
723	TCTTTTCTATAATCTCAC	1-1-4-8-4	TcTTTTctataatcTCAC	723_5	-20,82	30553
724	ATCTTTTCTATAATCTCACA	1-1-1-1-1-9-1-1-1-1-2	AtCtTttctataatCtCaCA	724_1	-20,93	30552
724	ATCTTTTCTATAATCTCACA	1-1-1-11-1-2-3	AtCttttctataatCtcACA	724_2	-20,51	30552
724	ATCTTTTCTATAATCTCACA	1-2-1-1-1-8-1-2-3	AtcTtTtctataatCtcACA	724_3	-20,35	30552
724	ATCTTTTCTATAATCTCACA	1-3-2-8-1-3-2	AtctTTtctataatCtcaCA	724_4	-20,10	30552
724	ATCTTTTCTATAATCTCACA	1-1-1-2-1-10-1-1-2	AtCttTtctataatctCaCA	724_5	-19,95	30552
725	ATCTTTTCTATAATCTCAC	1-1-1-9-1-1-1-1-3	AtCttttctataAtCtCAC	725_1	-19,62	30553
725	ATCTTTTCTATAATCTCAC	1-2-2-7-1-1-1-1-3	AtcTTttctataAtCtCAC	725_2	-19,97	30553
725	ATCTTTTCTATAATCTCAC	1-1-2-1-1-7-2-2-2	AtCTtTtctataaTCtcAC	725_3	-19,83	30553
725	ATCTTTTCTATAATCTCAC	1-2-1-1-1-9-4	AtcTtTtctataatcTCAC	725_4	-19,36	30553
725	ATCTTTTCTATAATCTCAC	3-13-3	ATCttttctataatctCAC	725_5	-20,25	30553
726	ATCTTTTCTATAATCTCA	1-1-2-8-1-1-1-1-2	AtCTtttctataAtCtCA	726_1	-18,77	30554
726	ATCTTTTCTATAATCTCA	3-1-1-7-1-2-3	ATCtTttctataAtcTCA	726_2	-20,03	30554
726	ATCTTTTCTATAATCTCA	3-10-2-1-2	ATCttttctataaTCtCA	726_3	-20,31	30554
726	ATCTTTTCTATAATCTCA	1-1-1-1-2-7-2-1-2	AtCtTTtctataaTCtCA	726_4	-19,49	30554
726	ATCTTTTCTATAATCTCA	1-1-3-9-4	AtCTTttctataatCTCA	726_5	-21,14	30554
727	CATCTTTTCTATAATCTCAC	2-11-1-1-1-2-2	CAtcttttctataAtCtcAC	727_1	-19,86	30553
727	CATCTTTTCTATAATCTCAC	1-1-2-9-1-1-1-2-2	CaTCttttctataAtCtcAC	727_2	-20,49	30553

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
727	CATCTTTTCTATAATCTCAC	1-3-1-1-1-8-1-1-3	CatcTtTtctataatCtCAC	727_3	-20,97	30553
727	CATCTTTTCTATAATCTCAC	1-2-1-1-1-9-1-2-2	CatCtTttctataatCtcAC	727_4	-19,35	30553
727	CATCTTTTCTATAATCTCAC	2-1-1-2-1-10-3	CAtCttTtctataatctCAC	727_5	-21,92	30553
728	CATCTTTTCTATAATCTCA	1-3-1-7-2-1-1-1-2	CatcTtttctatAAtCtCA	728_1	-19,26	30554
728	CATCTTTTCTATAATCTCA	2-3-1-6-2-2-3	CAtctTttctatAAtcTCA	728_2	-20,74	30554
728	CATCTTTTCTATAATCTCA	1-2-1-8-1-2-1-1-2	CatCttttctatAatCtCA	728_3	-19,21	30554
728	CATCTTTTCTATAATCTCA	2-1-1-1-1-9-1-1-2	CAtCtTttctataatCtCA	728_4	-20,86	30554
728	CATCTTTTCTATAATCTCA	1-1-2-13-2	CaTCttttctataatctCA	728_5	-19,23	30554
729	TCATCTTTTCTATAATCTCA	1-1-1-2-1-7-2-1-1-1-2	TcAtcTtttctatAAtCtCA	729_1	-20,53	30554
729	TCATCTTTTCTATAATCTCA	2-4-1-6-2-3-2	TCatctTttctatAAtctCA	729_2	-20,57	30554
729	TCATCTTTTCTATAATCTCA	2-2-1-8-1-2-1-1-2	TCatCttttctatAatCtCA	729_3	-21,70	30554
729	TCATCTTTTCTATAATCTCA	3-13-1-1-2	TCAtcttttctataatCtCA	729_4	-22,07	30554
729	TCATCTTTTCTATAATCTCA	3-1-1-13-2	TCAtCttttctataatctCA	729_5	-22,07	30554
730	TCATCTTTTCTATAATCTC	3-2-1-7-2-2-2	TCAtcTtttctatAAtcTC	730_1	-20,15	30555
730	TCATCTTTTCTATAATCTC	3-1-1-8-1-3-2	TCAtCttttctatAatcTC	730_2	-20,09	30555
730	TCATCTTTTCTATAATCTC	2-2-1-9-1-2-2	TCatCttttctataAtcTC	730_3	-18,83	30555
730	TCATCTTTTCTATAATCTC	3-13-3	TCAtcttttctataatCTC	730_4	-20,65	30555
730	TCATCTTTTCTATAATCTC	2-2-2-10-3	TCatCTtttctataatCTC	730_5	-21,35	30555
731	GTCATCTTTTCTATAATC	1-1-1-2-1-6-3-1-2	GtCatCttttctATAaTC	731_1	-19,76	30557
731	GTCATCTTTTCTATAATC	1-1-1-1-2-6-1-2-3	GtCaTCttttctAtaATC	731_2	-19,19	30557
731	GTCATCTTTTCTATAATC	4-9-1-2-2	GTCAtcttttctaTaaTC	731_3	-20,42	30557
731	GTCATCTTTTCTATAATC	3-2-1-8-4	GTCatCttttctatAATC	731_4	-20,51	30557
731	GTCATCTTTTCTATAATC	1-1-4-10-2	GtCATCttttctataaTC	731_5	-20,23	30557
732	TGTCATCTTTTCTATAAT	2-1-1-8-2-1-3	TGtCatcttttcTAtAAT	732_1	-19,36	30558

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
732	TGTCATCTTTTCTATAAT	2-1-2-7-2-2-2	TGtCAtcttttcTAtaAT	732_2	-20,51	30558
732	TGTCATCTTTTCTATAAT	1-1-3-7-1-3-2	TgTCAtcttttcTataAT	732_3	-19,51	30558
732	TGTCATCTTTTCTATAAT	4-10-4	TGTCatcttttctaTAAT	732_4	-21,42	30558
732	TGTCATCTTTTCTATAAT	2-2-1-9-4	TGtcAtcttttctaTAAT	732_5	-18,57	30558
733	ACTTAATTATACTTCCA	5-6-2-2-2	ACTTAattataCTtcCA	733_1	-21,55	30664
733	ACTTAATTATACTTCCA	2-1-2-6-1-2-3	ACtTAattataCttCCA	733_2	-21,02	30664
733	ACTTAATTATACTTCCA	1-2-2-7-5	ActTAattatacTTCCA	733_3	-20,65	30664
733	ACTTAATTATACTTCCA	4-8-1-1-3	ACTTaattatacTtCCA	733_4	-21,09	30664
733	ACTTAATTATACTTCCA	1-1-1-1-1-8-4	AcTtAattatactTCCA	733_5	-18,37	30664
734	CACTTAATTATACTTCC	2-1-2-6-2-2-2	CAcTTaattatACttCC	734_1	-20,10	30665
734	CACTTAATTATACTTCC	5-6-1-2-3	CACTTaattatActTCC	734_2	-21,76	30665
734	CACTTAATTATACTTCC	1-1-1-1-1-7-2-1-2	CaCtTaattataCTtCC	734_3	-19,09	30665
734	CACTTAATTATACTTCC	1-1-3-7-1-1-3	CaCTTaattataCtTCC	734_4	-20,59	30665
734	CACTTAATTATACTTCC	2-1-2-8-4	CAcTTaattatacTTCC	734_5	-20,52	30665
735	CACTTAATTATACTTCCA	2-2-1-7-2-1-3	CActTaattataCTtCCA	735_1	-22,96	30664
735	CACTTAATTATACTTCCA	2-1-1-1-1-6-1-3-2	CAcTtAattataCttcCA	735_2	-19,31	30664
735	CACTTAATTATACTTCCA	1-1-3-8-1-1-3	CaCTTaattatacTtCCA	735_3	-22,43	30664
735	CACTTAATTATACTTCCA	1-1-1-1-2-7-1-2-2	CaCtTAattatacTtcCA	735_4	-19,51	30664
735	CACTTAATTATACTTCCA	2-2-1-9-4	CActTaattatactTCCA	735_5	-21,76	30664
736	ACACTTAATTATACTTCCA	1-1-2-1-1-6-2-3-2	AcACtTaattatACttcCA	736_1	-20,93	30664
736	ACACTTAATTATACTTCCA	2-2-1-7-1-1-1-2-2	ACacTtaattatAcTtcCA	736_2	-19,38	30664
736	ACACTTAATTATACTTCCA	1-1-1-1-1-8-1-2-3	AcAcTtaattataCttCCA	736_3	-21,10	30664
736	ACACTTAATTATACTTCCA	1-1-1-2-1-9-4	AcActTaattatactTCCA	736_4	-21,31	30664
736	ACACTTAATTATACTTCCA	2-2-2-11-2	ACacTTaattatacttcCA	736_5	-19,91	30664

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
737	ACACTTAATTATACTTCC	1-3-1-7-2-1-3	AcacTtaattatACtTCC	737_1	-19,24	30665
737	ACACTTAATTATACTTCC	1-1-1-1-2-6-2-2-2	AcAcTTaattatACttCC	737_2	-19,64	30665
737	ACACTTAATTATACTTCC	2-1-2-7-1-1-1-1-2	ACaCTtaattatAcTtCC	737_3	-20,12	30665
737	ACACTTAATTATACTTCC	3-2-1-8-4	ACActTaattatacTTCC	737_4	-21,53	30665
737	ACACTTAATTATACTTCC	1-1-2-1-1-9-3	AcACtTaattatactTCC	737_5	-19,40	30665
738	ACACTTAATTATACTTC	5-7-5	ACACTtaattatACTTC	738_1	-20,47	30666
738	ACACTTAATTATACTTC	3-1-1-7-5	ACAcTtaattatACTTC	738_2	-18,40	30666
738	ACACTTAATTATACTTC	2-1-2-7-5	ACaCTtaattatACTTC	738_3	-18,51	30666
738	ACACTTAATTATACTTC	5-7-2-1-2	ACACTtaattatACtTC	738_4	-18,77	30666
738	ACACTTAATTATACTTC	5-7-1-1-3	ACACTtaattatAcTTC	738_5	-18,40	30666
738	ACACTTAATTATACTTC	5-8-4	ACACTtaattataCTTC	738_6	-19,88	30666
739	TACACTTAATTATACTTCC	3-2-1-7-2-2-2	TACacTtaattatACttCC	739_1	-21,57	30665
739	TACACTTAATTATACTTCC	1-4-1-7-1-1-4	TacacTtaattatAcTTCC	739_2	-19,87	30665
739	TACACTTAATTATACTTCC	1-2-3-8-1-2-2	TacACTtaattataCttCC	739_3	-20,88	30665
739	TACACTTAATTATACTTCC	4-11-4	TACActtaattatacTTCC	739_4	-23,04	30665
739	TACACTTAATTATACTTCC	2-1-1-1-1-10-3	TAcAcTtaattatactTCC	739_5	-20,03	30665
740	TACACTTAATTATACTTC	4-1-1-7-5	TACAcTtaattatACTTC	740_1	-20,63	30666
740	TACACTTAATTATACTTC	3-1-2-7-5	TACaCTtaattatACTTC	740_2	-20,74	30666
740	TACACTTAATTATACTTC	2-1-3-7-5	TAcACTtaattatACTTC	740_3	-20,21	30666
740	TACACTTAATTATACTTC	3-1-2-8-4	TACaCTtaattataCTTC	740_4	-20,14	30666
740	TACACTTAATTATACTTC	1-1-4-8-4	TaCACTtaattataCTTC	740_5	-20,48	30666
741	TTACACTTAATTATACTTC	2-1-2-7-4-1-2	TTaCActtaattATACtTC	741_1	-21,41	30666
741	TTACACTTAATTATACTTC	5-7-3-1-3	TTACActtaattATAcTTC	741_2	-22,67	30666
741	TTACACTTAATTATACTTC	4-1-1-6-2-1-4	TTACaCttaattATaCTTC	741_3	-22,54	30666

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
741	TTACACTTAATTATACTTC	2-1-2-7-2-1-4	TTaCActtaattATaCTTC	741_4	-21,48	30666
741	TTACACTTAATTATACTTC	5-7-1-1-5	TTACActtaattAtACTTC	741_5	-22,04	30666
742	TTACACTTAATTATACTT	5-7-3-1-2	TTACActtaattATAcTT	742_1	-20,18	30667
742	TTACACTTAATTATACTT	5-7-2-1-3	TTACActtaattATaCTT	742_2	-20,62	30667
742	TTACACTTAATTATACTT	5-7-1-1-4	TTACActtaattAtACTT	742_3	-19,54	30667
743	TTTACACTTAATTATACTT	4-1-1-6-4-1-2	TTTAcActtaatTATAcTT	743_1	-21,26	30667
743	TTTACACTTAATTATACTT	3-1-2-6-3-1-3	TTTaCActtaatTATaCTT	743_2	-22,57	30667
743	TTTACACTTAATTATACTT	4-8-2-1-4	TTTAcacttaatTAtACTT	743_3	-20,48	30667
743	TTTACACTTAATTATACTT	1-1-4-6-2-2-3	TtTACActtaatTAtaCTT	743_4	-21,20	30667
743	TTTACACTTAATTATACTT	2-2-2-6-1-1-5	TTtaCActtaatTaTACTT	743_5	-21,02	30667
744	TTTACACTTAATTATACT	3-1-2-6-3-1-2	TTTaCActtaatTATaCT	744_1	-20,75	30668
744	TTTACACTTAATTATACT	1-1-4-6-3-1-2	TtTACActtaatTATaCT	744_2	-21,06	30668
744	TTTACACTTAATTATACT	2-1-3-6-2-1-3	TTtACActtaatTAtACT	744_3	-19,03	30668
744	TTTACACTTAATTATACT	4-8-1-1-4	TTTAcacttaatTaTACT	744_4	-19,42	30668
744	TTTACACTTAATTATACT	1-1-1-1-2-6-1-1-4	TtTaCActtaatTaTACT	744_5	-19,12	30668
745	ATTTACACTTAATTATACT	4-1-1-6-4-1-2	ATTTaCacttaaTTATaCT	745_1	-22,20	30668
745	ATTTACACTTAATTATACT	2-1-3-6-3-1-3	ATtTACacttaaTTAtACT	745_2	-21,43	30668
745	ATTTACACTTAATTATACT	5-7-2-1-4	ATTTAcacttaaTTaTACT	745_3	-22,44	30668
745	ATTTACACTTAATTATACT	1-2-3-6-2-1-4	AttTACacttaaTTaTACT	745_4	-20,95	30668
745	ATTTACACTTAATTATACT	3-1-2-6-1-1-5	ATTtACacttaaTtATACT	745_5	-20,92	30668
746	ATTTACACTTAATTATAC	5-8-5	ATTTAcacttaatTATAC	746_1	-19,94	30669
746	ATTTACACTTAATTATAC	4-1-1-7-5	ATTTaCacttaatTATAC	746_2	-19,40	30669
746	ATTTACACTTAATTATAC	2-1-3-7-5	ATtTACacttaatTATAC	746_3	-19,70	30669
747	AATTTACACTTAATTATAC	3-1-2-6-3-1-3	AATtTAcacttaATTaTAC	747_1	-19,51	30669

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
747	AATTTACACTTAATTATAC	1-1-4-6-3-1-3	AaTTTAcacttaATTaTAC	747_2	-19,51	30669
747	AATTTACACTTAATTATAC	4-8-2-1-4	AATTtacacttaATtATAC	747_3	-18,04	30669
747	AATTTACACTTAATTATAC	5-7-1-1-5	AATTTacacttaAtTATAC	747_4	-19,79	30669
747	AATTTACACTTAATTATAC	2-1-3-6-1-1-5	AAtTTAcacttaAtTATAC	747_5	-19,26	30669
748	AATTTACACTTAATTATACT	3-2-2-6-4-1-2	AATttACacttaaTTATaCT	748_1	-21,50	30668
748	AATTTACACTTAATTATACT	5-1-1-6-3-1-3	AATTTaCacttaaTTAtACT	748_2	-21,87	30668
748	AATTTACACTTAATTATACT	3-1-3-6-2-1-4	AATtTACacttaaTTaTACT	748_3	-22,95	30668
748	AATTTACACTTAATTATACT	1-1-4-7-2-1-1-1-2	AaTTTAcacttaaTTaTaCT	748_4	-20,23	30668
748	AATTTACACTTAATTATACT	2-1-2-1-1-6-1-1-5	AAtTTaCacttaaTtATACT	748_5	-20,55	30668
749	TAATTTACACTTAATTATAC	2-1-4-6-4-1-2	TAaTTTAcacttaATTAtAC	749_1	-20,98	30669
749	TAATTTACACTTAATTATAC	5-8-3-1-3	TAATTtacacttaATTaTAC	749_2	-20,60	30669
749	TAATTTACACTTAATTATAC	2-2-3-6-3-1-3	TAatTTAcacttaATTaTAC	749_3	-20,80	30669
749	TAATTTACACTTAATTATAC	4-1-2-6-2-1-4	TAATtTAcacttaATtATAC	749_4	-21,41	30669
749	TAATTTACACTTAATTATAC	1-1-1-1-2-7-1-1-5	TaAtTTacacttaAtTATAC	749_5	-18,92	30669
750	TAATTTACACTTAATTAT	5-8-5	TAATTtacacttaATTAT	750_1	-18,27	30671
750	TAATTTACACTTAATTAT	4-1-1-7-5	TAATtTacacttaATTAT	750_2	-18,18	30671
750	TAATTTACACTTAATTAT	2-1-3-7-5	TAaTTTacacttaATTAT	750_3	-18,18	30671
750	TAATTTACACTTAATTAT	1-1-4-7-5	TaATTTacacttaATTAT	750_4	-18,16	30671
751	TAATTTACACTTAATTATA	5-7-4-1-2	TAATTtacacttAATTaTA	751_1	-18,87	30670
751	TAATTTACACTTAATTATA	5-7-2-1-4	TAATTtacacttAAtTATA	751_2	-19,05	30670
751	TAATTTACACTTAATTATA	3-1-2-6-2-1-4	TAAtTTacacttAAtTATA	751_3	-18,54	30670
751	TAATTTACACTTAATTATA	4-1-1-6-1-1-5	TAATtTacacttAaTTATA	751_4	-19,40	30670
751	TAATTTACACTTAATTATA	2-1-3-6-1-1-5	TAaTTTacacttAaTTATA	751_5	-19,41	30670
752	TTAATTTACACTTAATTATA	3-1-3-6-4-1-2	TTAaTTTacacttAATTaTA	752_1	-20,61	30670

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
752	TTAATTTACACTTAATTATA	5-1-1-6-3-1-3	TTAATtTacacttAATtATA	752_2	-20,28	30670
752	TTAATTTACACTTAATTATA	2-1-4-6-2-1-4	TTaATTTacacttAAtTATA	752_3	-20,77	30670
752	TTAATTTACACTTAATTATA	3-2-2-6-1-1-5	TTAatTTacacttAaTTATA	752_4	-20,28	30670
752	TTAATTTACACTTAATTATA	4-1-1-8-1-1-4	TTAAtTtacacttaAtTATA	752_5	-18,80	30670
753	TTAATTTACACTTAATTAT	4-1-1-6-3-1-3	TTAAtTtacactTAAtTAT	753_1	-18,65	30671
753	TTAATTTACACTTAATTAT	3-1-2-6-2-1-4	TTAaTTtacactTAaTTAT	753_2	-19,52	30671
753	TTAATTTACACTTAATTAT	2-1-2-7-2-1-4	TTaATttacactTAaTTAT	753_3	-18,68	30671
753	TTAATTTACACTTAATTAT	5-7-1-1-5	TTAATttacactTaATTAT	753_4	-20,00	30671
753	TTAATTTACACTTAATTAT	2-1-3-6-1-1-5	TTaATTtacactTaATTAT	753_5	-19,47	30671
754	TTTAATTTACACTTAATTA	3-1-2-6-3-1-3	TTTaATttacacTTAaTTA	754_1	-19,46	30672
754	TTTAATTTACACTTAATTA	5-7-2-1-4	TTTAAtttacacTTaATTA	754_2	-19,54	30672
754	TTTAATTTACACTTAATTA	4-1-1-6-2-1-4	TTTAaTttacacTTaATTA	754_3	-19,46	30672
754	TTTAATTTACACTTAATTA	1-1-1-1-2-6-2-1-4	TtTaATttacacTTaATTA	754_4	-18,11	30672
754	TTTAATTTACACTTAATTA	1-1-4-7-3-1-2	TtTAATttacactTAAtTA	754_5	-18,02	30672
755	TTTAATTTACACTTAATTAT	4-1-2-6-3-1-3	TTTAaTTtacactTAAtTAT	755_1	-20,90	30671
755	TTTAATTTACACTTAATTAT	3-1-2-7-2-1-4	TTTaATttacactTAaTTAT	755_2	-20,50	30671
755	TTTAATTTACACTTAATTAT	1-1-5-6-2-1-4	TtTAATTtacactTAaTTAT	755_3	-21,34	30671
755	TTTAATTTACACTTAATTAT	5-8-1-1-5	TTTAAtttacactTaATTAT	755_4	-20,58	30671
755	TTTAATTTACACTTAATTAT	2-2-3-6-1-1-5	TTtaATTtacactTaATTAT	755_5	-20,05	30671
756	ATTTAATTTACACTTAATTA	5-1-1-6-4-1-2	ATTTAaTttacacTTAAtTA	756_1	-21,11	30672
756	ATTTAATTTACACTTAATTA	3-2-2-6-3-1-3	ATTtaATttacacTTAaTTA	756_2	-20,29	30672
756	ATTTAATTTACACTTAATTA	4-1-2-6-2-1-4	ATTTaATttacacTTaATTA	756_3	-21,50	30672
756	ATTTAATTTACACTTAATTA	2-1-4-6-2-2-3	ATtTAATttacacTTaaTTA	756_4	-20,39	30672
756	ATTTAATTTACACTTAATTA	2-1-4-8-5	ATtTAATttacacttAATTA	756_5	-20,08	30672

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
757	ATTTAATTTACACTTAATT	5-7-3-1-3	ATTTAatttacaCTTaATT	757_1	-20,52	30673
757	ATTTAATTTACACTTAATT	4-1-1-7-2-1-3	ATTTaAtttacacTTaATT	757_2	-18,02	30673
757	ATTTAATTTACACTTAATT	2-1-3-7-2-1-3	ATtTAAtttacacTTaATT	757_3	-18,04	30673
757	ATTTAATTTACACTTAATT	4-1-1-8-5	ATTTaAtttacactTAATT	757_4	-18,34	30673
757	ATTTAATTTACACTTAATT	2-1-3-8-5	ATtTAAtttacactTAATT	757_5	-18,37	30673
758	TATTTAATTTACACTTAAT	3-1-2-6-4-1-2	TATtTAatttacACTTaAT	758_1	-20,16	30674
758	TATTTAATTTACACTTAAT	2-1-3-6-2-1-4	TAtTTAatttacACtTAAT	758_2	-19,37	30674
758	TATTTAATTTACACTTAAT	1-1-4-6-2-1-4	TaTTTAatttacACtTAAT	758_3	-19,19	30674
758	TATTTAATTTACACTTAAT	3-1-2-6-1-1-5	TATtTAatttacAcTTAAT	758_4	-19,44	30674
758	TATTTAATTTACACTTAAT	2-1-3-6-1-1-5	TAtTTAatttacAcTTAAT	758_5	-19,00	30674
759	TATTTAATTTACACTTAATT	2-1-4-6-4-1-2	TAtTTAAtttacaCTTAaTT	759_1	-21,54	30673
759	TATTTAATTTACACTTAATT	5-1-1-6-3-1-3	TATTTaAtttacaCTTaATT	759_2	-21,92	30673
759	TATTTAATTTACACTTAATT	4-1-2-7-3-1-2	TATTtAAtttacacTTAaTT	759_3	-19,35	30673
759	TATTTAATTTACACTTAATT	3-1-3-7-2-1-3	TATtTAAtttacacTTaATT	759_4	-20,28	30673
759	TATTTAATTTACACTTAATT	2-1-4-8-5	TAtTTAAtttacactTAATT	759_5	-20,16	30673
760	CTATTTAATTTACACTT	5-6-1-1-4	CTATTtaatttAcACTT	760_1	-19,07	30677
760	CTATTTAATTTACACTT	5-7-5	CTATTtaatttaCACTT	760_2	-20,97	30677
760	CTATTTAATTTACACTT	2-2-1-7-5	CTatTtaatttaCACTT	760_3	-18,08	30677
760	CTATTTAATTTACACTT	5-7-2-1-2	CTATTtaatttaCAcTT	760_4	-18,90	30677
760	CTATTTAATTTACACTT	5-7-1-1-3	CTATTtaatttaCaCTT	760_5	-19,01	30677
761	CTATTTAATTTACACTTAA	2-1-3-6-4-1-2	CTaTTTaatttaCACTtAA	761_1	-20,98	30675
761	CTATTTAATTTACACTTAA	3-1-2-6-3-1-3	CTAtTTaatttaCACtTAA	761_2	-21,73	30675
761	CTATTTAATTTACACTTAA	4-1-1-6-2-1-4	CTATtTaatttaCAcTTAA	761_3	-21,80	30675
761	CTATTTAATTTACACTTAA	5-7-2-2-3	CTATTtaatttaCActTAA	761_4	-20,86	30675

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
761	CTATTTAATTTACACTTAA	2-1-3-6-1-1-5	CTaTTTaatttaCaCTTAA	761_5	-21,29	30675
762	CTATTTAATTTACACTTA	5-7-3-1-2	CTATTtaatttaCACtTA	762_1	-21,50	30676
762	CTATTTAATTTACACTTA	3-2-1-6-3-1-2	CTAttTaatttaCACtTA	762_2	-20,17	30676
762	CTATTTAATTTACACTTA	3-1-1-7-2-1-3	CTAtTtaatttaCAcTTA	762_3	-19,37	30676
762	CTATTTAATTTACACTTA	2-1-3-6-2-1-3	CTaTTTaatttaCAcTTA	762_4	-20,43	30676
762	CTATTTAATTTACACTTA	2-1-3-6-1-1-4	CTaTTTaatttaCaCTTA	762_5	-20,54	30676
763	CTATTTAATTTACACTTAAT	2-1-4-6-3-2-2	CTaTTTAatttacACTtaAT	763_1	-21,79	30674
763	CTATTTAATTTACACTTAAT	4-1-2-6-2-1-4	CTATtTAatttacACtTAAT	763_2	-23,29	30674
763	CTATTTAATTTACACTTAAT	1-2-4-6-1-1-5	CtaTTTAatttacAcTTAAT	763_3	-20,68	30674
763	CTATTTAATTTACACTTAAT	3-1-3-6-1-1-2-1-2	CTAtTTAatttacAcTTaAT	763_4	-21,14	30674
763	CTATTTAATTTACACTTAAT	5-1-1-7-3-1-2	CTATTtAatttacaCTTaAT	763_5	-22,14	30674
764	TCTATTTAATTTACACTTA	2-1-3-6-4-1-2	TCtATTtaatttACACtTA	764_1	-21,94	30676
764	TCTATTTAATTTACACTTA	4-1-1-6-3-1-3	TCTAtTtaatttACAcTTA	764_2	-22,47	30676
764	TCTATTTAATTTACACTTA	3-1-2-7-2-1-3	TCTaTTtaatttaCAcTTA	764_3	-21,69	30676
764	TCTATTTAATTTACACTTA	1-1-4-7-2-2-2	TcTATTtaatttaCActTA	764_4	-20,33	30676
764	TCTATTTAATTTACACTTA	3-2-1-7-1-1-4	TCTatTtaatttaCaCTTA	764_5	-20,85	30676
765	TCTATTTAATTTACACTT	3-2-1-6-2-1-3	TCTatTtaatttACaCTT	765_1	-19,21	30677
765	TCTATTTAATTTACACTT	3-1-2-7-5	TCTaTTtaatttaCACTT	765_2	-21,53	30677
765	TCTATTTAATTTACACTT	2-1-3-7-5	TCtATTtaatttaCACTT	765_3	-20,81	30677
765	TCTATTTAATTTACACTT	4-1-1-7-2-1-2	TCTAtTtaatttaCAcTT	765_4	-19,64	30677
765	TCTATTTAATTTACACTT	1-1-4-7-2-1-2	TcTATTtaatttaCAcTT	765_5	-19,12	30677
766	TCTATTTAATTTACACTTAA	2-1-2-1-1-6-3-2-2	TCtATtTaatttaCACttAA	766_1	-20,25	30675
766	TCTATTTAATTTACACTTAA	4-1-1-7-2-1-4	TCTAtTtaatttaCAcTTAA	766_2	-22,62	30675
766	TCTATTTAATTTACACTTAA	1-1-1-1-3-6-2-2-3	TcTaTTTaatttaCActTAA	766_3	-20,38	30675

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
766	TCTATTTAATTTACACTTAA	3-1-2-7-1-1-2-1-2	TCTaTTtaatttaCaCTtAA	766_4	-20,27	30675
766	TCTATTTAATTTACACTTAA	2-3-2-6-1-1-1-1-3	TCtatTTaatttaCaCtTAA	766_5	-19,51	30675
767	ATCTATTTAATTTACACTT	2-1-2-7-4-1-2	ATcTAtttaattTACAcTT	767_1	-21,49	30677
767	ATCTATTTAATTTACACTT	1-1-4-6-3-1-3	AtCTATttaattTACaCTT	767_2	-23,18	30677
767	ATCTATTTAATTTACACTT	4-1-1-6-2-1-4	ATCTaTttaattTAcACTT	767_3	-22,64	30677
767	ATCTATTTAATTTACACTT	5-7-2-2-3	ATCTAtttaattTAcaCTT	767_4	-22,78	30677
767	ATCTATTTAATTTACACTT	1-1-4-6-1-1-5	AtCTATttaattTaCACTT	767_5	-23,52	30677
768	ATCTATTTAATTTACACTTA	1-2-4-6-2-1-1-1-2	AtcTATTtaatttACaCtTA	768_1	-21,10	30676
768	ATCTATTTAATTTACACTTA	1-1-3-1-1-6-1-1-5	AtCTAtTtaatttAcACTTA	768_2	-22,17	30676
768	ATCTATTTAATTTACACTTA	3-2-2-6-1-1-2-1-2	ATCtaTTtaatttAcACtTA	768_3	-20,60	30676
768	ATCTATTTAATTTACACTTA	1-1-2-1-2-7-2-2-2	AtCTaTTtaatttaCActTA	768_4	-20,80	30676
768	ATCTATTTAATTTACACTTA	3-1-1-1-1-7-1-2-3	ATCtAtTtaatttaCacTTA	768_5	-19,72	30676
769	TATCTATTTAATTTACACTT	1-1-2-1-2-6-4-1-2	TaTCtATttaattTACAcTT	769_1	-22,65	30677
769	TATCTATTTAATTTACACTT	2-1-1-1-2-6-2-1-4	TAtCtATttaattTAcACTT	769_2	-22,23	30677
769	TATCTATTTAATTTACACTT	2-1-4-6-2-3-2	TAtCTATttaattTAcacTT	769_3	-22,66	30677
769	TATCTATTTAATTTACACTT	1-3-3-6-1-1-5	TatcTATttaattTaCACTT	769_4	-22,96	30677
769	TATCTATTTAATTTACACTT	1-1-3-1-1-6-1-3-3	TaTCTaTttaattTacaCTT	769_5	-21,15	30677
770	TATCTATTTAATTTACACT	2-1-3-6-3-1-3	TAtCTAtttaatTTAcACT	770_1	-22,62	30678
770	TATCTATTTAATTTACACT	1-1-4-6-3-1-3	TaTCTAtttaatTTAcACT	770_2	-22,62	30678
770	TATCTATTTAATTTACACT	2-2-2-6-2-1-4	TAtcTAtttaatTTaCACT	770_3	-21,84	30678
770	TATCTATTTAATTTACACT	1-2-3-6-1-1-5	TatCTAtttaatTtACACT	770_4	-21,72	30678
770	TATCTATTTAATTTACACT	4-1-1-7-2-1-3	TATCtAtttaattTAcACT	770_5	-21,09	30678
771	TTATCTATTTAATTTACACT	2-4-1-6-4-1-2	TTatctAtttaatTTACaCT	771_1	-20,22	30678
771	TTATCTATTTAATTTACACT	2-2-3-6-3-2-2	TTatCTAtttaatTTAcaCT	771_2	-22,76	30678

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
771	TTATCTATTTAATTTACACT	1-1-5-6-2-2-3	TtATCTAtttaatTTacACT	771_3	-22,87	30678
771	TTATCTATTTAATTTACACT	2-2-3-6-1-2-4	TTatCTAtttaatTtaCACT	771_4	-22,94	30678
771	TTATCTATTTAATTTACACT	5-1-1-7-1-2-3	TTATCtAtttaattTacACT	771_5	-21,68	30678
772	TTTATCTATTTAATTTACA	1-1-3-7-4-1-2	TtTATctatttaATTTaCA	772_1	-19,96	30680
772	TTTATCTATTTAATTTACA	4-1-1-6-3-2-2	TTTAtCtatttaATTtaCA	772_2	-19,70	30680
772	TTTATCTATTTAATTTACA	3-1-2-6-2-1-4	TTTaTCtatttaATtTACA	772_3	-21,24	30680
772	TTTATCTATTTAATTTACA	5-7-2-2-3	TTTATctatttaATttACA	772_4	-19,82	30680
772	TTTATCTATTTAATTTACA	1-1-4-6-1-1-5	TtTATCtatttaAtTTACA	772_5	-21,42	30680
773	TTTTATCTATTTAATTTAC	2-1-3-6-3-1-3	TTtTATctatttAATtTAC	773_1	-19,10	30681
773	TTTTATCTATTTAATTTAC	1-1-4-6-2-1-4	TtTTATctatttAAtTTAC	773_2	-18,66	30681
773	TTTTATCTATTTAATTTAC	3-1-2-6-1-1-5	TTTtATctatttAaTTTAC	773_3	-18,15	30681
773	TTTTATCTATTTAATTTAC	1-2-3-6-1-1-5	TttTATctatttAaTTTAC	773_4	-18,29	30681
773	TTTTATCTATTTAATTTAC	2-1-3-6-1-2-4	TTtTATctatttAatTTAC	773_5	-18,15	30681
774	TTTTATCTATTTAATTTACA	1-1-2-1-1-7-4-1-2	TtTTaTctatttaATTTaCA	774_1	-19,84	30680
774	TTTTATCTATTTAATTTACA	2-1-1-1-2-6-3-1-3	TTtTaTCtatttaATTtACA	774_2	-20,79	30680
774	TTTTATCTATTTAATTTACA	4-2-1-6-2-1-4	TTTTatCtatttaATtTACA	774_3	-21,94	30680
774	TTTTATCTATTTAATTTACA	1-1-5-6-2-3-2	TtTTATCtatttaATttaCA	774_4	-21,32	30680
774	TTTTATCTATTTAATTTACA	2-2-3-6-1-2-4	TTttATCtatttaAttTACA	774_5	-20,67	30680
775	CTTTTATCTATTTAATTTA	5-7-4-1-2	CTTTTatctattTAATtTA	775_1	-21,18	30682
775	CTTTTATCTATTTAATTTA	5-7-2-1-4	CTTTTatctattTAaTTTA	775_2	-21,18	30682
775	CTTTTATCTATTTAATTTA	5-7-2-2-3	CTTTTatctattTAatTTA	775_3	-20,23	30682
775	CTTTTATCTATTTAATTTA	3-1-1-7-1-1-5	CTTtTatctattTaATTTA	775_4	-19,83	30682
775	CTTTTATCTATTTAATTTA	2-1-2-7-1-1-1-3	CTtTTatctattTaAtTTA	775_5	-18,07	30682
776	CTTTTATCTATTTAATTTAC	1-1-5-6-4-1-2	CtTTTATctatttAATTtAC	776_1	-21,25	30681

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
776	CTTTTATCTATTTAATTTAC	3-1-1-8-3-1-3	CTTtTatctatttAATtTAC	776_2	-20,13	30681
776	CTTTTATCTATTTAATTTAC	5-8-2-1-4	CTTTTatctatttAAtTTAC	776_3	-21,02	30681
776	CTTTTATCTATTTAATTTAC	1-1-2-1-2-6-2-1-4	CtTTtATetatttAAtTTAC	776_4	-19,49	30681
776	CTTTTATCTATTTAATTTAC	2-1-4-6-2-2-3	CTtTTATctatttAAttTAC	776_5	-21,33	30681
777	ACTTTTATCTATTTAATTT	4-1-1-6-4-1-2	ACTTtTatctatTTAAtTT	777_1	-20,04	30683
777	ACTTTTATCTATTTAATTT	3-1-2-6-3-1-3	ACTtTTatctatTTAaTTT	777_2	-20,48	30683
777	ACTTTTATCTATTTAATTT	5-7-2-1-4	ACTTTtatctatTTaATTT	777_3	-20,54	30683
777	ACTTTTATCTATTTAATTT	2-2-2-6-2-1-4	ACttTTatctatTTaATTT	777_4	-19,26	30683
777	ACTTTTATCTATTTAATTT	4-1-1-6-1-2-4	ACTTtTatctatTtaATTT	777_5	-19,21	30683
778	ACTTTTATCTATTTAATTTA	2-3-1-7-4-1-2	ACtttTatctattTAATtTA	778_1	-19,89	30682
778	ACTTTTATCTATTTAATTTA	1-1-4-7-2-1-1-1-2	AcTTTTatctattTAaTtTA	778_2	-19,82	30682
778	ACTTTTATCTATTTAATTTA	3-2-1-7-2-2-3	ACTttTatctattTAatTTA	778_3	-20,13	30682
778	ACTTTTATCTATTTAATTTA	4-9-1-1-5	ACTTttatctattTaATTTA	778_4	-21,14	30682
778	ACTTTTATCTATTTAATTTA	2-1-3-7-1-1-5	ACtTTTatctattTaATTTA	778_5	-21,49	30682
779	ACTTTTATCTATTTAATT	2-1-3-6-2-1-3	ACtTTTatctatTTaATT	779_1	-18,25	30684
779	ACTTTTATCTATTTAATT	4-1-1-7-5	ACTTtTatctattTAATT	779_2	-19,17	30684
779	ACTTTTATCTATTTAATT	3-1-2-7-5	ACTtTTatctattTAATT	779_3	-19,17	30684
779	ACTTTTATCTATTTAATT	2-1-3-7-5	ACtTTTatctattTAATT	779_4	-18,79	30684
779	ACTTTTATCTATTTAATT	1-1-4-7-5	AcTTTTatctattTAATT	779_5	-18,42	30684
780	AACTTTTATCTATTTAATT	5-7-3-1-3	AACTTttatctaTTTaATT	780_1	-19,61	30684
780	AACTTTTATCTATTTAATT	5-8-3-1-2	AACTTttatctatTTAaTT	780_2	-18,68	30684
780	AACTTTTATCTATTTAATT	4-1-1-7-3-1-2	AACTtTtatctatTTAaTT	780_3	-18,17	30684
780	AACTTTTATCTATTTAATT	1-1-4-7-2-1-3	AaCTTTtatctatTTaATT	780_4	-18,45	30684
780	AACTTTTATCTATTTAATT	5-9-5	AACTTttatctattTAATT	780_5	-19,19	30684

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
781	AACTTTTATCTATTTAAT	5-8-5	AACTTttatctatTTAAT	781_1	-18,18	30685
782	AACTTTTATCTATTTAATTT	1-1-1-1-3-6-4-1-2	AaCtTTTatctatTTAAtTT	782_1	-19,40	30683
782	AACTTTTATCTATTTAATTT	4-2-1-6-3-1-3	AACTttTatctatTTAaTTT	782_2	-20,41	30683
782	AACTTTTATCTATTTAATTT	5-1-1-6-2-1-4	AACTTtTatctatTTaATTT	782_3	-21,20	30683
782	AACTTTTATCTATTTAATTT	2-1-4-6-1-2-4	AAcTTTTatctatTtaATTT	782_4	-19,21	30683
782	AACTTTTATCTATTTAATTT	1-1-2-1-2-7-2-1-3	AaCTtTTatctattTAaTTT	782_5	-19,40	30683
783	TAACTTTTATCTATTTAAT	2-1-3-6-4-1-2	TAaCTTttatctATTTaAT	783_1	-19,91	30685
783	TAACTTTTATCTATTTAAT	2-1-3-6-2-1-4	TAaCTTttatctATtTAAT	783_2	-19,93	30685
783	TAACTTTTATCTATTTAAT	5-7-2-1-1-1-2	TAACTtttatctATtTaAT	783_3	-18,79	30685
783	TAACTTTTATCTATTTAAT	1-1-4-6-1-1-5	TaACTTttatctAtTTAAT	783_4	-19,16	30685
783	TAACTTTTATCTATTTAAT	5-9-5	TAACTtttatctatTTAAT	783_5	-19,60	30685
784	TAACTTTTATCTATTTAATT	4-1-1-7-1-1-2-1-2	TAACtTttatctaTtTAaTT	784_1	-18,83	30684
784	TAACTTTTATCTATTTAATT	2-1-4-7-3-1-2	TAaCTTTtatctatTTAaTT	784_2	-20,71	30684
784	TAACTTTTATCTATTTAATT	2-1-3-8-2-1-3	TAaCTTttatctatTTaATT	784_3	-19,87	30684
784	TAACTTTTATCTATTTAATT	1-1-5-7-2-1-3	TaACTTTtatctatTTaATT	784_4	-20,35	30684
784	TAACTTTTATCTATTTAATT	5-10-5	TAACTtttatctattTAATT	784_5	-20,61	30684
785	TAACTTTTATCTATTTAA	5-7-2-1-3	TAACTtttatctATtTAA	785_1	-18,07	30686
786	ATAACTTTTATCTATTTAA	3-1-2-6-4-1-2	ATAaCTtttatcTATTtAA	786_1	-20,14	30686
786	ATAACTTTTATCTATTTAA	4-1-1-6-3-1-3	ATAAcTtttatcTATtTAA	786_2	-20,03	30686
786	ATAACTTTTATCTATTTAA	2-1-3-6-2-1-4	ATaACTtttatcTAtTTAA	786_3	-20,33	30686
786	ATAACTTTTATCTATTTAA	3-1-2-6-2-2-3	ATAaCTtttatcTAttTAA	786_4	-19,84	30686
786	ATAACTTTTATCTATTTAA	5-7-1-1-5	ATAACttttatcTaTTTAA	786_5	-20,30	30686
787	ATAACTTTTATCTATTTAAT	3-1-3-6-3-2-2	ATAaCTTttatctATTtaAT	787_1	-20,73	30685
787	ATAACTTTTATCTATTTAAT	2-1-4-6-2-1-4	ATaACTTttatctATtTAAT	787_2	-21,66	30685

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
787	ATAACTTTTATCTATTTAAT	3-1-2-7-1-2-4	ATAaCTtttatctAttTAAT	787_3	-19,93	30685
787	ATAACTTTTATCTATTTAAT	4-2-1-7-3-1-2	ATAActTttatctaTTTaAT	787_4	-18,98	30685
787	ATAACTTTTATCTATTTAAT	2-1-4-8-5	ATaACTTttatctatTTAAT	787_5	-21,13	30685
788	TATAACTTTTATCTATTTA	1-1-2-1-1-6-4-1-2	TaTAaCttttatCTATtTA	788_1	-21,10	30687
788	TATAACTTTTATCTATTTA	2-2-2-6-3-1-3	TAtaACttttatCTAtTTA	788_2	-20,60	30687
788	TATAACTTTTATCTATTTA	3-1-2-6-2-1-4	TATaACttttatCTaTTTA	788_3	-22,09	30687
788	TATAACTTTTATCTATTTA	5-7-1-1-5	TATAActtttatCtATTTA	788_4	-21,33	30687
788	TATAACTTTTATCTATTTA	4-1-1-7-2-2-2	TATAaCttttatcTAttTA	788_5	-20,13	30687
789	TATAACTTTTATCTATTTAA	4-1-1-7-4-1-2	TATAaCttttatcTATTtAA	789_1	-21,18	30686
789	TATAACTTTTATCTATTTAA	2-2-3-6-3-1-3	TAtaACTtttatcTATtTAA	789_2	-21,32	30686
789	TATAACTTTTATCTATTTAA	1-1-5-6-2-1-4	TaTAACTtttatcTAtTTAA	789_3	-21,97	30686
789	TATAACTTTTATCTATTTAA	3-1-2-7-1-1-1-1-3	TATaACttttatcTaTtTAA	789_4	-19,86	30686
789	TATAACTTTTATCTATTTAA	4-2-1-6-1-2-4	TATAacTtttatcTatTTAA	789_5	-20,09	30686
790	TTATAACTTTTATCTATTT	2-1-3-6-4-1-2	TTaTAActtttaTCTAtTT	790_1	-21,00	30688
790	TTATAACTTTTATCTATTT	5-7-2-2-3	TTATAacttttaTCtaTTT	790_2	-20,52	30688
790	TTATAACTTTTATCTATTT	4-1-1-6-1-1-5	TTATaActtttaTcTATTT	790_3	-21,08	30688
790	TTATAACTTTTATCTATTT	4-1-1-7-3-1-2	TTATaActtttatCTAtTT	790_4	-20,46	30688
790	TTATAACTTTTATCTATTT	2-1-3-8-5	TTaTAActtttatcTATTT	790_5	-19,98	30688
791	TTATAACTTTTATCTATT	5-7-3-1-2	TTATAacttttaTCTaTT	791_1	-20,32	30689
791	TTATAACTTTTATCTATT	5-7-1-1-4	TTATAacttttaTcTATT	791_2	-19,99	30689
791	TTATAACTTTTATCTATT	4-1-1-7-5	TTATaActtttatCTATT	791_3	-20,40	30689
791	TTATAACTTTTATCTATT	4-9-5	TTATaacttttatCTATT	791_4	-19,98	30689
791	TTATAACTTTTATCTATT	2-1-3-7-5	TTaTAActtttatCTATT	791_5	-19,81	30689
792	TTATAACTTTTATCTATTTA	1-2-1-1-2-6-3-2-2	TtaTaACttttatCTAttTA	792_1	-20,10	30687

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
792	TTATAACTTTTATCTATTTA	3-2-1-7-1-1-2-1-2	TTAtaActtttatCtATtTA	792_2	-18,80	30687
792	TTATAACTTTTATCTATTTA	4-1-2-6-1-3-3	TTATaACttttatCtatTTA	792_3	-21,34	30687
792	TTATAACTTTTATCTATTTA	2-1-2-1-1-7-2-1-3	TTaTAaCttttatcTAtTTA	792_4	-20,83	30687
792	TTATAACTTTTATCTATTTA	1-1-4-8-1-1-4	TtATAActtttatcTaTTTA	792_5	-19,94	30687
793	CTTATAACTTTTATCTATT	1-1-1-1-2-6-3-2-2	CtTaTAacttttATCtaTT	793_1	-19,45	30689
793	CTTATAACTTTTATCTATT	1-2-3-6-1-1-5	CttATAacttttAtCTATT	793_2	-21,25	30689
793	CTTATAACTTTTATCTATT	3-2-1-8-5	CTTatAacttttatCTATT	793_3	-20,78	30689
793	CTTATAACTTTTATCTATT	1-1-3-9-2-1-2	CtTATaacttttatCTaTT	793_4	-19,82	30689
793	CTTATAACTTTTATCTATT	5-9-1-1-3	CTTATaacttttatCtATT	793_5	-20,81	30689
794	CTTATAACTTTTATCTAT	5-7-3-1-2	CTTATaacttttATCtAT	794_1	-21,02	30690
794	CTTATAACTTTTATCTAT	1-1-3-7-1-1-4	CtTATaacttttAtCTAT	794_2	-20,04	30690
794	CTTATAACTTTTATCTAT	2-2-1-8-5	CTtaTaacttttaTCTAT	794_3	-19,59	30690
794	CTTATAACTTTTATCTAT	3-1-2-8-4	CTTaTAacttttatCTAT	794_4	-20,86	30690
794	CTTATAACTTTTATCTAT	5-10-3	CTTATaacttttatcTAT	794_5	-19,99	30690
795	CTTATAACTTTTATCTATTT	1-1-1-2-2-6-2-1-1-1-2	CtTatAActtttaTCtAtTT	795_1	-18,22	30688
795	CTTATAACTTTTATCTATTT	1-1-1-1-2-8-2-1-3	CtTaTAacttttatCTaTTT	795_2	-20,86	30688
795	CTTATAACTTTTATCTATTT	2-1-2-1-1-7-2-2-2	CTtATaActtttatCTatTT	795_3	-20,54	30688
795	CTTATAACTTTTATCTATTT	3-2-1-8-1-1-1-1-2	CTTatAacttttatCtAtTT	795_4	-18,19	30688
795	CTTATAACTTTTATCTATTT	1-2-2-1-1-9-4	CttATaActtttatctATTT	795_5	-18,61	30688
796	CTTATAACTTTTATCTA	5-6-2-1-3	CTTATaactttTAtCTA	796_1	-21,44	30691
796	CTTATAACTTTTATCTA	5-6-1-2-3	CTTATaactttTatCTA	796_2	-20,31	30691
796	CTTATAACTTTTATCTA	1-1-3-7-5	CtTATaacttttATCTA	796_3	-19,90	30691
796	CTTATAACTTTTATCTA	3-1-1-8-4	CTTaTaacttttaTCTA	796_4	-18,77	30691
796	CTTATAACTTTTATCTA	2-1-2-8-4	CTtATaacttttaTCTA	796_5	-18,43	30691

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
797	GCTTATAACTTTTATCTA	2-2-2-6-2-2-2	GCttATaactttTAtcTA	797_1	-21,32	30691
797	GCTTATAACTTTTATCTA	4-9-1-1-3	GCTTataactttttAtCTA	797_2	-21,88	30691
797	GCTTATAACTTTTATCTA	2-12-4	GCttataacttttaTCTA	797_3	-20,47	30691
797	GCTTATAACTTTTATCTA	2-1-1-1-1-9-3	GCtTaTaacttttatCTA	797_4	-20,94	30691
797	GCTTATAACTTTTATCTA	1-1-4-10-2	GcTTATaacttttatcTA	797_5	-19,62	30691
798	GCTTATAACTTTTATCT	2-9-1-2-3	GCttataacttTtaTCT	798_1	-18,54	30692
798	GCTTATAACTTTTATCT	2-10-5	GCttataactttTATCT	798_2	-20,90	30692
798	GCTTATAACTTTTATCT	4-8-1-1-3	GCTTataactttTaTCT	798_3	-21,40	30692
798	GCTTATAACTTTTATCT	2-1-2-8-4	GCtTAtaacttttATCT	798_4	-21,00	30692
798	GCTTATAACTTTTATCT	5-10-2	GCTTAtaacttttatCT	798_5	-20,68	30692
799	TGCTTATAACTTTTATC	3-8-3-1-2	TGCttataactTTTaTC	799_1	-19,59	30693
799	TGCTTATAACTTTTATC	3-8-2-1-3	TGCttataactTTtATC	799_2	-19,26	30693
799	TGCTTATAACTTTTATC	2-10-5	TGcttataacttTTATC	799_3	-18,08	30693
799	TGCTTATAACTTTTATC	5-8-4	TGCTTataactttTATC	799_4	-22,34	30693
799	TGCTTATAACTTTTATC	3-10-4	TGCttataactttTATC	799_5	-19,90	30693
800	TGCTTATAACTTTTATCT	3-9-3-1-2	TGCttataacttTTAtCT	800_1	-22,27	30692
800	TGCTTATAACTTTTATCT	2-2-2-7-5	TGctTAtaactttTATCT	800_2	-22,61	30692
800	TGCTTATAACTTTTATCT	3-10-1-1-3	TGCttataactttTaTCT	800_3	-21,45	30692
800	TGCTTATAACTTTTATCT	1-1-1-1-2-8-4	TgCtTAtaacttttATCT	800_4	-20,79	30692
800	TGCTTATAACTTTTATCT	4-1-1-10-2	TGCTtAtaacttttatCT	800_5	-20,89	30692
801	CTGCTTATAACTTTTATC	2-1-1-8-2-1-3	CTgCttataactTTtATC	801_1	-20,05	30693
801	CTGCTTATAACTTTTATC	4-8-1-3-2	CTGCttataactTttaTC	801_2	-21,02	30693
801	CTGCTTATAACTTTTATC	2-1-1-10-4	CTgCttataactttTATC	801_3	-20,69	30693
801	CTGCTTATAACTTTTATC	1-1-2-10-1-1-2	CtGCttataactttTaTC	801_4	-18,86	30693

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
801	CTGCTTATAACTTTTATC	1-1-4-9-3	CtGCTTataacttttATC	801_5	-21,47	30693
802	CTCTGCTTATAACTTTT	1-1-1-1-1-6-2-1-3	CtCtGcttataACtTTT	802_1	-18,92	30696
802	CTCTGCTTATAACTTTT	1-1-1-1-1-7-2-1-2	CtCtGcttataaCTtTT	802_2	-18,47	30696
802	CTCTGCTTATAACTTTT	1-1-2-8-1-1-3	CtCTgcttataaCtTTT	802_3	-19,44	30696
802	CTCTGCTTATAACTTTT	1-2-2-7-1-1-3	CtcTGcttataaCtTTT	802_4	-19,02	30696
802	CTCTGCTTATAACTTTT	3-1-1-10-2	CTCtGcttataacttTT	802_5	-18,16	30696
803	CCTCTGCTTATAACTTT	1-1-2-7-2-1-3	CcTCtgcttatAAcTTT	803_1	-20,60	30697
803	CCTCTGCTTATAACTTT	2-9-1-3-2	CCtctgcttatAactTT	803_2	-19,28	30697
803	CCTCTGCTTATAACTTT	2-2-1-7-1-2-2	CCtcTgcttataActTT	803_3	-20,58	30697
803	CCTCTGCTTATAACTTT	1-2-1-8-1-2-2	CctCtgcttataActTT	803_4	-18,06	30697
803	CCTCTGCTTATAACTTT	2-1-1-9-1-1-2	CCtCtgcttataaCtTT	803_5	-21,12	30697
804	CTACTATACTTTCCTCT	3-8-2-2-2	CTActatactttTCctCT	804_1	-22,54	30709
804	CTACTATACTTTCCTCT	1-1-1-9-2-1-2	CtActatactttCCtCT	804_2	-21,39	30709
804	CTACTATACTTTCCTCT	1-2-1-8-1-2-2	CtaCtatactttCctCT	804_3	-19,70	30709
804	CTACTATACTTTCCTCT	2-11-1-1-2	CTactatactttcCtCT	804_4	-20,45	30709
804	CTACTATACTTTCCTCT	1-3-1-8-1-1-2	CtacTatactttcCtCT	804_5	-19,77	30709
805	TCTACTATACTTTCCTCT	2-1-1-9-1-2-2	TCtActatactttCctCT	805_1	-21,40	30709
805	TCTACTATACTTTCCTCT	2-2-1-8-1-2-2	TCtactatactttCctCT	805_2	-22,20	30709
805	TCTACTATACTTTCCTCT	2-11-1-2-2	TCtactatactttCctCT	805_3	-21,20	30709
805	TCTACTATACTTTCCTCT	2-1-1-10-1-1-2	TCtActatactttcCtCT	805_4	-21,52	30709
805	TCTACTATACTTTCCTCT	2-2-1-9-1-1-2	TCtaCtatactttcCtCT	805_5	-22,32	30709
806	TTCTACTATACTTTCCT	1-1-1-8-1-3-2	TtCtactatacTttcCT	806_1	-18,06	30711
806	TTCTACTATACTTTCCT	1-2-1-7-1-3-2	TtcTactatacTttcCT	806_2	-18,02	30711
806	TTCTACTATACTTTCCT	1-1-1-1-1-7-1-1-3	TtCtActatactTtCCT	806_3	-20,41	30711

(continued)

Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
806	TTCTACTATACTTTCCT	1-1-1-10-4	TtCtactatacttT CCT	806_4	-20,90	30711
806	TTCTACTATACTTTCCT	1-1-1-1-1-9-3	TtCtActatactttCCT	806_5	-20,11	30711
807	TTCTACTATACTTTCCTC	1-2-1-8-1-1-1-1-2	TtcTactatactTtCcTC	807_1	-19,51	30710
807	TTCTACTATACTTTCCTC	1-1-1-2-1-6-1-3-2	TtCtaCtatactTtccTC	807_2	-19,77	30710
807	TTCTACTATACTTTCCTC	1-1-1-1-1-9-1-1-2	TtCtActatactttCcTC	807_3	-19,44	30710
807	TTCTACTATACTTTCCTC	1-1-1-12-3	TtCtactatactttcCTC	807_4	-20,04	30710
807	TTCTACTATACTTTCCTC	1-2-1-1-1-10-2	TtcTaCtatactttccTC	807_5	-19,43	30710
808	TTTCCATCTACTATTAAT	1-1-3-7-3-1-2	TtTCCatctactATTaAT	808_1	-21,43	39804
808	TTTCCATCTACTATTAAT	2-1-2-7-1-1-1-1-2	TTtCCatctactAtTaAT	808_2	-19,50	39804
808	TTTCCATCTACTATTAAT	1-1-4-6-1-2-3	TtTCCAtctactAttAAT	808_3	-20,72	39804
808	TTTCCATCTACTATTAAT	2-1-2-8-1-1-3	TTtCCatctactaTtAAT	808_4	-19,43	39804
808	TTTCCATCTACTATTAAT	4-1-1-8-4	TTTCcAtctactatTAAT	808_5	-20,12	39804
809	TTTCCATCTACTATTAA	5-6-3-1-2	TTTCCatctacTATtAA	809_1	-21,74	39805
809	TTTCCATCTACTATTAA	2-1-2-6-2-1-3	TTtCCatctacTAtTAA	809_2	-20,76	39805
809	TTTCCATCTACTATTAA	1-1-3-6-1-1-4	TtTCCatctacTaTTAA	809_3	-20,75	39805
809	TTTCCATCTACTATTAA	2-1-2-7-5	TTtCCatctactATTAA	809_4	-20,54	39805
809	TTTCCATCTACTATTAA	5-9-3	TTTCCatctactatTAA	809_5	-20,18	39805
810	GTTTCCATCTACTATTA	3-9-2-1-2	GTTtccatctacTAtTA	810_1	-20,81	39806
810	GTTTCCATCTACTATTA	1-1-1-1-1-7-1-1-3	GtTtCcatctacTaTTA	810_2	-19,35	39806
810	GTTTCCATCTACTATTA	2-2-1-7-1-2-2	GTttCcatctacTatTA	810_3	-19,64	39806
810	GTTTCCATCTACTATTA	3-1-1-8-4	GTTtCcatctactATTA	810_4	-21,37	39806
810	GTTTCCATCTACTATTA	1-2-2-10-2	GttTCcatctactatTA	810_5	-18,14	39806
811	AATACAAAATCATCTTAC	3-1-2-6-1-1-4	AATaCAaaatcaTcTTAC	811_1	-18,05	39836
811	AATACAAAATCATCTTAC	4-9-5	AATAcaaaatcatCTTAC	811_2	-18,25	39836

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
811	AATACAAAATCATCTTAC	3-1-2-7-5	AATaCAaaatcatCTTAC	811_3	-19,20	39836
811	AATACAAAATCATCTTAC	2-1-3-7-5	AAtACAaaatcatCTTAC	811_4	-18,12	39836
811	AATACAAAATCATCTTAC	1-1-4-7-5	AaTACAaaatcatCTTAC	811_5	-19,50	39836
812	AATACAAAATCATCTTACA	2-2-2-6-4-1-2	AAtaCAaaatcaTCTTaCA	812_1	-20,31	39835
812	AATACAAAATCATCTTACA	4-8-3-2-2	AATAcaaaatcaTCTtaCA	812_2	-19,80	39835
812	AATACAAAATCATCTTACA	3-1-2-6-2-1-4	AATaCAaaatcaTCtTACA	812_3	-21,91	39835
812	AATACAAAATCATCTTACA	1-1-4-7-2-2-2	AaTACAaaatcatCTtaCA	812_4	-19,93	39835
812	AATACAAAATCATCTTACA	5-8-1-1-4	AATACaaaatcatCtTACA	812_5	-20,93	39835
813	TAATACAAAATCATCTTA	1-1-4-6-3-1-2	TaATACaaaatcATCtTA	813_1	-18,46	39837
813	TAATACAAAATCATCTTA	5-8-5	TAATAcaaaatcaTCTTA	813_2	-19,57	39837
813	TAATACAAAATCATCTTA	5-9-4	TAATAcaaaatcatCTTA	813_3	-18,44	39837
813	TAATACAAAATCATCTTA	2-1-3-8-4	TAaTACaaaatcatCTTA	813_4	-18,20	39837
813	TAATACAAAATCATCTTA	1-1-4-8-4	TaATACaaaatcatCTTA	813_5	-18,18	39837
814	TAATACAAAATCATCTTAC	2-1-3-6-4-1-2	TAaTACaaaatcATCTtAC	814_1	-19,95	39836
814	TAATACAAAATCATCTTAC	4-1-1-6-3-1-3	TAATaCaaaatcATCtTAC	814_2	-20,22	39836
814	TAATACAAAATCATCTTAC	1-2-3-6-1-1-5	TaaTACaaaatcAtCTTAC	814_3	-19,14	39836
814	TAATACAAAATCATCTTAC	5-8-2-1-3	TAATAcaaaatcaTCtTAC	814_4	-19,90	39836
814	TAATACAAAATCATCTTAC	4-1-1-8-5	TAATaCaaaatcatCTTAC	814_5	-19,94	39836
815	TAATACAAAATCATCTTACA	3-2-2-6-2-1-1-1-2	TAAtaCAaaatcaTCtTaCA	815_1	-20,84	39835
815	TAATACAAAATCATCTTACA	2-3-1-8-2-1-3	TAataCaaaatcatCTtACA	815_2	-18,77	39835
815	TAATACAAAATCATCTTACA	2-1-2-1-1-7-2-2-2	TAaTAcAaaatcatCTtaCA	815_3	-19,66	39835
815	TAATACAAAATCATCTTACA	1-1-1-1-2-8-1-1-4	TaAtACaaaatcatCtTACA	815_4	-19,11	39835
815	TAATACAAAATCATCTTACA	4-10-1-1-1-1-2	TAATacaaaatcatCtTaCA	815_5	-19,22	39835
816	TCTGTATACACCATCCCA	2-10-1-1-1-1-2	TCtgtatacaccAtCcCA	816_1	-24,49	46389

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Seq ID NO	Motif	Design	Compound	CMP ID NO	ΔG°	Start SEQ ID NO 1
816	TCTGTATACACCATCCCA	2-3-1-6-1-3-2	TCtgtAtacaccAtccCA	816_2	-23,81	46389
816	TCTGTATACACCATCCCA	2-10-1-3-2	TCtgtatacaccAtCcCA	816_3	-23,72	46389
816	TCTGTATACACCATCCCA	2-1-1-10-1-1-2	TCtGtatacaccatCcCA	816_4	-24,75	46389
816	TCTGTATACACCATCCCA	2-3-1-8-1-1-2	TCtgtAtacaccatCcCA	816_5	-24,53	46389
816	TCTGTATACACCATCCCA	2-3-1-10-2	TCtgtAtacaccatccCA	816_6	-23,76	46389
817	TTCTGACTCCCTATCCA	1-1-1-12-2	TtCtgactccctatcCA	817_1	-22,56	46417
818	TTTCTGACTCCCTATCC	1-2-1-11-2	TttCtgactccctatCC	818_1	-22,64	46418

[0272] Designs refer to the gapmer design, F-G-F', where each number represents the number of consecutive modified nucleosides, e.g 2' modified nucleosides (first number = 5' flank), followed by the number of DNA nucleosides (second number = gap region), followed by the number of modified nucleosides, e.g 2' modified nucleosides (third number = 3' flank), optionally preceded by or followed by further repeated regions of DNA and LNA, which are not necessarily part of the contiguous sequence that is complementary to the target nucleic acid. For some oligonucleotides in table 3 the flanks are mixed flanks, such flanks start and end with a 2' modified nucleosides, in these cases the gap region is the number above 5 not located at the 5' or 3' terminal in of the design.

[0273] For the oligonucleotide compounds capital letters represent beta-D-oxy LNA nucleosides, lowercase letters represent DNA nucleosides, all LNA C are 5-methyl cytosine, and 5-methyl DNA cytosines are presented by "e", all internucleoside linkages are phosphorothioate internucleoside linkages.

[0274] Oligonucleotides with an EX-EX indication as Start on SEQ ID NO: 1 are exon-exon spanning oligonucleotides designed to be complementary across exon-exon junctions of SNHG14-023 (ENST00000554726). The oligonucleotides primarily span exon2 and exon3 (i.e. are complementary to a region in exon2 and a region in exon 3)

Oligonucleotide synthesis

[0275] Oligonucleotide synthesis is generally known in the art. Below is a protocol which may be applied. The oligonucleotides of the present invention may have been produced by slightly varying methods in terms of apparatus, support and concentrations used.

[0276] Oligonucleotides are synthesized on uridine universal supports using the phosphoramidite approach on a MerMade12 or an Oligomaker DNA/RNA synthesizer at 1-4 μmol scale. At the end of the synthesis, the oligonucleotides are cleaved from the solid support using aqueous ammonia for 5-16 hours at 60°C. The oligonucleotides are purified by reverse phase HPLC (RP-HPLC) or by solid phase extractions and characterized by UPLC, and the molecular mass is further confirmed by ESI-MS.

Elongation of the oligonucleotide:

[0277] The coupling of β-cyanoethyl- phosphoramidites (DNA-A(Bz), DNA- G(ibu), DNA- C(Bz), DNA-T, LNA-5-methyl-C(Bz), LNA-A(Bz), LNA- G(dmf), LNA-T or amino-C6 linker) is performed by using a solution of 0.1 M of the 5'-O-DMT-protected amidite in acetonitrile and DCI (4,5-dicyanoimidazole) in acetonitrile (0.25 M) as activator. For the final cycle a phosphoramidite with desired modifications can be used, e.g. a C6 linker for attaching a conjugate group or a conjugate group as such. Thiolation for introduction of phosphorthioate linkages is carried out by using xanthane hydride (0.01 M in acetonitrile/pyridine 9:1). Phosphordiester linkages can be introduced using 0.02 M iodine in THF/Pyridine/water 7:2:1. The rest of the reagents are the ones typically used for oligonucleotide synthesis.

Purification by RP-HPLC:

[0278] The crude compounds are purified by preparative RP-HPLC on a Phenomenex Jupiter C18 10μ 150x10 mm column. 0.1 M ammonium acetate pH 8 and acetonitrile is used as buffers at a flow rate of 5 mL/min. The collected fractions are lyophilized to give the purified compound typically as a white solid.

Abbreviations:

[0279]

DCI:	4,5-Dicyanoimidazole
DCM:	Dichloromethane
DMF:	Dimethylformamide
DMT:	4,4'-Dimethoxytrityl
THF:	Tetrahydrofurane
Bz:	Benzoyl
Ibu:	Isobutyryl
RP-HPLC:	Reverse phase high performance liquid chromatography

T_m Assay

[0280] Oligonucleotide and RNA target duplexes are diluted to 3 mM in 500 ml RNase-free water and mixed with 500 ml 2x T_m-buffer (200mM NaCl, 0.2mM EDTA, 20mM Naphosphate, pH 7.0). The solution is heated to 95°C for 3 min and then allowed to anneal in room temperature for 30 min. The duplex melting temperatures (T_m) is measured on a Lambda 40 UV/VIS Spectrophotometer equipped with a Peltier temperature programmer PTP6 using PE Templab software (Perkin Elmer). The temperature is ramped up from 20°C to 95°C and then down to 25°C, recording absorption at 260 nm. First derivative and the local maximums of both the melting and annealing are used to assess the duplex T_m.

Preparation of mouse primary cortical neuron cell cultures

[0281] Primary cortical neuron cultures were prepared from mouse embryo brains of 15 days of age according to standard procedure. In brief, culture plates were coated with Poly-L-Lysine (50 μg/ml Poly-L-Lysine, 10 mM Na-tetraborate, pH 8 buffer) for 2-3 hrs at room temperature. The plates were washed with 1xPBS before use. Harvested mouse embryo brains were dissected and homogenized by a razor blade and submerged into 38 ml dissection medium (HBSS, 0.01 M Hepes, Penicillin/Streptomycin). Then, 2 ml trypsin was added and cells were incubated for 30 min at 37 °C and centrifuged down. The cells were dissolved in 20 ml DMEM (+ 10% FBS) and passed through a syringe for further homogenization. This was followed by centrifugation at 500 rpm for 15 mins. The cells were dissolved in DMEM (+10% FBS) and seeded in 96 well plates (0.1 × 10^6 cells/well in 100 μl). The neuronal cell cultures were ready for use directly after seeding.

Screening oligonucleotides in mouse primary cortical neuron cell cultures

[0282] Cells were cultured in growth medium (Gibco Neurobasal medium, B27 supplement, Glutamax, Pencillin-streptomycin) in 96-well plates and incubated with oligonucleotides for 3 days at the desired concentrations. Total RNA was isolated from the cells and the knock-down efficacy was measured by qPCR analysis using the qScript™ XLT One-Step RT-qPCR ToughMix®, Low ROX™ kit from Quanta Bioscience (95134-500). A commercial taqman assays from Thermo Fisher Scientific was used to measure Ube3a_ATS including GAPDH for normalization.

Generation of human primary neuronal cell cultures

[0283] Any cell lines at any described time point was incubated at 37°C, 5% CO2 concentration and 95% relative humidity.

Human induced pluripotent stem cells (hiPSC) culture

[0284] Whole human blood samples were obtained from patients diagnosed with Angelman syndrome. The subsequent cultures of primary Peripheral Blood Mononuclear Cells (PMCSs) were enriched for erythroblasts. Patient-specific iPSC lines were generated by reprogramming erythroblast with CytoTune-iPS Sendai Reprogramming Kit (Thermo Fisher Scientific). Derived iPSC lines were maintained in feeder-free conditions using hESC-qualified Matrigel (Corning) in mTESR1 (STEMCELL Technologies) with daily medium replacement. Upon reaching confluence, colonies were dissociated into cell cluster of 50 - 200 μm in size using Gentle Cell Dissociation Reagent (STEMCELL Technologies) and subcultured at a ratio of 1:10 - 1:20 in the presence of 10 μM Y-27632 (Calbiochem).

Differentiation into Neural progenitor cells (NPC)

[0285] Upon induction of neural differentiation iPSC-derived cells were maintained in basal medium composed of equal volumes of DMEM:F12 Glutamax medium and Neurobasal medium (Gibco, Invitrogen), supplemented with 1x B27 (Gibco, Invitrogen), 1x N2 (Gibco, Invitrogen), 0.1 mM beta-mercaptoethanol (Gibco, Invitrogen) and indicated supplements.

[0286] Neural progenitor cells (NPCs) were derived from hiPSCs by dual SMAD inhibition and according to published procedures with slight modifications (Chambers et al. 2009 Nat Biotechnol. Vol. 3 pp.275-80, Boissart et al., 2013 Transl Psychiatry. 3:e294). HiPSCs were dissociated with Accutase (Innovative Cell Technologies Inc.) into a single cell suspension and resuspended in basic medium further supplemented with 10 μM Y-27632 (Calbiochem), 5 ng/ml FGF (Peprotech), 10 μM SB-431542 (Calbiochem) and 100 nM LDN (Calbiochem). Single cell suspension was transferred to AggreWell800 plates (STEMCELL Technologies) enabling the formation of aggregates consisting of 8000 cells. After 5 days neural aggregates were transferred onto plates coated with poly-L-ornithine (Sigma) and laminin (Roche) and allowed to form neural rosettes under continued dual SMAD inhibition (SB-431542 and LDN) in basic medium supplemented with FGF. Neural rosettes were selectively isolated using STEMdiff™ Neural Rosette Selection Reagent (STEMCELL Technologies), replated onto dishes coated with poly-L-ornithine and Laminin521 (BioLamina) and expanded in basic medium supplemented with 10 ng/ml FGF (Peprotech), 10 ng/ml EGF (RnD), and 20 ng/ml BDNF (Peprotech). When reaching confluency, cells were enzymatically dissociated with 0.05% Trypsin/EDTA (Gibco, Invitrogen) and subcultured. Continued passaging in basic medium supplemented with FGF, EGF and BDNF leads to a stable neural progenitor cell line (NPC line) within 10 to 20 passages. A stable neural progenitor cell line is defined by its capacity to self-renew and by the expression of the developmental stage-specific markers Sox2 and Nestin. Upon specific stimuli, NPCs differentiate into neuronal (MAP2+, Tau+, HuC/D+) and astroglial (GFAP+) progenies (Dunkley et al., 2015 Proteomics Clin Appl. Vol. 7-8 pp.684-94).

NPC culture

[0287] Conditions for NPC culture have been described previously and were used with slight modifications (Boissart et al., 2013 Transl Psychiatry. 3:e294). In brief, cells were maintained in dishes coated with Laminin521 (BioLamina) and cultured in basic medium [composed of equal volumes of DMEM:F12 Glutamax medium and Neurobasal medium (Gibco, Invitrogen), supplemented with 1x B27 (Gibco, Invitrogen), 1x N2 (Gibco, Invitrogen), 0.1 mM beta-mercaptoethanol (Gibco, Invitrogen)] and supplemented with 10 ng/ml FGF (Peprotech), 10 ng/ml EGF (RnD), and 20 ng/ml BDNF (Peprotech).

Differentiation into neuronal cell culture

[0288] To induce neuronal differentiation of NPC, cells were dissociated with 0.05% Trypsin/EDTA (Gibco, Invitrogen) into single cell suspension and seeded onto Laminin521 (BioLamina) coated dishes at a density of 12.000 cells/cm2 and maintained in basic medium supplemented with 200 ng/ml Shh (Peprotech), 100 ng/ml FGF8 (Peprotech), and 100 μM ascorbic acid phosphate (Sigma) for a period of 7 days. Subsequently, cells were replated in basal medium supplemented with 20 ng/ml BDNF (Peprotech), 10 ng/ml GDNF (Peprotech), 0.5 mM cAMP (BIOLOG Life Science), and 100 μM ascorbic acid phosphate (Sigma) at a density of 45000 cells/cm2 and differentiated for a period of 21 days. At day 21 of differentiation, differentiated neuronal cultures were replated onto the screening-compatible plate format. Replating was performed by dissociating the cultures with Accutase (Innovative Cell Technologies Inc.) into a single cell suspension. Cells were seeded at a density of 200.000 cells/cm2 in presence of 10 μM Y-27632 (a cell-permeable, reversible, inhibitor of Rho kinases from Calbiochem) into the 384 well microtiter plates for final oligonucleotides screening assay. Neuronal cultures were further differentiated for additional 7 days in basal medium supplemented with 20 ng/ml BDNF (Peprotech), 10 ng/ml GDNF (Peprotech), 0.5 mM cAMP (BIOLOG Life Science), and 100 μM ascorbic acid phosphate (Sigma). Differentiation medium was exchanged twice per week. After a total differentiation period of 35 days neuronal cell cultures were ready for oligonucleotide treatment.

Screening oligonucleotides in human neuronal cell cultures - 384 well system

[0289] For screening, oligonucleotide stocks were pre-diluted to the indicated concentrations with water into 384 well microtiter plates (compound plate). The plate layout served as a treatment template. Two microliter oligonucleotide dilution from each well was transferred from the compound plate to a respective culture plate. All liquid handling was done under sterile conditions in a laminar flow using a semi-automated laboratory robotic system (Beckmancoulter). Neuronal cell cultures were incubated with oligonucleotides for 5 days without media change. Subsequently, neuronal cultures were lysed and processed for qPCR assay with RealTime ready Cell lysis and RNA Virus Master kit (Roche). Liquid handling was performed using a semi-automated laboratory robotic system (Beckmancoulter). Samples were analyzed by a Lightcycler480 real-time PCR system (Roche).

[0290] Activity of the oligonucleotides was assessed by qPCR monitoring transcript abundance of UBE3A using the following primers and probes

UBE3a-Sense: Forward primer: ATATGTGGAAGCCGGAATCT (SEQ ID NO: 837),
Reverse primer: TCCCAGAACTCCCTAATCAGAA (SEQ ID NO: 838),
Internal probe labeled with dye FAM: ATGACGGTGGCTATACCAGG (SEQ ID NO: 839)

[0291] The RT-qPCR was multiplexed with PPIA (peptidylprolyl isomerase A) as housekeeping gene for normalization. PPIA primers and probe labeled with the dye VIC were purchased from Thermo Fisher Scientific (assay ID Hs99999904_m1). Each plate includes a non-targeting oligonucleotide (mock) as negative control (TTGaataagtggaTGT (SEQ ID NO: 846)) and a reference oligonucleotide CMP ID NO: 41_1, resulting in up-regulation of UBE3A mRNA.

[0292] Selectivity of oligonucleotides was verified by counter screening for SNORD 115 transcript, which is located upstream of SNORD109B on chromosome 15. Expression of SNORD115 was monitored by qPCR using the following primers and probe

Forward primer: GGGTCAATGATGAGAACCTTAT (SEQ ID NO: 840),

Reverse primer GGGCCTCAGCGTAATCCTATT (SEQ ID NO: 841),
Internal probe labeled with the dye FAM: TTCTGAAGAGAGGTGATGACTTAAAA (SEQ ID NO: 842)

[0293] The RT-qPCR was multiplexed with PPIA (Thermo Fisher Scientific) upon oligonucleotide treatment.

[0294] The reduction of the SNHG14 transcript downstream of SNORD109B (also termed the UBE3A suppressor) was measured by RT-qPCR using the following primers and probe Forward primer: ATCCGAGGCATGAATCTCAC (SEQ ID NO: 843),

Reverse primer: CAGGCCAAAACCCTTGATAA (SEQ ID NO: 844),
Internal probe labeled with dye FAM: TTGCTGAGCATTTTTGCATC (SEQ ID NO: 845)

[0295] The RT-qPCR was multiplexed with PPIA (Thermo Fisher Scientific).

[0296] Data are presented as average % expression relative to mock across all plates and normalized to the reference oligonucleotide to account for plate to plate variation.

Screening oligonucleotides in human neuronal cell cultures - 96 well system

[0297] For screening, oligonucleotide stocks were pre-diluted to the indicated concentrations with water into 96 well microtiter plates (compound plate). The plate layout served as a treatment template. Two microliter oligonucleotide dilution from each well was transferred from the compound plate to a respective culture plate. All liquid handling was done under sterile conditions in a laminar flow using a semi-automated laboratory robotic system (Beckman Coulter). Neuronal cell cultures were incubated with oligonucleotides for 5 days without media change. Subsequently, neuronal cultures were lysed and RNA purified using RNA purification kit Pure Link Pro96 (12173011A) LifeTechnologies. Liquid handling was performed using a semi-automated laboratory robotic system (Beckmancoulter). qPCR analysis of Ube3a and Ube3a-ATS was carried out on a ViiA™ 7 Real-Time PCR System Thermo Fisher Scientific using the qScriptTM XLT 1-Step RT-qPCR ToughMix Low ROX, from Quanta (95134-50).

[0298] The following primers and probes were used:
qPCR UBE3a-Sense:

Forward primer: ATATGTGGAAGCCGGAATCT (SEQ ID NO: 697),
Reverse primer: TCCCAGAACTCCCTAATCAGAA (SEQ ID NO: 698),
Internal probe labeled with dye FAM: ATGACGGTGGCTATACCAGG (SEQ ID NO: 699)

[0299] qPCR SNHG14 transcript downstream of SNORD109B (also termed the UBE3A suppressor): Commercially available primer and probe set from ThermoFisher: Hs01372957_m1. These primers amplifies a 87 bp exon-exon spanning sequence in the Genbank transcript AF400500.1

QPCR GAPDH transcript:

[0300] Commercially available primer and probe set from Thermofisher: Gene Symbol: with following assay details: RefSeq: NM_002046.3, Probe Exon Location:3, Amplicon Size: 122 bp. Corresponding TaqMan Assay ID: Hs99999905_m1.

[0301] The RT-qPCR for both Ube3a and Ube3a-ATS was multiplexed with GAPDH as housekeeping gene for normalization. Each plate includes a non-targeting oligonucleotide (mock) as negative control (TTGaataagtggaTGT (SEQ ID NO: 846)) and a reference oligonucleotide CMP ID NO: 21_1, resulting in up-regulation of UBE3A mRNA. Moreover panel of oligos not targeting Ub3a or SNHG14 transcript downstream of SNORD109B (also termed the UBE3A suppressor) were included to monitor the assay noise and risk of detecting false positives. These were randomly distributed over the plates.

Control oligonucleotides:

[0302]

CGAaccactgaaCAA	(SEQ ID NO: 819)
CGAaccactgaacAAA	(SEQ ID NO: 820)
CGAagtgcacaCG	(SEQ ID NO: 821)
GCGtaaagagaGGT	(SEQ ID NO: 822)

(continued)

GAGAaggcacagaCGG	(SEQ ID NO: 823)
GCGaagtgcacaCGG	(SEQ ID NO: 824)
GAGaaggcacagaCGG	(SEQ ID NO: 825)
CGAaccactgAACA	(SEQ ID NO: 826)
GAAccactgaacAAA	(SEQ ID NO: 827)
caGCGtaaagagaGG	(SEQ ID NO: 828)
GCgtaaagagAGG	(SEQ ID NO: 829)
CGAaccactgaAC	(SEQ ID NO: 830)
CGAAccactgaaCAAA	(SEQ ID NO: 831)
AGCgaagtgcacaCGG	(SEQ ID NO: 832)
AGGtgaagcgaAGTG	(SEQ ID NO: 833)
TAGTaaactgagCCA	(SEQ ID NO: 834)
AGAaggcacagaCGG	(SEQ ID NO: 835)
CCGcagtatggaTCG	(SEQ ID NO: 836)

Example 1 - Oligonucleotide activity in mouse primary neuronal cell cultures

[0303] Oligonucleotides targeting the part of SNHG14 long non-coding RNA which is antisense to the UBE3A pre-mRNA (position 55319 to 141053 of SEQ ID NO: 1) were tested for their ability to reduce the SNHG14 long non-coding RNA transcript preventing UBE3A expression (also termed UBE3A suppressor or UBE3A-SUP in the data table) and their ability to induce UBE3A mRNA re-expression in mouse primary cortical neuron cell cultures, obtained as described in the "Materials and methods" section above. The oligonucleotide concentration was 5 microM.

[0304] The oligonucleotides were screened according to the protocol for screening in mouse cortical neuron cell cultures described in the section "Materials and methods". The results are shown in table 4.

Table 4: Oligonucleotide activity in primary mouse neuronal cell cultures.

CMP ID NO	oligonucleotide	% of Mock UBE3A_SUP	sd	% of Mock UBE3A	sd
95_1	CTCAtacttgctttaAT	3,6	0,1	154,1	15,1
95_2	CTcatacttgctttaAT	15,9	2,6	119,8	12,4
96_1	ACatctcatacttGCTT	4,0	0,5	149,9	11,5
96_2	ACatctcatacttgcTT	9,3	3,9	139,9	36,4
96_3	ACatctcatacttgCTT	3,1	0,2	143,2	3,9
97_1	ACatctcatactTGCT	4,0	1,5	154,5	10,0
97_2	ACatctcatacttgCT	6,1	1,7	141,1	14,1
97_3	ACatctcatacttGCT	3,7	0,6	162,7	15,0
97_4	ACATctcatacttgCT	5,2	0,4	156,7	24,4
98_1	TAcatctcatactTGCT	5,0	0,9	159,0	15,6
98_2	TAcatctcatacttgCT	15,5	5,3	130,4	3,4
98_3	TACAtctcatacttgCT	4,7	0,4	140,3	38,2
101_1	TACatctcatactTGC	2,6	0,5	152,6	10,2
101_2	TAcatctcatacttGC	19,2	6,0	112,0	15,0
101_3	TAcatctcatactTGC	3,5	0,4	117,2	13,7
101_4	TACAtctcatacttGC	3,0	0,7	140,5	12,4
100_1	CTAcatctcatactTGC	5,4	0,8	160,4	4,1
100_2	CTacatctcatacttGC	9,6	3,7	159,2	14,5

(continued)

CMP ID NO	oligonucleotide	% of Mock UBE3A_SUP	sd	% of Mock UBE3A	sd
100_3	CTacatctcatactTGC	3,0	0,1	133,2	5,9
99_2	CCtacatctcatacttGC	7,8	1,4	150,7	11,0
99_3	CCtacatctcatactTGC	3,2	0,6	134,7	12,5
99_4	CCtacatctcatacTTGC	2,7	0,2	145,2	4,7
102_1	CCTAcatctcatactTG	5,8	1,7	127,0	24,5
102 2	CCtacatctcatactTG	20,2	6,6	129,7	9,2
102_4	CCTacatctcatacTTG	4,0	0,6	140,2	7,2
102_3	CCTacatctcatactTG	3,9	1,0	133,3	10,0
104_1	CCTacatctcataCTT	6,6	1,5	136,5	8,7
104_3	CCtacatctcatACTT	3,5	0,4	131,4	6,0
103_1	ACCtacatctcataCTT	5,8	1,4	130,8	0,7
103_2	ACctacatctcatacTT	11,4	2,2	123,6	12,4
103_3	ACctacatctcatACTT	5,8	0,8	132,2	4,5
105_1	TACCtacatctcatacTT	5,2	0,8	152,3	7,2
106_1	TTAcctacatctcataCTT	13,3	3,0	140,1	17,5
106_2	TTacctacatctcatacTT	21,0	1,4	116,9	15,0
107_1	ACCTacatctcataCT	6,2	0,9	119,2	3,4
107_2	ACctacatctcataCT	14,3	7,4	142,9	13,7
108_1	TACCtacatctcataCT	5,6	1,0	127,0	10,7
108_2	TAcctacatctcataCT	21,4	12,5	117,1	8,5
109_1	TTacctacatctcaTACT	4,4	0,4	138,9	1,2
109_2	TTacctacatctcataCT	22,9	3,3	117,1	13,0
110_1	TTAcctacatctcaTAC	8,7	2,1	133,2	5,1
110_2	TTacctacatctcatAC	21,0	5,1	111,4	11,1
111_1	GTtacctacatctCATA	8,0	2,4	143,8	14,8
111_2	GTtacctacatctcaTA	19,0	2,3	115,4	4,1
112_1	GTTacctacatctCAT	6,6	1,4	145,5	16,8
112_2	GTtacctacatctcAT	15,8	4,5	120,3	8,1
126_1	TCACtttccagatatCA	8,0	1,9	133,8	5,4
126_3	TCactttccagatatCA	53,4	75,9	112,0	11,4
128_1	ACATgtccctttataTT	16,3	2,5	114,7	11,1
128_2	ACatgtccctttataTT	14,8	1,1	136,9	6,2
129_1	ACAtgtccctttaTAT	11,8	1,9	135,0	14,3
132_1	CTCAtccctccaagaAA	9,1	1,6	131,7	8,4
132_2	CTcatccctccaagaAA	11,2	3,9	159,3	17,7

Example 2 - Oligonucleotide activity in human neuronal cell cultures

[0305] Oligonucleotides targeting human SNHG14 in the region downstream of SNORD109B corresponding to position

25278410 to 25419462 on chromosome 15 (SEQ ID NO: 1) were tested in patient derived human neuronal cell cultures (see protocol in "Materials and methods" section). The oligonucleotides ability to reduce the SNHG14 transcript in the region downstream of SNORD109B (also termed UBE3A suppressor or UBE3A-SUP in the data table), without affecting expression of SNORD115 was analyzed. Furthermore, the ability to induce UBE3A mRNA re-expression was analyzed.

[0306] The oligonucleotides were screened according to the protocol for screening oligonucleotides in human neuronal cell cultures described in the section "Materials and methods" above.

[0307] The results are shown in table 5. The expression of UBE3A mRNA has been measured for all compounds, whereas the knock-down of the UBE3A suppressor and the maintenance of SNORD1115 levels have not been analyzed for all compounds.

Table 5: Oligonucleotide activity in patient derived human neuronal cell cultures.

Start SEQ ID NO 1	**CMP ID NO**	**Target**	**% of Mock** Oligo conc 0.2 µM	**sd**	**% of Mock** Oligo conc 1.0 µM	**sd**	**% of Mock** Oligo conc 5.0 µM	**sd**
1678	10_1	UBE3A	107	14	88	10	151	8
1679	12_2	UBE3A	100	9	87	14	158	16
1687	20_1	UBE3A	87	7	102	22	213	44
1712	21_1	UBE3A	127	23	166	6	178	13
1712	21_1	UBE3A-SUP	81	3	82	8	72	12
1712	21_1	SNORD115	115	6	142	24	169	26
4167	22_1	UBE3A	87	5	90	8	146	20
4170	27_1	UBE3A	94	16	106	11	170	10

Start SEQ ID NO 1	CMP ID NO	Target	% of Mock Oligo conc 0.2 µM	sd	% of Mock Oligo conc 1.0 µM	sd	% of Mock Oligo conc 5.0 µM	sd
4171	29_2	UBE3A	86	13	100	12	194	35
4172	30_1	UBE3A	96	6	121	12	209	27
9210	35_1	UBE3A	88	5	112	23	195	27
10838	37_1	UBE3A	77	7	85	9	169	24
15565	38_2	UBE3A	93	11	108	6	167	34
22209	42_1	UBE3A	125	16	143	14	180	17
22209	42_1	UBE3A-SUP	108	14	98	15	85	18
22209	42_1	SNORD115	101	14	93	25	127	21
30449	43_1	UBE3A	99	5	95	13	115	8
30451	44_1	UBE3A	99	15	80	20	141	17
30451	44_2	UBE3A	98	31	104	16	119	7
30697	46_1	UBE3A	91	8	87	5	167	20
36066	49_1	UBE3A	95	6	111	10	155	29
36066	49_1	UBE3A-SUP	76	7	84	24	110	31
36066	49_1	SNORD115	99	14	111	20	94	6
36068	50_1	UBE3A	109	15	105	11	92	14
36068	50_1	UBE3A-SUP	122	24	93	28	73	7
36068	50_1	SNORD115	120	15	113	12	99	6
37206	51_1	UBE3A	114	16	101	7	101	3
37206	51_1	UBE3A-SUP	128	21	67	9	84	13
37206	51_1	SNORD115	140	26	110	9	100	11
46130	52_1	UBE3A	139	3	160	1	236	36
46130	52_1	UBE3A-SUP	135	16	133	26	160	32
46130	52_1	SNORD115	104	8	119	14	100	8
48145	59_1	UBE3A	179	3	122	17	115	NA
48170	76_1	UBE3A	85	16	100	8	155	12
48171	80_1	UBE3A	120	7	114	10	172	20
48171	78_1	UBE3A	136	31	103	20	169	11
48172	82_2	UBE3A	96	11	121	4	186	32
48172	84_1	UBE3A	95	14	100	8	158	14
49343	85_1	UBE3A	97	22	121	10	189	17
49722	87_1	UBE3A	111	9	126	11	177	22
52417	92_1	UBE3A	133	7	140	30	140	8
52417	92_1	UBE3A-SUP	88	14	80	14	82	8
52417	92_1	SNORD115	102	8	114	20	91	9
52420	93_1	UBE3A	111	14	120	9	126	16
52420	93_1	UBE3A-SUP	104	23	82	20	79	8
52420	93_1	SNORD115	110	11	114	17	95	7
53953	94_1	UBE3A	117	12	147	15	166	15
53953	94_1	UBE3A-SUP	92	18	81	5	86	22

Start SEQ ID NO 1	CMP ID NO	Target	% of Mock Oligo conc 0.2 µM	sd	% of Mock Oligo conc 1.0 µM	sd	% of Mock Oligo conc 5.0 µM	sd
53953	94_1	SNORD115	124	33	122	17	106	14
60819	95_1	UBE3A	103	11	131	14	175	7
60819	95_1	UBE3A-SUP	93	13	87	3	74	6
60819	95_1	SNORD115	162	19	158	20	201	11
60819	95_2	UBE3A	147	10	129	20	117	2
60819	95_2	UBE3A-SUP	118	24	87	13	83	8
60819	95_2	SNORD115	104	17	118	10	129	6
60823	96_1	UBE3A	115	16	135	19	174	17
60823	96_1	UBE3A-SUP	104	25	93	32	91	11
60823	96_2	UBE3A	108	7	114	9	115	13
60823	96_2	UBE3A-SUP	99	17	92	19	93	10
60824	97_1	UBE3A	111	12	134	23	169	14
60824	97_1	UBE3A-SUP	110	27	105	33	92	10
60824	97_2	UBE3A	124	13	126	12	124	11
60824	97_2	UBE3A-SUP	113	17	107	33	96	20
60824	98_1	UBE3A	111	16	119	11	138	14
60824	98_1	UBE3A-SUP	118	34	98	23	82	19
60824	98_1	SNORD115	109	11	123	18	114	16
60824	98_2	UBE3A	128	10	109	7	136	12
60824	98_2	UBE3A-SUP	91	15	77	11	110	16
60824	98_2	SNORD115	101	3	110	7	124	11
60825	99_1	UBE3A	125	6	115	5	131	10
60825	99_1	UBE3A-SUP	139	18	121	34	127	45
60825	99_1	SNORD115	110	18	112	12	99	19
60825	99_2	UBE3A	120	21	111	11	135	22
60825	99_2	UBE3A-SUP	96	21	79	15	75	11
60825	99_2	SNORD115	104	34	113	22	131	24
60825	100_1	UBE3A	123	34	139	34	145	21
60825	100_1	UBE3A-SUP	104	37	127	46	99	17
60825	100_2	UBE3A	124	46	138	37	145	31
60825	100_2	UBE3A-SUP	111	36	120	47	92	11
60825	101_1	UBE3A	112	18	123	15	150	13
60825	101_1	UBE3A-SUP	96	18	102	14	88	12
60825	101_2	UBE3A	118	15	138	24	139	32
60825	101_2	UBE3A-SUP	100	29	110	39	92	10
60826	102_1	UBE3A	132	17	120	7	125	9
60826	102_1	UBE3A-SUP	113	16	83	5	88	18
60826	102_1	SNORD115	121	36	131	23	100	9
60826	102_2	UBE3A	90	6	116	23	103	7
60826	102_2	UBE3A-SUP	91	7	90	12	64	18

Start SEQ ID NO 1	CMP ID NO	Target	% of Mock Oligo conc 0.2 µM	sd	% of Mock Oligo conc 1.0 µM	sd	% of Mock Oligo conc 5.0 µM	sd
60826	102_2	SNORD115	116	15	146	27	183	28
60827	103_1	UBE3A	106	8	112	10	115	9
60827	103_1	UBE3A-SUP	99	15	110	28	94	8
60827	103_2	UBE3A	107	14	120	13	112	14
60827	103_2	UBE3A-SUP	97	14	118	38	93	20
60827	104_1	UBE3A	128	14	111	9	111	6
60827	104_1	UBE3A-SUP	111	12	97	9	87	19
60827	104_1	SNORD115	114	10	110	12	109	13
60827	104_2	UBE3A	108	10	111	16	109	10
60827	104_2	UBE3A-SUP	103	13	103	33	89	9
60827	105_1	UBE3A	122	13	121	12	121	4
60827	105_1	UBE3A-SUP	119	7	97	15	93	7
60827	105_1	SNORD115	114	21	128	12	118	9
60827	105_2	UBE3A	123	5	110	9	114	8
60827	105_2	UBE3A-SUP	110	11	89	17	94	21
60827	105_2	SNORD115	102	15	108	16	107	18
60827	106_1	UBE3A	114	17	133	23	125	9
60827	106_1	UBE3A-SUP	112	35	103	15	87	12
60827	106_2	UBE3A	110	12	130	22	123	14
60827	106_2	UBE3A-SUP	105	19	107	27	93	10
60828	107_1	UBE3A	83	11	117	13	112	6
60828	107_1	UBE3A-SUP	86	11	114	16	67	7
60828	107_1	SNORD115	108	17	130	21	137	24
60828	107_2	UBE3A	143	42	117	10	122	11
60828	107_2	UBE3A-SUP	116	12	92	4	100	8
60828	107_2	SNORD115	108	4	127	16	108	14
60828	108_1	UBE3A	120	7	127	31	132	31
60828	108_1	UBE3A-SUP	153	33	118	34	89	17
60828	108_1	SNORD115	114	9	114	9	105	15
60828	108_2	UBE3A	122	18	133	26	128	9
60828	108_2	UBE3A-SUP	101	19	100	28	89	17
60828	109_1	UBE3A	108	10	129	14	128	5
60828	109_1	UBE3A-SUP	106	21	107	24	84	8
60828	109_2	UBE3A	109	11	110	8	111	13
60828	109_2	UBE3A-SUP	95	15	86	14	83	9
60829	110_1	UBE3A	104	6	83	3	101	15
60829	110_1	UBE3A-SUP	100	13	95	12	79	4
60829	110_1	SNORD115	126	21	125	6	182	13
60829	110_2	UBE3A	92	7	87	8	96	7
60829	110_2	UBE3A-SUP	99	7	108	9	81	5

Start SEQ ID NO 1	CMP ID NO	Target	% of Mock Oligo conc 0.2 µM	sd	% of Mock Oligo conc 1.0 µM	sd	% of Mock Oligo conc 5.0 µM	sd
60829	110_2	SNORD115	118	15	139	22	198	39
60830	111_1	UBE3A	110	6	122	13	124	10
60830	111_1	UBE3A-SUP	104	14	90	28	79	11
60830	111_2	UBE3A	115	10	120	15	121	10
60830	111_2	UBE3A-SUP	114	20	89	19	87	9
60831	112_1	UBE3A	93	8	94	13	106	10
60831	112_1	UBE3A-SUP	97	1	68	29	82	7
60831	112_1	SNORD115	116	20	110	13	158	20
60831	112_2	UBE3A	83	8	78	7	83	6
60831	112_2	UBE3A-SUP	106	35	80	23	69	9
60831	112_2	SNORD115	107	6	106	8	159	21
62198	113_1	UBE3A	110	3	122	6	134	9
62198	113_1	UBE3A-SUP	113	20	85	19	79	24
62198	113_1	SNORD115	116	18	123	9	91	9
62284	115_1	UBE3A	105	14	98	19	141	36
62422	116_1	UBE3A	130	19	142	29	172	18
62423	117_1	UBE3A	76	8	93	13	171	17
62439	118_1	UBE3A	75	7	88	9	150	19
66378	119_1	UBE3A	96	14	93	5	110	10
77565	126_1	UBE3A	94	6	113	5	125	14
77565	126_1	UBE3A-SUP	83	17	95	33	85	5
77565	126_1	SNORD115	105	11	123	19	152	15
77565	126_2	UBE3A	95	5	126	9	111	2
77565	126_2	UBE3A-SUP	77	27	106	21	83	15
77565	126_2	SNORD115	115	17	157	13	180	15
92321	128_1	UBE3A	102	7	91	5	111	13
92321	128_1	UBE3A-SUP	115	3	104	25	91	13
92321	128_1	SNORD115	135	9	132	12	196	35
92321	128_2	UBE3A	91	5	96	8	104	8
92321	128_2	UBE3A-SUP	112	20	92	20	79	7
92321	128_2	SNORD115	125	7	111	13	169	12
92322	129_1	UBE3A	101	5	103	2	110	7
92322	129_1	UBE3A-SUP	99	39	113	12	94	13
92322	129_1	SNORD115	124	25	114	6	140	13
92322	129_2	UBE3A	93	2	100	4	113	16
92322	129_2	UBE3A-SUP	109	4	102	22	85	7
92322	129_2	SNORD115	103	11	99	9	152	31
97154	132_1	UBE3A	100	10	128	13	142	13
97154	132_1	UBE3A-SUP	103	9	115	8	109	6
97154	132_1	SNORD115	49	7	90	12	143	25

Start SEQ ID NO 1	CMP ID NO	Target	% of Mock Oligo conc 0.2 µM	sd	% of Mock Oligo conc 1.0 µM	sd	% of Mock Oligo conc 5.0 µM	sd
97154	132_2	UBE3A	111	8	128	17	128	17
97154	132_2	UBE3A-SUP	95	7	116	9	105	13
97154	133_2	SNORD115	86	7	106	9	121	9
97154	133_1	UBE3A	101	3	107	11	124	19
97154	133_1	UBE3A-SUP	112	9	117	7	146	25
97154	133_1	SNORD115	60	7	110	15	141	15
97154	133_2	UBE3A	94	13	116	14	138	12
97154	133_2	UBE3A-SUP	116	6	128	13	148	38
97154	132_2	SNORD115	70	5	108	9	160	34
106137	137_1	UBE3A	83	12	74	11	124	20
109404	138_1	UBE3A	80	20	92	7	120	21
110766	139_1	UBE3A	76	5	85	12	121	17
114826	140_1	UBE3A	87	10	88	11	136	9
118637	143_1	UBE3A	83	7	104	30	141	28
118639	144_1	UBE3A	74	17	31	39	106	33
124160	145_2	UBE3A	89	6	95	10	115	25
125499	146_1	UBE3A	83	13	76	7	124	16
125499	146_2	UBE3A	123	30	79	14	102	23
125538	150_2	UBE3A	82	17	82	7	119	24

[0308] Of the 187 compounds tested approximately 90 % showed re-expression of UBE3A when compared to the mock oligonucleotide at the 5 micro Molar concentration. The number of oligonucleotides capable of inducing re-expression of UBE3A is higher in the region between position 1 to 55318 of SEQ ID NO: 1 (non-overlapping region) then in the region complementary to UBE3A coding region (overlapping region. Figure 2 plots the distribution of the oligonucleotides according to their position on chromosome 15 versus the UBE3A mRNA expression relative to the mock oligonucleotide.

[0309] For the oligonucleotides where SNORD115 has been tested there is no significant down regulation when compared to mock at 1 and 5 microM.

Example 3 - Activity of oligonucleotides targeting the SNHG14 transcript in the region downstream of SNORD109B and upstream of the region antisense to to the UBE3A pre-mRNA

[0310] Oligonucleotides targeting position 4806-54939 of SEQ ID NO: 1 were tested in patient derived human neuronal cell cultures (see protocol in "Materials and methods" section). The oligonucleotides ability to reduce the SNHG14 transcript in the region downstream of SNORD109B (also termed UBE3A suppressor or UBE3A-SUP in the data table. Furthermore, the ability to induce UBE3A mRNA re-expression was analyzed.

[0311] The oligonucleotides were screened according to the protocol for screening oligonucleotides in human neuronal cell cultures described in the section "Materials and methods" - "Screening oligonucleotides in human neuronal cell cultures - 96 well system"

[0312] The results are shown in table 6.

Table 6: Oligonucleotide activity in patient derived human neuronal cell cultures.

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
4806	151_1	0,2	66	2	125	NA

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
4806	151_1	1	53	10	NA	NA
4808	152_1	0,2	49	6	167	NA
4808	152_1	1	33	4	289	NA
4809	153_1	0,2	41	1	208	NA
4809	153_1	1	29	10	NA	NA
4811	154_1	0,2	48	3	282	NA
4811	154_1	1	37	5	331	NA
4812	155_1	0,2	35	5	286	64
4812	155_1	1	32	3	327	21
4972	156_1	0,2	60	6	145	6
4972	156_1	1	46	14	145	NA
4973	157_1	0,2	75	9	128	6
4973	157_1	1	59	NA	158	NA
4979	158_1	0,2	46	9	131	NA
4979	158_1	1	37	5	219	8
5058	159_1	0,2	69	6	133	19
5058	159_1	1	51	14	NA	NA
5071	160_1	0,2	55	8	98	NA
5071	160_1	1	39	7	136	34
5078	161_1	0,2	65	7	205	18
5078	161_1	1	51	10	306	31
5094	162_1	0,2	53	5	154	27
5094	162_1	1	34	8	300	65
5096	163_1	0,2	44	1	206	49
5096	163_1	1	36	6	316	NA
5100	164_1	0,2	34	3	220	NA
5100	164_1	1	30	3	227	32
5101	165_1	0,2	38	7	245	NA
5101	165_1	1	36	4	246	55
5218	166_1	0,2	45	4	240	NA
5218	166_1	1	36	6	280	44
5218	167_1	0,2	46	2	261	NA
5218	167_1	1	31	4	346	30
5224	168_1	0,2	39	3	377	40
5224	168_1	1	33	5	338	65
5224	169_1	0,2	37	4	313	NA
5224	169_1	1	31	2	308	3
5427	170_1	0,2	89	13	105	26

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
5427	170_1	1	117	35	124	NA
5434	171_1	0,2	51	5	164	10
5434	171_1	1	33	6	213	46
5785	172_1	0,2	46	5	210	NA
5785	172_1	1	38	4	342	NA
5786	173_1	0,2	54	4	292	61
5786	173_1	1	39	6	552	NA
6341	174_1	0,2	97	11	126	3
6341	174_1	1	90	33	NA	NA
6694	175_1	0,2	44	4	226	NA
6694	175_1	1	35	4	296	NA
6695	176_1	0,2	32	7	297	87
6695	176_1	1	29	4	263	9
6958	177_1	0,2	58	7	244	76
6958	177_1	1	47	NA	NA	NA
7159	179_1	0,2	33	4	282	NA
7159	179_1	1	29	5	289	7
7159	178_1	0,2	43	5	248	NA
7159	178_1	1	32	4	258	NA
7720	180_1	0,2	75	6	144	36
7720	180_1	1	54	7	233	26
7724	181_1	0,2	72	6	177	20
7724	181_1	1	45	19	224	62
7725	182_1	0,2	65	5	139	37
7725	182_1	1	47	4	208	76
7725	183_1	0,2	103	13	140	2
7725	183_1	1	74	6	NA	NA
7727	184_1	0,2	45	2	300	107
7727	184_1	1	35	2	272	16
8117	185_1	0,2	87	17	122	13
8117	185_1	1	63	17	175	NA
8118	186_1	0,2	40	5	368	105
8118	186_1	1	33	5	NA	NA
8119	187_1	0,2	62	5	197	NA
8119	187_1	1	43	13	517	143
8120	188_1	0,2	96	10	136	41
8120	188_1	1	79	22	146	19
8571	189_1	0,2	53	11	204	NA

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
8571	189_1	1	49	24	298	15
8573	190_1	0,2	54	9	140	9
8573	190_1	1	50	10	267	4
8574	191_1	0,2	56	1	117	NA
8574	191_1	1	57	13	199	NA
8575	192_1	0,2	56	9	165	10
8575	192_1	1	54	13	246	NA
8576	193_1	0,2	56	6	185	7
8576	193_1	1	52	8	330	35
8585	194_1	0,2	47	2	302	NA
8585	194_1	1	39	7	NA	NA
8819	195_1	0,2	62	10	155	10
8819	195_1	1	41	3	192	7
8820	196_1	0,2	55	12	237	69
8820	196_1	1	40	3	278	26
8887	197_1	0,2	69	15	301	59
8887	197_1	1	58	7	383	92
9150	198_1	0,2	49	6	NA	NA
9150	198_1	1	43	3	365	38
9201	199_1	0,2	79	23	88	42
9201	199_1	1	64	24	140	22
9202	201_1	0,2	61	10	NA	NA
9202	201_1	1	45	8	343	27
9202	200_1	0,2	47	3	287	76
9202	200_1	1	41	4	281	NA
9203	202_1	0,2	55	17	166	92
9203	202_1	1	40	5	297	54
9209	203_1	0,2	60	1	122	NA
9209	203_1	1	40	14	204	8
9210	204_1	0,2	43	2	216	NA
9210	204_1	1	37	3	409	NA
9210	205_1	0,2	45	8	187	NA
9210	205_1	1	37	22	336	18
9211	206_1	0,2	51	10	384	17
9211	206_1	1	42	3	381	35
9211	207_1	0,2	65	8	301	28
9211	207_1	1	50	5	272	53
9212	35_2	0,2	42	11	203	16

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc μM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
9212	35_2	1	44	18	335	NA
9212	208_1	0,2	64	5	147	58
9212	208_1	1	50	6	260	73
9213	209_1	0,2	57	7	NA	NA
9213	209_1	1	49	4	346	31
9214	210_1	0,2	49	7	139	NA
9214	210_1	1	45	7	223	59
10832	211_1	0,2	70	6	147	10
10832	211_1	1	56	9	200	38
10837	212_1	0,2	59	9	146	46
10837	212_1	1	41	6	226	47
10838	213_1	0,2	50	8	247	69
10838	213_1	1	44	12	307	NA
10877	214_1	0,2	108	21	115	1
10877	214_1	1	92	37	88	32
11434	215_1	0,2	97	12	81	23
11434	215_1	1	80	26	111	11
11435	216_1	0,2	90	16	87	NA
11435	216_1	1	82	29	82	21
11436	217_1	0,2	87	6	83	11
11436	217_1	1	68	26	123	NA
11438	218_1	0,2	57	5	133	NA
11438	218_1	1	44	16	188	NA
11439	219_1	0,2	84	1	93	NA
11439	219_1	1	66	22	113	29
11464	220_1	0,2	67	9	209	51
11464	220_1	1	41	6	256	33
11507	221_1	0,2	59	6	237	NA
11507	221_1	1	40	63	320	NA
11508	222_1	0,2	53	7	195	NA
11508	222_1	1	48	12	302	NA
11511	223_1	0,2	41	3	210	6
11511	223_1	1	37	9	273	NA
11513	224_1	0,2	22	8	288	91
11513	224_1	1	26	5	360	46
11514	225_1	0,2	98	17	98	31
11514	225_1	1	68	16	129	11
11736	226_1	0,2	69	8	197	80

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc μM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
11736	226_1	1	55	7	329	66
12361	227_1	0,2	48	8	183	56
12361	227_1	1	37	4	193	46
12794	228_1	0,2	38	9	201	71
12794	228_1	1	32	2	362	48
12795	229_1	0,2	50	12	161	30
12795	229_1	1	34	7	301	35
12796	230_1	0,2	44	12	237	86
12796	230_1	1	32	3	379	106
12894	232_1	0,2	91	17	79	27
12894	232_1	1	66	10	99	24
12894	231_1	0,2	80	5	89	NA
12894	231_1	1	57	14	164	31
12895	234_1	0,2	88	11	75	32
12895	234_1	1	68	19	91	24
12895	233_1	0,2	57	5	199	37
12895	233_1	1	38	7	249	57
12896	235_1	0,2	72	3	176	9
12896	235_1	1	45	3	251	42
13223	236_1	0,2	40	3	267	66
13223	236_1	1	31	3	270	23
13224	238_1	0,2	33	3	265	NA
13224	238_1	1	28	4	265	6
13224	237_1	0,2	38	2	212	NA
13224	237_1	1	31	1	254	31
13225	239_1	0,2	42	5	317	113
13225	239_1	1	29	7	215	26
13226	240_1	0,2	38	7	223	NA
13226	240_1	1	32	5	232	16
15115	241_1	0,2	61	8	377	15
15115	241_1	1	41	3	377	43
15258	242_1	0,2	66	14	133	35
15258	242_1	1	55	10	170	17
15568	243_1	0,2	62	13	192	58
15568	243_1	1	41	11	309	5
15570	244_1	0,2	53	17	252	59
15570	244_1	1	44	5	332	52
15572	245_1	0,2	57	21	321	122

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc μM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
15572	245_1	1	49	7	407	77
15573	246_1	0,2	47	16	348	129
15573	246_1	1	40	7	410	69
15574	247_1	0,2	48	14	326	116
15574	247_1	1	44	8	411	36
15722	248_1	0,2	51	3	258	17
15722	248_1	1	36	3	230	NA
16597	249_1	0,2	66	19	111	39
16597	249_1	1	54	14	174	44
16603	250_1	0,2	67	26	89	31
16603	250_1	1	56	6	172	32
16730	251_1	0,2	36	5	354	41
16730	251_1	1	31	2	326	75
16849	252_1	0,2	74	17	188	81
16849	252_1	1	48	17	282	1
17089	253_1	0,2	70	17	98	37
17089	253_1	1	62	19	153	13
17401	254_1	0,2	42	6	209	83
17401	254_1	1	29	3	327	49
24290	255_1	0,2	106	13	105	36
24290	255_1	1	109	21	136	NA
24296	256_1	0,2	92	20	117	30
24296	256_1	1	93	15	138	21
24811	257_1	0,2	85	12	126	4
24811	257_1	1	74	12	137	17
25032	258_1	0,2	50	11	329	131
25032	258_1	1	39	5	411	53
25033	259_1	0,2	40	10	343	50
25033	259_1	1	31	3	483	84
25250	260_1	0,2	33	10	279	42
25250	260_1	1	33	4	338	65
25251	261_1	0,2	40	8	209	97
25251	261_1	1	34	3	370	57
25718	262_1	0,2	56	20	113	48
25718	262_1	1	45	8	198	65
25720	263_1	0,2	84	7	121	39
25720	263_1	1	72	11	88	10
25721	264_1	0,2	83	15	87	40

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
25721	264_1	1	84	22	NA	NA
26331	265_1	0,2	93	5	88	38
26331	265_1	1	81	8	NA	NA
27165	266_1	0,2	63	3	117	39
27165	266_1	1	46	9	174	15
27248	267_1	0,2	81	10	124	17
27248	267_1	1	59	10	190	112
29330	268_1	0,2	109	4	124	48
29330	268_1	1	98	28	114	35
29635	269_1	0,2	45	1	218	50
29635	269_1	1	33	9	267	NA
29635	270_1	0,2	55	5	225	41
29635	270_1	1	45	8	NA	NA
29636	271_1	0,2	48	2	285	56
29636	271_1	1	40	7	359	99
29636	272_1	0,2	48	3	166	5
29636	272_1	1	35	8	293	40
29637	273_1	0,2	56	5	255	47
29637	273_1	1	46	4	300	105
29637	274_1	0,2	67	7	134	35
29637	274_1	1	54	7	234	19
29661	275_1	0,2	51	3	167	15
29661	275_1	1	42	11	251	NA
29661	276_1	0,2	54	5	127	17
29661	276_1	1	39	8	229	NA
29684	277_1	0,2	40	3	168	73
29684	277_1	1	31	13	NA	NA
29684	278_1	0,2	46	7	179	2
29684	278_1	1	36	8	NA	NA
30455	279_1	0,2	102	20	96	34
30455	279_1	1	86	22	118	23
30456	280_1	0,2	94	23	91	28
30456	280_1	1	83	18	134	36
30457	281_1	0,2	89	23	97	37
30457	281_1	1	94	23	106	39
30458	282_1	0,2	99	14	77	27
30458	282_1	1	103	17	96	20
30462	283_1	0,2	66	26	98	36

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
30462	283_1	1	56	14	129	13
30465	284_1	0,2	73	11	114	47
30465	284_1	1	57	10	197	63
30601	285_1	0,2	41	31	311	29
30601	285_1	1	30	16	373	40
30605	286_1	0,2	40	2	221	86
30605	286_1	1	33	6	375	NA
30609	287_1	0,2	43	3	267	65
30609	287_1	1	37	5	332	27
30610	288_1	0,2	46	6	253	79
30610	288_1	1	38	3	338	NA
30667	289_1	0,2	38	15	325	144
30667	289_1	1	36	3	461	68
30668	290_1	0,2	74	19	124	54
30668	290_1	1	58	14	183	20
30669	291_1	0,2	86	18	98	40
30669	291_1	1	78	12	133	26
30670	292_1	0,2	93	10	86	31
30670	292_1	1	94	16	127	22
30679	293_1	0,2	85	19	83	21
30679	293_1	1	87	21	113	23
30681	294_1	0,2	92	17	78	20
30681	294_1	1	100	19	86	22
30682	295_1	0,2	93	22	101	40
30682	295_1	1	94	33	101	8
30699	296_1	0,2	80	24	134	6
30699	296_1	1	47	21	232	36
30700	297_1	0,2	53	5	146	26
30700	297_1	1	32	8	NA	NA
30700	298_1	0,2	47	4	221	NA
30700	298_1	1	38	0	294	NA
30701	299_1	0,2	49	4	140	NA
30701	299_1	1	23	NA	NA	NA
30701	300_1	0,2	50	9	163	19
30701	300_1	1	39	11	346	11
30702	301_1	0,2	66	9	116	36
30702	301_1	1	44	14	230	51
30711	302_1	0,2	41	14	288	120

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc μM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
30711	302_1	1	40	5	422	132
30714	303_1	0,2	45	9	355	94
30714	303_1	1	31	5	355	8
30715	305_1	0,2	39	4	292	56
30715	305_1	1	34	12	253	5
30715	304_1	0,2	50	13	263	87
30715	304_1	1	43	7	285	12
31630	306_1	0,2	92	32	134	48
31630	306_1	1	85	25	177	26
31632	307_1	0,2	94	24	92	32
31632	307_1	1	86	17	109	33
31633	308_1	0,2	92	18	78	13
31633	308_1	1	102	23	98	7
32755	310_1	0,2	47	12	220	40
32755	310_1	1	40	16	285	NA
32755	309_1	0,2	62	6	167	NA
32755	309_1	1	40	10	225	NA
32756	311_1	0,2	55	9	128	9
32756	311_1	1	56	NA	224	NA
33366	312_1	0,2	64	23	121	4
33366	312_1	1	56	10	137	1
33367	313_1	0,2	81	7	91	NA
33367	313_1	1	79	22	115	12
33368	314_1	0,2	70	4	103	NA
33368	314_1	1	57	15	157	NA
33369	315_1	0,2	73	12	87	20
33369	315_1	1	67	19	155	NA
33375	316_1	0,2	79	18	100	18
33375	316_1	1	51	14	159	39
33377	317_1	0,2	46	21	248	72
33377	317_1	1	41	9	313	NA
33378	318_1	0,2	38	17	273	63
33378	318_1	1	36	7	321	1
36606	319_1	0,2	79	10	154	21
36606	319_1	1	48	9	233	65
36607	320_1	0,2	60	9	157	18
36607	320_1	1	49	9	206	25
38092	321_1	0,2	51	10	221	59

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
38092	321_1	1	41	5	328	39
38297	322_1	0,2	43	9	298	31
38297	322_1	1	34	6	365	91
39173	323_1	0,2	98	8	119	27
39173	323_1	1	82	20	177	21
39174	324_1	0,2	89	8	139	24
39174	324_1	1	84	23	192	15
39175	325_1	0,2	93	18	167	13
39175	325_1	1	68	17	203	33
39176	326_1	0,2	79	12	185	83
39176	326_1	1	55	17	374	107
39228	327_1	0,2	75	12	151	29
39228	327_1	1	57	8	207	32
39230	328_1	0,2	65	11	176	19
39230	328_1	1	52	19	357	NA
39231	329_1	0,2	63	19	150	35
39231	329_1	1	46	6	257	43
39563	330_1	0,2	69	10	116	34
39563	330_1	1	56	11	196	NA
39808	331_1	0,2	40	8	201	17
39808	331_1	1	25	5	300	NA
39808	332_1	0,2	40	14	282	109
39808	332_1	1	33	7	404	81
39931	333_1	0,2	80	11	107	53
39931	333_1	1	70	16	112	26
41114	334_1	0,2	64	4	113	NA
41114	334_1	1	28	NA	179	NA
41444	335_1	0,2	57	17	165	39
41444	335_1	1	46	4	290	40
41445	336_1	0,2	51	2	134	NA
41445	336_1	1	42	15	238	NA
41446	337_1	0,2	63	1	108	NA
41446	337_1	1	56	14	151	22
41725	338_1	0,2	91	16	130	50
41725	338_1	1	75	23	154	27
41726	339_1	0,2	66	20	142	23
41726	339_1	1	55	14	193	NA
41728	340_1	0,2	60	16	137	23

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
41728	340_1	1	51	13	233	NA
42167	341_1	0,2	70	9	138	7
42167	341_1	1	51	11	182	20
42168	343_1	0,2	67	9	210	92
42168	343_1	1	52	6	193	NA
42168	342_1	0,2	51	6	183	NA
42168	342_1	1	46	10	275	14
42169	344_1	0,2	55	1	231	32
42169	344_1	1	35	3	NA	NA
42169	345_1	0,2	55	7	164	41
42169	345_1	1	45	5	284	27
42287	346_1	0,2	66	7	144	32
42287	346_1	1	53	5	279	34
42289	347_1	0,2	75	20	125	10
42289	347_1	1	68	7	241	69
43452	348_1	0,2	62	12	231	92
43452	348_1	1	48	23	257	72
43453	349_1	0,2	52	11	142	41
43453	349_1	1	44	23	257	34
43562	350_1	0,2	50	13	148	35
43562	350_1	1	36	10	NA	NA
43565	351_1	0,2	71	10	116	43
43565	351_1	1	60	11	154	37
43566	352_1	0,2	65	19	139	14
43566	352_1	1	44	8	255	23
43634	353_1	0,2	63	25	172	75
43634	353_1	1	51	22	214	NA
44180	355_1	0,2	60	6	165	8
44180	355_1	1	57	25	145	NA
44180	354_1	0,2	76	17	149	55
44180	354_1	1	48	10	240	29
44181	356_1	0,2	60	5	170	27
44181	356_1	1	43	15	154	55
44183	357_1	0,2	50	15	214	33
44183	357_1	1	37	17	196	19
44184	358_1	0,2	57	5	155	31
44184	358_1	1	47	10	257	94
44439	359_1	0,2	46	4	220	53

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc μM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
44439	359_1	1	45	2	347	52
44440	360_1	0,2	48	9	261	37
44440	360_1	1	44	6	NA	NA
44440	361_1	0,2	43	5	218	46
44440	361_1	1	29	3	291	19
44441	362_1	0,2	50	5	192	60
44441	362_1	1	45	7	290	58
44441	363_1	0,2	45	10	185	51
44441	363_1	1	43	10	247	NA
44442	364_1	0,2	54	8	124	24
44442	364_1	1	39	5	271	54
44442	365_1	0,2	59	6	166	9
44442	365_1	1	44	8	313	47
44443	367_1	0,2	55	10	161	29
44443	367_1	1	40	7	314	67
44443	366_1	0,2	51	5	202	44
44443	366_1	1	41	10	300	31
44477	368_1	0,2	73	6	155	58
44477	368_1	1	52	3	362	141
44478	369_1	0,2	82	18	130	35
44478	369_1	1	58	11	228	66
44776	370_1	0,2	60	7	128	20
44776	370_1	1	46	5	274	NA
45216	371_1	0,2	50	10	149	33
45216	371_1	1	41	8	260	59
45217	372_1	0,2	59	7	132	45
45217	372_1	1	39	4	270	12
45217	373_1	0,2	47	3	167	52
45217	373_1	1	38	4	330	62
45218	374_1	0,2	51	9	189	27
45218	374_1	1	42	9	359	93
45246	375_1	0,2	61	8	175	29
45246	375_1	1	50	7	257	NA
45247	376_1	0,2	84	4	116	40
45247	376_1	1	74	10	144	NA
45248	378_1	0,2	61	10	226	2
45248	378_1	1	50	5	367	141
45248	377_1	0,2	74	11	138	29

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
45248	377_1	1	62	4	251	NA
45249	379_1	0,2	48	5	232	NA
45249	379_1	1	50	NA	312	NA
45249	380_1	0,2	54	4	203	16
45249	380_1	1	53	1	353	12
45250	381_1	0,2	48	6	230	25
45250	381_1	1	40	7	387	79
45250	382_1	0,2	60	7	153	30
45250	382_1	1	46	3	288	43
45258	383_1	0,2	46	4	211	NA
45258	383_1	1	34	6	307	29
45266	385_1	0,2	80	34	85	8
45266	385_1	1	55	13	128	25
45266	384_1	0,2	92	4	128	50
45266	384_1	1	79	12	108	23
45267	386_1	0,2	93	23	105	13
45267	386_1	1	80	23	139	14
45268	387_1	0,2	90	17	111	1
45268	387_1	1	109	9	122	44
45270	388_1	0,2	97	7	146	47
45270	388_1	1	88	9	113	22
45271	390_1	0,2	79	12	141	14
45271	390_1	1	58	14	197	38
45271	389_1	0,2	70	3	97	28
45271	389_1	1	53	6	150	26
45272	391_1	0,2	61	4	128	24
45272	391_1	1	55	14	208	39
45560	392_1	0,2	86	22	97	26
45560	392_1	1	71	19	125	18
45627	393_1	0,2	48	14	150	64
45627	393_1	1	39	1	209	35
45628	394_1	0,2	51	4	174	34
45628	394_1	1	44	8	309	30
45629	395_1	0,2	60	5	151	24
45629	395_1	1	48	7	297	43
45629	396_1	0,2	86	24	139	55
45629	396_1	1	64	13	203	38
45635	397_1	0,2	50	10	289	61

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc μM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
45635	397_1	1	46	2	401	56
45709	398_1	0,2	47	6	207	61
45709	398_1	1	49	6	233	NA
45709	399_1	0,2	56	6	206	13
45709	399_1	1	45	4	287	93
46215	400_1	0,2	78	14	122	13
46215	400_1	1	60	9	114	19
46256	401_1	0,2	62	7	164	56
46256	401_1	1	45	5	213	20
46257	404_1	0,2	44	4	207	44
46257	404_1	1	41	3	288	45
46257	402_1	0,2	48	5	197	57
46257	402_1	1	41	1	300	11
46257	403_1	0,2	51	4	265	50
46257	403_1	1	44	5	382	NA
46259	405_1	0,2	46	4	NA	NA
46259	405_1	1	39	10	359	10
46260	406_1	0,2	52	9	153	63
46260	406_1	1	48	7	262	71
46263	407_1	0,2	52	9	148	9
46263	407_1	1	41	5	262	45
46264	408_1	0,2	51	17	269	72
46264	408_1	1	42	8	280	55
46392	409_1	0,2	38	10	359	91
46392	409_1	1	38	8	NA	NA
46393	410_1	0,2	39	12	295	30
46393	410_1	1	32	12	NA	NA
46420	411_1	0,2	75	10	69	3
46420	411_1	1	86	3	101	21
46505	412_1	0,2	65	11	97	7
46505	412_1	1	53	5	226	59
46505	413_1	0,2	74	16	124	19
46505	413_1	1	69	13	117	11
46506	414_1	0,2	75	7	149	17
46506	414_1	1	71	10	169	118
46507	415_1	0,2	86	31	119	36
46507	415_1	1	66	17	129	28
46508	416_1	0,2	86	22	87	22

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc μM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
46508	416_1	1	67	10	142	16
47364	417_1	0,2	49	2	166	22
47364	417_1	1	47	13	295	NA
47365	418_1	0,2	54	3	131	29
47365	418_1	1	41	3	230	42
48110	419_1	0,2	77	9	101	45
48110	419_1	1	58	8	178	68
48111	420_1	0,2	63	7	121	32
48111	420_1	1	51	2	238	59
48186	421_1	0,2	69	5	176	52
48186	421_1	1	44	12	307	62
48221	422_1	0,2	58	15	149	63
48221	422_1	1	39	6	235	50
48222	423_1	0,2	60	12	143	9
48222	423_1	1	43	10	209	57
49345	85_2	0,2	43	14	242	38
49345	85_2	1	37	5	275	NA
50282	424_1	0,2	75	20	138	19
50282	424_1	1	56	9	226	62
51241	426_1	0,2	61	6	144	NA
51241	426_1	1	46	9	264	44
51241	425_1	0,2	46	8	164	22
51241	425_1	1	44	4	244	35
51242	428_1	0,2	57	6	138	30
51242	428_1	1	48	7	290	39
51242	427_1	0,2	40	15	341	NA
51242	427_1	1	30	8	286	63
51244	429_1	0,2	46	5	184	25
51244	429_1	1	44	6	283	4
51245	430_1	0,2	47	7	203	9
51245	430_1	1	37	5	271	29
51358	431_1	0,2	51	7	265	10
51358	431_1	1	40	4	363	70
51358	432_1	0,2	60	4	202	51
51358	432_1	1	37	7	275	NA
51359	433_1	0,2	40	3	238	20
51359	433_1	1	32	3	NA	NA
51359	434_1	0,2	39	6	424	83

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
51359	434_1	1	35	6	360	NA
51438	435_1	0,2	78	15	144	62
51438	435_1	1	60	14	201	27
51438	436_1	0,2	71	4	125	32
51438	436_1	1	54	6	205	71
51953	437_1	0,2	46	6	217	35
51953	437_1	1	37	4	277	52
52150	438_1	0,2	67	6	131	39
52150	438_1	1	53	13	177	NA
52549	439_1	0,2	56	5	162	31
52549	439_1	1	50	10	215	39
52550	440_1	0,2	69	13	137	40
52550	440_1	1	50	5	156	53
52551	441_1	0,2	66	3	132	8
52551	441_1	1	49	5	169	27
52579	442_1	0,2	38	7	280	60
52579	442_1	1	37	5	257	51
53012	443_1	0,2	79	10	197	61
53012	443_1	1	65	7	212	36
53013	445_1	0,2	64	6	211	13
53013	445_1	1	56	4	264	42
53013	444_1	0,2	68	11	137	33
53013	444_1	1	58	9	198	35
53014	446_1	0,2	59	6	125	NA
53014	446_1	1	47	3	216	22
53014	447_1	0,2	53	2	188	94
53014	447_1	1	51	10	192	47
54198	448_1	0,2	54	15	161	66
54198	448_1	1	48	11	243	NA
54199	449_1	0,2	63	12	166	20
54199	449_1	1	45	8	185	41
54232	450_1	0,2	84	17	112	67
54232	450_1	1	83	8	157	15
54233	451_1	0,2	67	14	118	44
54233	451_1	1	51	8	192	34
54235	452_1	0,2	50	3	162	NA
54235	452_1	1	42	7	190	NA
54236	453_1	0,2	47	21	234	17

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
54236	453_1	1	42	5	295	NA
54238	454_1	0,2	76	14	85	NA
54238	454_1	1	48	12	162	NA
54239	455_1	0,2	62	6	132	69
54239	455_1	1	46	7	149	57
54609	456_1	0,2	66	10	130	57
54609	456_1	1	56	11	141	60
54924	457_1	0,2	78	3	137	29
54924	457_1	1	61	4	178	25

Example 4 - Activity of oligonucleotides targeting the SNHG14 transcript in the region antisense to to the UBE3A pre-mRNA

[0313] Oligonucleotides targeting position 55337-136214 of SEQ ID NO: 1 were tested in patient derived human neuronal cell cultures (see protocol in "Materials and methods" section). The oligonucleotides ability to reduce the SNHG14 transcript in the region downstream of SNORD109B (also termed UBE3A suppressor or UBE3A-SUP in the data table). Furthermore, the ability to induce UBE3A mRNA re-expression was analyzed.

[0314] The oligonucleotides were screened according to the protocol for screening oligonucleotides in human neuronal cell cultures described in the section "Materials and methods" - "Screening oligonucleotides in human neuronal cell cultures - 96 well system".

[0315] The results are shown in table 7.

Table 7: Oligonucleotide activity in patient derived human neuronal cell cultures.

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
55337	458_1	0,2	64	0	177	6
55337	458_1	1	50	10	233	9
55338	459_1	0,2	48	1	186	6
55338	459_1	1	44	9	213	NA
59565	460_1	0,2	66	4	110	24
59565	460_1	1	66	9	131	23
59574	461_1	0,2	56	5	162	19
59574	461_1	1	45	13	149	6
59575	462_1	0,2	56	7	114	84
59575	462_1	1	39	11	101	13
59576	463_1	0,2	82	19	52	NA
59576	463_1	1	65	15	95	18
60012	464_1	0,2	47	5	129	71
60012	464_1	1	41	3	160	64
60298	465_1	0,2	49	7	206	95
60298	465_1	1	37	9	222	44
60448	466_1	0,2	47	7	130	NA
60448	466_1	1	33	8	167	31

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc μM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
60821	467_1	0,2	87	1	73	NA
60821	467_1	1	62	18	101	3
61925	468_1	0,2	108	19	105	19
61925	468_1	1	95	17	101	19
62287	469_1	0,2	62	8	180	57
62287	469_1	1	48	5	196	38
62422	470_1	0,2	71	2	130	20
62422	470_1	1	57	9	116	18
62443	471_1	0,2	51	2	NA	NA
62443	471_1	1	43	2	160	34
64113	472_1	0,2	95	4	83	22
64113	472_1	1	76	14	74	36
64461	473_1	0,2	79	23	141	22
64461	473_1	1	59	12	279	53
64462	474_1	0,2	80	12	138	3
64462	474_1	1	84	15	202	3
65272	475_1	0,2	77	3	104	2
65272	475_1	1	75	23	113	10
66840	476_1	0,2	67	5	86	5
66840	476_1	1	72	10	100	12
67426	477_1	0,2	62	15	101	8
67426	477_1	1	65	13	170	52
68194	478_1	0,2	53	10	109	6
68194	478_1	1	59	4	178	7
68328	479_1	0,2	74	6	94	2
68328	479_1	1	79	16	111	38
68805	480_1	0,2	58	15	157	63
68805	480_1	1	49	2	190	26
68921	481_1	0,2	58	7	210	58
68921	481_1	1	55	10	281	NA
70133	482_1	0,2	50	9	149	6
70133	482_1	1	54	8	247	41
72377	483_1	0,2	44	2	143	NA
72377	483_1	1	52	6	195	37
72378	484_1	0,2	47	12	111	8
72378	484_1	1	56	3	201	NA
72826	485_1	0,2	54	12	116	0
72826	485_1	1	64	13	172	1

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc μM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
72861	486_1	0,2	52	9	93	6
72861	486_1	1	54	6	167	16
72887	487_1	0,2	55	3	128	5
72887	487_1	1	59	4	193	24
73474	488_1	0,2	55	10	132	20
73474	488_1	1	55	5	202	56
73992	489_1	0,2	60	7	146	17
73992	489_1	1	67	7	197	31
74791	490_1	0,2	42	5	167	65
74791	490_1	1	46	6	277	19
74851	491_1	0,2	69	14	78	1
74851	491_1	1	73	6	114	11
74853	492_1	0,2	64	6	84	1
74853	492_1	1	68	5	136	25
75840	493_1	0,2	40	10	90	6
75840	493_1	1	61	8	155	32
75841	494_1	0,2	65	10	131	30
75841	494_1	1	57	4	119	16
76238	495_1	0,2	70	9	109	41
76238	495_1	1	50	8	156	22
76254	496_1	0,2	67	13	134	34
76254	496_1	1	55	7	201	NA
76811	497_1	0,2	83	7	134	41
76811	497_1	1	77	8	148	32
77114	498_1	0,2	59	2	128	13
77114	498_1	1	64	10	206	NA
80468	499_1	0,2	55	2	105	34
80468	499_1	1	61	6	151	42
81047	500_1	0,2	103	17	80	6
81047	500_1	1	143	25	122	7
82233	501_1	0,2	57	NA	104	NA
82233	501_1	1	61	3	199	39
84166	502_1	0,2	49	6	89	0
84166	502_1	1	57	5	115	NA
85392	503_1	0,2	61	6	90	14
85392	503_1	1	62	8	118	15
86974	504_1	0,2	73	7	82	4
86974	504_1	1	79	3	104	19

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc μM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
87728	505_1	0,2	79	14	76	2
87728	505_1	1	80	19	97	35
87810	506_1	0,2	69	9	101	20
87810	506_1	1	73	6	155	2
88417	507_1	0,2	45	NA	116	3
88417	507_1	1	61	14	168	6
88991	508_1	0,2	51	6	113	20
88991	508_1	1	59	2	154	31
90228	509_1	0,2	65	6	76	10
90228	509_1	1	62	7	118	4
90474	510_1	0,2	71	7	83	14
90474	510_1	1	81	3	125	NA
91625	511_1	0,2	57	17	105	3
91625	511_1	1	65	11	150	NA
91885	512_1	0,2	57	5	105	1
91885	512_1	1	66	7	155	30
92976	513_1	0,2	67	6	136	44
92976	513_1	1	68	11	138	38
94304	514_1	0,2	81	11	110	7
94304	514_1	1	87	6	153	28
94528	515_1	0,2	48	5	128	6
94528	515_1	1	55	3	191	25
95653	516_1	0,2	57	3	108	7
95653	516_1	1	62	3	131	16
96751	517_1	0,2	63	9	90	19
96751	517_1	1	62	4	106	NA
97636	518_1	0,2	49	5	107	14
97636	518_1	1	44	9	137	NA
98480	519_1	0,2	55	1	106	NA
98480	519_1	1	54	5	112	23
98481	520_1	0,2	55	2	116	6
98481	520_1	1	62	4	129	6
99646	521_1	0,2	74	10	105	1
99646	521_1	1	87	13	119	27
100334	522_1	0,2	49	7	157	28
100334	522_1	1	57	2	120	37
101110	523_1	0,2	51	10	96	10
101110	523_1	1	72	14	114	25

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc μM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
101898	524_1	0,2	85	11	79	3
101898	524_1	1	93	21	92	46
102558	525_1	0,2	82	9	104	8
102558	525_1	1	86	18	104	30
103589	526_1	0,2	85	17	114	14
103589	526_1	1	94	39	126	6
104309	527_1	0,2	63	11	148	2
104309	527_1	1	70	26	155	NA
105686	528_1	0,2	66	11	91	24
105686	528_1	1	66	14	140	36
107972	529_1	0,2	84	15	109	15
107972	529_1	1	94	14	127	24
108257	530_1	0,2	63	7	114	19
108257	530_1	1	67	12	141	40
109407	531_1	0,2	84	24	87	16
109407	531_1	1	82	11	127	26
110210	532_1	0,2	72	12	91	14
110210	532_1	1	80	14	122	40
110768	533_1	0,2	67	8	126	16
110768	533_1	1	87	21	176	45
111811	534_1	0,2	77	2	98	17
111811	534_1	1	74	6	143	14
111812	535_1	0,2	64	4	97	0
111812	535_1	1	77	3	136	37
112149	536_1	0,2	73	2	63	2
112149	536_1	1	77	18	127	36
112150	537_1	0,2	76	6	78	8
112150	537_1	1	90	29	91	11
112945	538_1	0,2	69	4	121	2
112945	538_1	1	83	14	102	39
113533	539_1	0,2	95	17	85	2
113533	539_1	1	91	27	87	17
114274	540_1	0,2	89	11	103	17
114274	540_1	1	87	26	132	20
114495	541_1	0,2	76	5	88	1
114495	541_1	1	83	15	120	6
114831	542_1	0,2	59	3	76	4
114831	542_1	1	74	3	104	4

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
115355	543_1	0,2	66	8	91	9
115355	543_1	1	74	16	110	NA
116105	544_1	0,2	55	12	77	NA
116105	544_1	1	74	6	110	8
116106	545_1	0,2	58	18	96	9
116106	545_1	1	66	8	130	10
117096	546_1	0,2	69	9	118	20
117096	546_1	1	65	4	146	NA
117189	547_1	0,2	69	6	98	9
117189	547_1	1	74	11	146	25
117476	548_1	0,2	59	4	87	5
117476	548_1	1	65	3	104	10
118293	549_1	0,2	55	8	92	3
118293	549_1	1	66	10	105	24
118294	550_1	0,2	55	18	90	4
118294	550_1	1	72	21	119	5
118756	551_1	0,2	60	13	86	18
118756	551_1	1	88	24	120	26
119621	552_1	0,2	77	21	117	4
119621	552_1	1	102	19	146	NA
120655	553_1	0,2	55	9	124	19
120655	553_1	1	57	7	185	14
123733	554_1	0,2	74	6	87	14
123733	554_1	1	77	4	127	4
124163	555_1	0,2	89	12	117	46
124163	555_1	1	67	20	152	13
125512	556_1	0,2	70	5	114	26
125512	556_1	1	69	11	119	47
126882	557_1	0,2	78	15	106	8
126882	557_1	1	84	10	113	33
127105	558_1	0,2	71	7	91	13
127105	558_1	1	68	5	108	28
127809	559_1	0,2	59	4	74	NA
127809	559_1	1	58	7	101	26
129020	560_1	0,2	82	11	103	39
129020	560_1	1	77	9	103	27
129205	561_1	0,2	75	24	78	16
129205	561_1	1	89	11	102	23

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc μM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
129928	562_1	0,2	57	0	98	21
129928	562_1	1	63	9	107	18
130020	563_1	0,2	65	5	85	9
130020	563_1	1	65	3	145	12
130884	564_1	0,2	81	24	117	31
130884	564_1	1	83	4	139	17
130886	565_1	0,2	80	8	103	13
130886	565_1	1	69	7	122	11
131404	566_1	0,2	79	4	85	3
131404	566_1	1	80	7	116	24
132514	567_1	0,2	71	8	98	28
132514	567_1	1	69	9	97	29
133367	568_1	0,2	78	9	88	16
133367	568_1	1	91	17	88	32
136198	569_1	0,2	88	5	87	2
136198	569_1	1	81	6	109	35

Example 5 -Activity of oligonucleotides targeting the SNHG14 transcript in the region downstream of SNORD109B and upstream of the region antisense to to the UBE3A pre-mRNA

[0316] Oligonucleotides targeting position 5224-51257 of SEQ ID NO: 1 were tested in patient derived human neuronal cell cultures (see protocol in "Materials and methods" section). The oligonucleotides ability to reduce the SNHG14 transcript in the region downstream of SNORD109B (also termed UBE3A suppressor or UBE3A-SUP in the data table. Furthermore, the ability to induce UBE3A mRNA re-expression was analyzed.

[0317] The oligonucleotides were screened according to the protocol for screening oligonucleotides in human neuronal cell cultures described in the section "Materials and methods" "Screening oligonucleotides in human neuronal cell cultures - 96 well system" with the following modifications:

UBE3a-Sense primer
Using commercially available primers and probe from ThermoFisher: Hs00166580_m1 amplifying a 94 bp sequence in position 838 of refseq ID NM_000462.3.

[0318] Each plate include PBS controls (instead on a non-targeting ologinucleotide) and a positive control oligonucleotide CMP ID NO: 271_1, resulting in up-regulation of UBE3A mRNA. The additional control oligonucleotides were not included.

[0319] Data are presented as average % expression relative to PBS controls across all plates and normalized to the positive control oligonucleotide to manage plate to plate variation in efficacy levels.The results are shown in table 8.

Table 8: Oligonucleotide activity in patient derived human neuronal cell cultures.

Start SEQ ID NO 1	CMP ID NO	Conc μM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
5224	169_2	7.5 μM	49	4	209	9
5224	169_3	7.5 μM	47	5	282	5
5224	169_4	7.5 μM	57	14	202	12
5224	169_5	7.5 μM	84	36	148	4
5224	169_6	7.5 μM	42	1	285	16

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
5224	169_7	7.5 µM	52	6	233	27
5224	169_8	7.5 µM	51	7	278	11
5224	169_9	7.5 µM	51	4	228	20
5224	169_10	7.5 µM	78	17	143	5
5224	169_11	7.5 µM	74	15	146	2
5224	169_12	7.5 µM	47	1	277	26
5224	169_13	7.5 µM	56	23	244	42
5224	169_14	7.5 µM	74	16	141	1
5224	169_15	7.5 µM	95	32	122	13
5224	169_16	7.5 µM	44	4	276	23
5224	169_17	7.5 µM	85	5	118	5
5224	169_18	7.5 µM	75	18	131	4
5224	169_19	7.5 µM	95	18	126	11
5224	169_20	7.5 µM	61	12	169	20
5224	169_21	7.5 µM	79	18	156	3
5224	169_22	7.5 µM	63	14	173	16
5224	169_23	7.5 µM	43	2	233	27
5224	169_24	7.5 µM	56	1	183	9
5224	169_25	7.5 µM	48	0	220	24
5224	169_26	7.5 µM	41	1	244	39
5224	169_27	7.5 µM	55	16	260	42
5224	169_28	7.5 µM	48	1	265	65
5224	169_29	7.5 µM	56	2	197	18
5224	169_30	7.5 µM	57	12	189	12
5224	169_31	7.5 µM	53	4	196	9
5224	169_32	7.5 µM	50	1	220	3
5224	169_33	7.5 µM	64	19	227	8
5224	169_34	7.5 µM	58	4	193	10
5224	169_35	7.5 µM	45	2	229	3
5224	169_36	7.5 µM	44	6	262	14
5224	169_37	7.5 µM	55	2	180	21
5224	169_38	7.5 µM	75	22	158	13
5224	169_39	7.5 µM	76	15	159	17
5224	169_40	7.5 µM	60	18	232	31
5224	169_41	7.5 µM	46	3	230	10
5224	169_42	7.5 µM	47	3	240	11
5224	169_43	7.5 µM	48	9	273	30
5224	169_44	7.5 µM	83	32	196	11

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
5224	169_45	7.5 µM	69	4	185	20
5224	169_46	7.5 µM	45	9	256	3
5224	169_47	7.5 µM	41	2	304	4
5224	169_48	7.5 µM	44	1	260	16
5224	169_49	7.5 µM	38	1	245	32
5224	169_50	7.5 µM	35	2	314	28
5224	169_51	7.5 µM	41	5	281	5
5224	169_52	7.5 µM	36	1	282	1
5224	169_53	7.5 µM	38	7	301	7
5224	169_54	7.5 µM	36	3	304	6
5224	169_55	7.5 µM	52	5	246	23
5224	169_56	7.5 µM	33	15	302	15
5224	169_57	7.5 µM	34	16	273	16
5784	570_1	7.5 µM	47	0	274	7
5784	570_2	7.5 µM	47	8	232	8
5784	570_3	7.5 µM	55	25	280	54
5784	570_4	7.5 µM	61	11	235	54
5784	570_5	7.5 µM	72	10	198	30
5784	570_6	7.5 µM	66	8	244	50
5784	570_7	7.5 µM	42	1	284	13
5784	570_8	7.5 µM	43	6	257	11
5784	570_9	7.5 µM	32	9	242	30
5785	571_1	7.5 µM	40	1	269	35
5785	571_2	7.5 µM	42	3	187	6
5785	571_3	7.5 µM	46	6	242	8
5785	571_4	7.5 µM	37	4	282	19
5785	571_5	7.5 µM	48	16	296	2
5785	571_6	7.5 µM	37	6	274	10
5785	571_7	7.5 µM	39	1	260	8
5785	571_8	7.5 µM	35	1	252	3
5785	571_9	7.5 µM	30	5	297	10
5786	572_1	7.5 µM	34	4	279	29
5786	572_2	7.5 µM	63	10	152	4
5786	572_3	7.5 µM	39	0	280	42
5786	572_4	7.5 µM	40	1	283	14
5786	572_5	7.5 µM	38	6	310	11
5786	572_6	7.5 µM	33	1	316	18
5786	572_7	7.5 µM	35	1	318	11

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
5786	572_8	7.5 µM	47	9	310	19
5786	572_9	7.5 µM	31	7	321	12
8116	573_1	7.5 µM	39	8	316	28
8116	573_2	7.5 µM	49	15	305	41
8116	573_3	7.5 µM	46	13	308	3
8116	573_4	7.5 µM	39	3	332	6
8116	573_5	7.5 µM	34	6	278	12
8116	573_6	7.5 µM	42	1	285	10
8116	573_7	7.5 µM	38	0	289	33
8116	573_8	7.5 µM	40	4	311	20
8116	573_9	7.5 µM	57	9	315	5
8117	574_1	7.5 µM	40	2	291	35
8117	574_2	7.5 µM	42	3	343	18
8117	574_3	7.5 µM	36	6	325	8
8117	574_4	7.5 µM	38	1	279	15
8117	574_5	7.5 µM	42	6	308	10
8117	574_6	7.5 µM	47	8	340	11
8117	574_7	7.5 µM	43	0	308	42
8117	574_8	7.5 µM	44	6	268	10
8117	574_9	7.5 µM	41	8	241	22
8118	575_1	7.5 µM	47	0	198	28
8118	575_2	7.5 µM	83	26	253	31
8118	575_3	7.5 µM	48	4	348	5
8118	575_4	7.5 µM	37	2	269	7
8118	575_5	7.5 µM	43	6	258	17
8118	575_6	7.5 µM	50	6	286	3
8118	575_7	7.5 µM	37	2	331	30
8118	575_8	7.5 µM	47	7	264	1
8118	575_9	7.5 µM	64	23	243	3
8119	576_1	7.5 µM	47	1	272	14
8119	576_2	7.5 µM	109	31	119	3
8119	576_3	7.5 µM	36	3	287	6
8119	576_4	7.5 µM	35	3	285	23
8119	576_5	7.5 µM	49	10	222	1
8119	576_6	7.5 µM	79	12	132	10
8119	576_7	7.5 µM	76	4	132	3
8119	576_8	7.5 µM	62	1	147	5
8119	576_9	7.5 µM	43	3	230	5

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
8120	577_1	7.5 µM	57	3	158	15
8120	577_2	7.5 µM	39	4	279	60
8120	577_3	7.5 µM	38	1	290	68
8120	577_4	7.5 µM	77	11	148	11
8120	577_5	7.5 µM	31	6	272	36
8120	577_6	7.5 µM	38	8	228	32
8120	577_7	7.5 µM	40	8	246	39
8120	577_8	7.5 µM	43	11	256	26
8120	577_9	7.5 µM	85	32	109	6
8584	578_1	7.5 µM	57	7	199	7
8584	578_2	7.5 µM	40	5	263	3
8584	578_3	7.5 µM	40	2	289	23
8584	578_4	7.5 µM	43	8	199	16
8584	578_5	7.5 µM	42	1	256	15
8584	578_6	7.5 µM	42	6	241	10
8584	578_7	7.5 µM	42	5	329	20
8584	578_8	7.5 µM	49	7	271	13
8584	578_9	7.5 µM	45	3	222	3
8585	579_1	7.5 µM	45	0	208	8
8585	579_2	7.5 µM	51	4	226	6
8585	579_3	7.5 µM	54	5	178	8
8585	579_4	7.5 µM	41	4	328	13
8585	579_5	7.5 µM	50	5	272	3
8585	579_6	7.5 µM	86	12	161	0
8585	579_7	7.5 µM	72	5	155	15
8585	579_8	7.5 µM	57	3	230	14
8585	579_9	7.5 µM	83	0	123	1
8586	580_1	7.5 µM	37	2	313	13
8586	580_2	7.5 µM	43	1	266	3
8586	580_3	7.5 µM	42	5	303	5
8586	580_4	7.5 µM	57	4	225	26
8586	580_5	7.5 µM	51	4	228	35
8586	580_6	7.5 µM	44	4	253	15
8586	580_7	7.5 µM	50	1	241	10
8586	580_8	7.5 µM	44	0	227	26
8586	580_9	7.5 µM	31	5	323	31
8587	581_1	7.5 µM	50	6	223	30
8587	581_2	7.5 µM	66	7	199	19

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
8587	581_3	7.5 µM	56	8	197	9
8587	581_4	7.5 µM	57	12	270	24
8587	581_5	7.5 µM	51	12	259	12
8587	581_6	7.5 µM	39	4	282	2
8587	581_7	7.5 µM	38	11	263	5
8587	581_8	7.5 µM	45	10	203	19
8587	581_9	7.5 µM	43	2	234	10
9209	582_1	7.5 µM	61	7	225	7
9209	582_2	7.5 µM	46	9	341	36
9209	582_3	7.5 µM	44	9	306	38
9209	582_4	7.5 µM	43	1	249	5
9209	582_5	7.5 µM	33	16	306	6
9209	582_6	7.5 µM	37	8	329	19
9209	582_7	7.5 µM	44	9	289	4
9209	582_8	7.5 µM	39	3	314	20
9209	582_9	7.5 µM	41	4	299	25
9210	583_1	7.5 µM	43	5	319	25
9210	583_2	7.5 µM	53	9	352	5
9210	583_3	7.5 µM	42	2	362	42
9210	583_4	7.5 µM	46	5	225	13
9210	583_5	7.5 µM	39	6	343	21
9210	583_6	7.5 µM	44	9	298	8
9210	583_7	7.5 µM	37	5	332	9
9210	583_8	7.5 µM	42	6	343	25
9210	583_9	7.5 µM	36	2	341	9
9211	584_1	7.5 µM	45	5	343	39
9211	584_2	7.5 µM	42	2	298	22
9211	584_3	7.5 µM	44	10	321	2
9211	584_4	7.5 µM	50	1	299	5
9211	584_5	7.5 µM	44	1	319	25
9211	584_6	7.5 µM	50	6	323	13
9211	584_7	7.5 µM	42	4	316	27
9211	584_8	7.5 µM	53	3	217	11
9212	208_2	7.5 µM	44	7	312	26
9212	208_3	7.5 µM	38	2	331	21
9212	208_4	7.5 µM	47	3	353	11
9212	208_5	7.5 µM	54	11	348	14
9212	208_6	7.5 µM	51	12	310	8

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
9212	208_7	7.5 µM	60	9	224	11
9213	209_2	7.5 µM	44	12	242	21
9213	209_3	7.5 µM	37	12	335	12
9213	209_4	7.5 µM	55	7	350	2
9213	209_5	7.5 µM	47	7	337	19
9213	209_6	7.5 µM	51	8	300	19
9213	209_7	7.5 µM	47	15	342	23
9213	209_8	7.5 µM	45	12	289	5
9213	209_9	7.5 µM	41	1	368	37
9213	209_10	7.5 µM	40	4	315	1
11511	585_1	7.5 µM	41	7	350	12
11511	585_2	7.5 µM	44	4	233	7
11511	585_3	7.5 µM	40	8	310	31
11511	585_4	7.5 µM	33	8	324	41
11511	585_5	7.5 µM	29	3	314	23
11511	585_6	7.5 µM	38	4	332	15
11511	585_7	7.5 µM	30	2	315	15
11511	585_8	7.5 µM	36	11	328	37
11511	585_9	7.5 µM	39	5	303	49
11512	586_1	7.5 µM	60	3	236	5
11512	586_2	7.5 µM	40	9	282	53
11512	586_3	7.5 µM	36	1	279	11
11512	586_4	7.5 µM	34	3	288	21
11512	586_5	7.5 µM	30	1	270	4
11512	586_6	7.5 µM	29	5	269	24
11512	586_7	7.5 µM	33	4	263	6
11512	586_8	7.5 µM	32	4	270	4
11512	586_9	7.5 µM	33	5	310	48
11513	587_1	7.5 µM	45	2	237	34
11513	587_2	7.5 µM	44	3	307	4
11513	587_3	7.5 µM	37	1	285	24
11513	587_4	7.5 µM	44	1	252	41
11513	587_5	7.5 µM	51	7	220	29
11513	587_6	7.5 µM	41	2	262	35
11513	587_7	7.5 µM	39	7	280	21
11513	587_8	7.5 µM	48	9	230	11
11513	587_9	7.5 µM	41	5	270	9
11514	588_1	7.5 µM	54	9	204	25

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
11514	588_2	7.5 µM	98	5	143	4
11514	588_3	7.5 µM	55	9	180	1
11514	588_4	7.5 µM	113	24	109	17
11514	588_5	7.5 µM	66	26	150	5
11514	588_6	7.5 µM	74	1	131	1
11514	588_7	7.5 µM	79	4	140	9
11514	588_8	7.5 µM	49	2	235	2
11514	588_9	7.5 µM	51	10	281	2
11515	589_1	7.5 µM	61	2	154	9
11515	589_2	7.5 µM	70	9	126	12
11515	589_3	7.5 µM	53	3	212	32
11515	589_4	7.5 µM	93	14	108	14
11515	589_5	7.5 µM	69	11	191	7
11515	589_6	7.5 µM	53	9	183	20
11515	589_7	7.5 µM	45	8	257	4
11515	589_8	7.5 µM	35	5	213	5
11515	589_9	7.5 µM	41	2	290	22
13223	236_2	7.5 µM	39	6	286	21
13223	236_3	7.5 µM	32	10	256	29
13223	236_4	7.5 µM	37	5	285	12
13223	236_5	7.5 µM	33	8	280	19
13223	236_6	7.5 µM	40	16	295	7
13223	236_7	7.5 µM	45	10	254	50
13223	236_8	7.5 µM	41	22	306	50
13223	236_9	7.5 µM	32	11	292	47
13223	236_10	7.5 µM	31	10	307	3
13223	236_11	7.5 µM	52	32	198	29
13223	236_12	7.5 µM	31	7	261	18
13223	236_13	7.5 µM	34	3	279	32
13223	236_14	7.5 µM	38	0	285	75
13223	236_15	7.5 µM	40	17	307	53
13223	236_16	7.5 µM	41	6	321	30
13224	237_2	7.5 µM	49	18	251	38
13224	237_3	7.5 µM	53	14	236	33
13224	237_4	7.5 µM	39	0	283	26
13224	237_5	7.5 µM	43	2	243	2
13224	237_6	7.5 µM	39	10	265	48
13224	237_7	7.5 µM	50	3	302	19

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
13224	237_8	7.5 µM	46	7	327	43
13224	237_9	7.5 µM	38	9	287	12
13224	237_10	7.5 µM	35	6	248	35
13224	237_11	7.5 µM	41	1	259	24
13224	237_12	7.5 µM	33	6	303	35
13224	237_13	7.5 µM	26	4	265	53
13224	237_14	7.5 µM	30	8	321	15
13224	237_15	7.5 µM	33	11	315	24
13224	237_16	7.5 µM	36	11	292	19
13225	239_2	7.5 µM	35	16	291	30
13225	239_3	7.5 µM	40	15	311	42
13225	239_4	7.5 µM	81	6	144	16
13225	239_5	7.5 µM	90	16	127	11
13225	239_6	7.5 µM	49	29	282	3
13225	239_7	7.5 µM	35	4	296	23
13225	239_8	7.5 µM	40	1	292	48
13225	239_9	7.5 µM	36	1	318	44
13225	239_10	7.5 µM	49	NA	304	NA
13225	239_11	7.5 µM	45	NA	258	NA
13225	239_12	7.5 µM	43	1	285	1
13225	239_13	7.5 µM	31	1	308	31
13225	239_14	7.5 µM	41	8	253	6
13225	239_15	7.5 µM	28	3	291	16
13225	239_16	7.5 µM	29	3	314	14
13226	590_1	7.5 µM	34	1	283	18
13226	590_2	7.5 µM	49	7	213	17
13226	590_3	7.5 µM	40	1	274	51
13226	590_4	7.5 µM	36	1	300	2
13226	590_5	7.5 µM	37	3	280	36
13226	590_6	7.5 µM	38	2	204	17
13226	590_7	7.5 µM	38	5	245	16
13226	590_8	7.5 µM	30	6	219	34
13226	590_9	7.5 µM	33	1	269	2
13226	590_10	7.5 µM	33	2	258	49
13226	590_11	7.5 µM	48	17	297	31
13226	590_12	7.5 µM	33	4	317	65
13226	590_13	7.5 µM	35	7	337	43
13226	590_14	7.5 µM	25	1	306	22

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
13226	590_15	7.5 µM	30	5	299	2
15113	591_1	7.5 µM	43	3	313	14
15113	591_2	7.5 µM	52	2	295	24
15114	592_1	7.5 µM	53	2	232	17
15114	592_2	7.5 µM	39	1	309	23
15114	592_3	7.5 µM	46	1	278	12
15114	592_4	7.5 µM	36	1	328	13
15114	592_5	7.5 µM	49	9	295	40
15114	592_6	7.5 µM	46	3	297	10
15114	592_7	7.5 µM	75	21	160	23
15114	592_8	7.5 µM	41	10	325	23
15114	592_9	7.5 µM	55	15	265	3
15115	241_2	7.5 µM	66	18	168	2
15115	241_3	7.5 µM	51	15	265	11
15115	241_4	7.5 µM	49	4	239	7
15115	241_5	7.5 µM	52	11	314	20
15115	241_6	7.5 µM	41	13	307	7
15115	241_7	7.5 µM	38	6	344	33
15115	241_8	7.5 µM	39	10	329	9
15115	241_9	7.5 µM	50	11	321	32
15115	241_10	7.5 µM	48	9	316	1
15563	593_1	7.5 µM	38	10	282	14
15563	593_2	7.5 µM	31	5	279	16
15563	593_3	7.5 µM	34	7	281	16
15563	593_4	7.5 µM	32	16	318	2
15563	594_1	7.5 µM	40	2	320	21
15563	594_2	7.5 µM	54	7	237	14
15563	594_3	7.5 µM	35	6	300	45
15563	594_4	7.5 µM	37	7	254	6
15564	596_1	7.5 µM	47	7	225	35
15564	596_2	7.5 µM	49	2	184	14
15564	596_3	7.5 µM	34	8	271	18
15564	596_4	7.5 µM	45	8	277	29
15564	595_1	7.5 µM	42	4	254	6
15564	595_2	7.5 µM	36	9	277	35
15564	595_3	7.5 µM	40	8	295	31
15564	595_4	7.5 µM	45	5	173	20
15566	597_1	7.5 µM	48	6	296	22

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
15566	597_2	7.5 µM	44	12	293	8
15566	597_3	7.5 µM	41	6	318	23
15566	597_4	7.5 µM	60	9	340	72
15567	38_3	7.5 µM	41	3	306	14
15567	38_4	7.5 µM	45	1	303	48
15567	38_5	7.5 µM	39	15	292	28
15567	38_6	7.5 µM	46	12	261	40
15567	598_1	7.5 µM	42	2	257	31
15567	598_2	7.5 µM	41	12	272	46
15567	598_3	7.5 µM	54	9	281	29
15567	598_4	7.5 µM	45	8	307	6
15568	599_1	7.5 µM	47	3	326	68
15568	599_2	7.5 µM	60	14	307	30
15568	599_3	7.5 µM	50	8	274	24
15568	599_4	7.5 µM	45	6	250	12
15568	600_1	7.5 µM	37	6	251	1
15568	600_2	7.5 µM	45	11	267	15
15568	600_3	7.5 µM	44	5	278	1
15568	600_4	7.5 µM	41	10	265	5
15569	601_1	7.5 µM	42	12	271	18
15569	601_2	7.5 µM	38	6	269	24
15569	601_3	7.5 µM	39	4	260	34
15569	601_4	7.5 µM	56	8	146	1
15570	244_2	7.5 µM	46	1	338	6
15570	244_3	7.5 µM	47	0	275	47
15570	244_4	7.5 µM	47	8	281	67
15570	244_5	7.5 µM	41	8	258	52
15570	39_2	7.5 µM	53	4	339	25
15570	39_3	7.5 µM	65	5	200	17
15570	39_4	7.5 µM	47	7	321	6
15570	39_5	7.5 µM	46	3	289	20
15571	602_1	7.5 µM	34	5	278	29
15571	602_2	7.5 µM	39	8	254	37
15571	602_3	7.5 µM	41	10	266	23
15571	602_4	7.5 µM	42	8	256	40
15571	40_2	7.5 µM	58	0	325	4
15571	40_3	7.5 µM	58	2	326	35
15571	40_4	7.5 µM	54	1	306	3

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
15571	40_5	7.5 µM	44	2	322	4
15571	40_6	7.5 µM	43	4	293	17
15571	40_7	7.5 µM	53	7	343	20
15571	40_8	7.5 µM	52	1	337	17
15572	604_1	7.5 µM	58	1	289	3
15572	604_2	7.5 µM	63	12	230	5
15572	604_3	7.5 µM	57	3	306	23
15572	604_4	7.5 µM	46	6	324	4
15572	603_1	7.5 µM	60	7	339	31
15572	603_2	7.5 µM	70	0	279	19
15572	603_3	7.5 µM	59	9	290	48
15572	603_4	7.5 µM	85	11	123	24
15573	605_1	7.5 µM	56	5	288	3
15573	605_2	7.5 µM	58	4	286	6
15573	605_3	7.5 µM	59	3	261	9
15573	605_4	7.5 µM	69	24	328	17
15573	606_1	7.5 µM	50	4	282	19
15573	606_2	7.5 µM	112	NA	133	NA
15573	606_3	7.5 µM	55	22	254	43
15573	606_4	7.5 µM	107	59	116	2
15574	607_1	7.5 µM	56	2	337	31
15574	607_2	7.5 µM	59	1	254	10
15574	607_3	7.5 µM	53	0	295	26
15574	607_4	7.5 µM	48	3	268	15
25248	608_1	7.5 µM	86	7	189	5
25248	608_2	7.5 µM	102	13	136	3
25248	608_3	7.5 µM	54	17	280	12
25248	608_4	7.5 µM	71	8	219	31
25248	608_5	7.5 µM	59	20	179	16
25248	608_6	7.5 µM	71	2	198	0
25248	608_7	7.5 µM	47	3	230	21
25248	608_8	7.5 µM	55	12	287	13
25248	608_9	7.5 µM	66	19	297	18
25249	609_1	7.5 µM	58	19	264	7
25249	609_2	7.5 µM	88	6	156	5
25249	609_3	7.5 µM	76	19	140	13
25249	609_4	7.5 µM	50	15	185	6
25249	609_5	7.5 µM	95	29	139	1

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
25249	609_6	7.5 µM	86	15	126	7
25249	609_7	7.5 µM	72	9	174	1
25249	609_8	7.5 µM	64	3	189	18
25249	609_9	7.5 µM	77	12	223	35
25250	610_1	7.5 µM	55	17	233	7
25250	610_2	7.5 µM	52	15	233	9
25250	610_3	7.5 µM	77	5	151	11
25250	610_4	7.5 µM	48	0	242	21
25250	610_5	7.5 µM	59	8	234	0
25250	610_6	7.5 µM	59	12	208	23
25250	610_7	7.5 µM	69	7	216	5
25250	610_8	7.5 µM	70	16	211	2
25250	610_9	7.5 µM	77	22	157	19
25251	611_1	7.5 µM	43	4	306	10
25251	611_2	7.5 µM	43	1	300	36
25251	611_3	7.5 µM	43	17	306	6
25251	611_4	7.5 µM	40	1	320	37
25251	611_5	7.5 µM	48	9	273	7
25251	611_6	7.5 µM	51	2	302	26
25251	611_7	7.5 µM	40	8	326	8
25251	611_8	7.5 µM	55	10	330	17
25251	611_9	7.5 µM	40	3	297	11
25252	612_1	7.5 µM	58	9	219	5
25252	612_2	7.5 µM	54	9	282	4
25252	612_3	7.5 µM	56	13	265	35
25252	612_4	7.5 µM	81	16	239	51
25252	612_5	7.5 µM	57	2	234	25
25252	612_6	7.5 µM	76	18	221	8
25252	612_7	7.5 µM	45	7	285	11
25252	612_8	7.5 µM	50	8	231	4
25252	612_9	7.5 µM	51	3	305	17
29636	271_1	7.5 µM	35	4	345	29
29636	271_1	7.5 µM	32	6	383	31
29636	271_1	7.5 µM	42	7	292	13
29636	271_1	7.5 µM	40	1	309	41
29636	271_1	7.5 µM	41	10	339	17
29636	271_1	7.5 µM	35	8	306	40
29636	271_1	7.5 µM	33	1	320	12

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
29636	271_1	7.5 µM	43	1	347	7
29636	271_1	7.5 µM	36	2	339	19
29636	271_1	7.5 µM	36	1	315	5
29636	271_1	7.5 µM	41	1	326	16
29636	271_1	7.5 µM	38	2	344	1
29636	271_1	7.5 µM	34	6	341	8
29636	271_1	7.5 µM	42	9	320	1
29636	271_1	7.5 µM	31	8	344	37
29636	271_1	7.5 µM	44	2	335	11
29636	271_1	7.5 µM	32	0	316	17
29636	271_1	7.5 µM	43	11	323	2
29636	271_1	7.5 µM	35	7	340	2
29636	271_1	7.5 µM	43	1	340	8
29636	271_1	7.5 µM	33	4	296	27
29636	271_1	7.5 µM	38	5	334	4
29636	271_1	7.5 µM	36	4	341	22
29636	271_1	7.5 µM	48	4	334	3
29636	271_1	7.5 µM	36	8	303	13
29636	271_1	7.5 µM	36	0	343	7
29636	271_1	7.5 µM	39	1	326	1
29636	271_1	7.5 µM	38	2	346	14
29636	271_1	7.5 µM	32	0	332	11
29636	271_1	7.5 µM	39	4	330	23
29636	271_1	7.5 µM	39	7	346	33
29636	271_1	7.5 µM	40	1	329	14
29636	271_1	7.5 µM	34	6	316	38
29636	271_1	7.5 µM	33	4	317	14
29636	271_1	7.5 µM	41	6	328	11
29636	271_1	7.5 µM	45	2	345	3
29636	271_1	7.5 µM	37	1	330	3
29636	271_1	7.5 µM	45	7	322	18
29636	271_1	7.5 µM	36	3	334	13
29636	271_1	7.5 µM	33	8	333	3
29636	271_1	7.5 µM	35	10	321	43
29636	271_1	7.5 µM	41	3	323	18
29636	271_1	7.5 µM	39	8	354	39
29636	271_1	7.5 µM	35	2	327	23
30599	613_1	7.5 µM	73	29	172	22

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
30599	613_2	7.5 µM	87	40	114	9
30599	613_3	7.5 µM	59	23	168	23
30599	613_4	7.5 µM	43	15	281	31
30599	613_5	7.5 µM	51	3	271	28
30600	614_1	7.5 µM	56	11	179	22
30600	614_2	7.5 µM	96	40	100	7
30600	614_3	7.5 µM	41	7	246	27
30600	614_4	7.5 µM	47	19	283	14
30600	614_5	7.5 µM	52	21	209	16
30600	615_1	7.5 µM	61	19	197	12
30600	615_2	7.5 µM	45	11	287	25
30600	615_3	7.5 µM	102	NA	115	NA
30600	615_4	7.5 µM	72	NA	170	NA
30600	615_5	7.5 µM	95	NA	138	NA
30601	285_2	7.5 µM	83	NA	165	NA
30601	285_3	7.5 µM	124	NA	111	NA
30601	285_4	7.5 µM	69	NA	183	NA
30601	285_5	7.5 µM	47	23	211	7
30601	285_6	7.5 µM	46	12	183	6
30601	617_1	7.5 µM	67	26	190	19
30601	617_2	7.5 µM	74	35	137	6
30601	617_3	7.5 µM	51	16	211	4
30601	617_4	7.5 µM	65	22	142	11
30601	617_5	7.5 µM	43	8	298	26
30601	616_1	7.5 µM	50	22	181	12
30601	616_2	7.5 µM	37	13	276	33
30601	616_3	7.5 µM	38	16	264	9
30601	616_4	7.5 µM	43	NA	304	NA
30601	616_5	7.5 µM	50	NA	229	NA
30602	619_1	7.5 µM	90	43	131	22
30602	619_2	7.5 µM	78	40	138	2
30602	619_3	7.5 µM	66	22	123	8
30602	619_4	7.5 µM	100	43	96	5
30602	619_5	7.5 µM	75	17	157	5
30602	618_1	7.5 µM	46	16	226	12
30602	618_2	7.5 µM	68	NA	151	NA
30602	618_3	7.5 µM	52	4	207	18
30602	618_4	7.5 µM	57	12	223	2

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
30602	618_5	7.5 µM	54	2	211	3
30603	620_1	7.5 µM	106	23	110	16
30603	620_2	7.5 µM	48	10	243	18
30603	620_3	7.5 µM	53	1	174	32
30603	620_4	7.5 µM	81	0	138	15
30603	620_5	7.5 µM	56	5	218	9
30604	621_1	7.5 µM	39	4	304	10
30604	621_2	7.5 µM	35	7	311	3
30604	621_3	7.5 µM	67	18	142	8
30604	621_4	7.5 µM	34	6	273	21
30604	621_5	7.5 µM	36	5	266	18
30605	622_1	7.5 µM	42	1	242	28
30605	622_2	7.5 µM	31	10	300	8
30605	622_3	7.5 µM	35	3	319	11
30605	622_4	7.5 µM	37	4	281	5
30605	622_5	7.5 µM	39	5	306	11
30606	623_1	7.5 µM	47	3	287	1
30606	623_2	7.5 µM	74	23	166	7
30606	623_3	7.5 µM	82	1	149	8
30606	623_4	7.5 µM	66	9	135	8
30606	623_5	7.5 µM	78	7	128	12
30608	624_1	7.5 µM	84	13	185	25
30608	624_2	7.5 µM	35	2	245	9
30608	624_3	7.5 µM	31	3	267	9
30608	624_4	7.5 µM	39	16	257	13
30608	624_5	7.5 µM	34	3	283	4
30666	625_1	7.5 µM	45	5	286	39
30666	625_2	7.5 µM	39	3	280	13
30666	625_3	7.5 µM	40	10	258	9
30666	625_4	7.5 µM	41	14	234	39
30666	625_5	7.5 µM	42	5	293	26
30666	625_6	7.5 µM	44	0	284	25
30666	625_7	7.5 µM	46	3	271	4
30666	625_8	7.5 µM	47	5	256	17
30666	625_9	7.5 µM	40	7	302	2
30667	626_1	7.5 µM	38	1	279	10
30667	626_2	7.5 µM	39	21	329	22
30667	626_3	7.5 µM	59	12	265	65

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
30667	626_4	7.5 µM	39	5	318	25
30667	626_5	7.5 µM	36	2	302	33
30667	626_6	7.5 µM	36	6	273	34
30667	626_7	7.5 µM	30	0	299	29
30667	626_8	7.5 µM	35	4	277	43
30667	626_9	7.5 µM	32	3	275	22
30668	627_1	7.5 µM	71	3	131	11
30668	627_2	7.5 µM	49	4	226	30
30668	627_3	7.5 µM	64	5	147	8
30668	627_4	7.5 µM	52	6	176	9
30668	627_5	7.5 µM	78	14	108	3
30668	627_6	7.5 µM	40	1	183	23
30668	627_7	7.5 µM	85	8	116	2
30668	627_8	7.5 µM	45	1	128	7
30668	627_9	7.5 µM	42	5	215	36
30669	628_1	7.5 µM	90	11	120	15
30669	628_2	7.5 µM	73	12	124	4
30669	628_3	7.5 µM	88	2	115	4
30669	628_4	7.5 µM	54	4	190	18
30669	628_5	7.5 µM	64	1	138	3
30669	628_6	7.5 µM	62	4	138	11
30669	628_7	7.5 µM	55	1	138	13
30669	628_8	7.5 µM	62	1	140	5
30669	628_9	7.5 µM	79	10	134	22
30711	629_1	7.5 µM	42	1	252	47
30711	629_2	7.5 µM	40	2	295	30
30711	629_3	7.5 µM	46	1	302	78
30711	629_4	7.5 µM	41	3	260	16
30711	629_5	7.5 µM	41	1	284	3
30711	629_6	7.5 µM	43	0	262	1
30711	629_7	7.5 µM	43	3	278	65
30711	629_8	7.5 µM	53	5	234	24
30711	629_9	7.5 µM	37	4	289	1
30711	629_10	7.5 µM	47	6	292	6
30711	629_11	7.5 µM	50	5	224	20
30712	630_1	7.5 µM	44	2	282	22
30712	630_2	7.5 µM	45	6	297	23
30712	630_3	7.5 µM	46	2	272	10

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
30713	631_1	7.5 µM	45	2	294	10
30713	631_2	7.5 µM	42	0	285	14
30713	631_3	7.5 µM	38	3	319	21
30713	631_4	7.5 µM	43	3	282	4
30713	631_5	7.5 µM	54	2	173	17
30713	631_6	7.5 µM	37	0	315	10
30713	631_7	7.5 µM	40	4	317	2
30713	631_8	7.5 µM	44	1	275	5
30713	631_9	7.5 µM	47	2	233	8
30713	631_10	7.5 µM	108	18	101	3
30714	632_1	7.5 µM	48	4	210	4
30714	632_2	7.5 µM	53	5	256	5
30714	632_3	7.5 µM	60	5	224	19
30714	632_4	7.5 µM	89	12	117	11
30714	632_5	7.5 µM	39	6	312	6
30714	632_6	7.5 µM	40	2	278	31
30714	632_7	7.5 µM	86	1	160	21
30714	632_8	7.5 µM	57	17	278	40
30714	632_9	7.5 µM	51	7	236	13
30715	304_2	7.5 µM	53	5	206	18
30715	304_3	7.5 µM	70	11	142	24
30715	304_4	7.5 µM	88	1	120	10
30715	304_5	7.5 µM	82	15	123	7
30715	304_6	7.5 µM	43	4	264	12
30715	304_7	7.5 µM	41	5	266	49
30715	304_8	7.5 µM	43	1	291	12
30715	304_9	7.5 µM	36	3	285	18
30715	304_10	7.5 µM	42	1	280	40
33376	633_1	7.5 µM	53	1	234	50
33376	633_2	7.5 µM	45	5	301	7
33376	633_3	7.5 µM	53	7	263	17
33376	633_4	7.5 µM	53	4	229	22
33376	633_5	7.5 µM	43	3	264	36
33376	633_6	7.5 µM	53	5	247	12
33376	633_7	7.5 µM	49	6	289	6
33376	633_8	7.5 µM	64	11	238	24
33376	633_9	7.5 µM	63	2	249	28
33377	634_1	7.5 µM	57	9	250	14

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
33377	634_2	7.5 µM	53	10	265	3
33377	634_3	7.5 µM	48	2	275	10
33377	634_4	7.5 µM	39	6	287	12
33377	634_5	7.5 µM	49	1	255	22
33377	634_6	7.5 µM	51	2	291	15
33377	634_7	7.5 µM	47	5	297	16
33377	634_8	7.5 µM	42	9	311	14
33377	634_9	7.5 µM	47	5	271	23
33378	635_1	7.5 µM	56	11	257	3
33378	635_2	7.5 µM	56	5	213	23
33378	635_3	7.5 µM	61	8	215	8
33378	635_4	7.5 µM	58	15	232	16
33378	635_5	7.5 µM	48	3	316	20
33378	635_6	7.5 µM	59	5	262	30
33378	635_7	7.5 µM	55	7	287	15
33378	635_8	7.5 µM	42	1	284	3
33378	635_9	7.5 µM	40	0	277	23
33379	636_1	7.5 µM	50	2	239	7
33379	636_2	7.5 µM	74	16	204	10
33379	636_3	7.5 µM	55	4	201	3
33379	636_4	7.5 µM	54	2	238	7
33379	636_5	7.5 µM	52	5	207	43
33379	636_6	7.5 µM	47	3	249	6
33379	636_7	7.5 µM	48	5	241	1
33379	636_8	7.5 µM	37	7	304	12
33379	636_9	7.5 µM	62	9	245	5
33380	637_1	7.5 µM	39	1	219	25
33380	637_2	7.5 µM	59	1	197	11
33380	637_3	7.5 µM	56	1	250	19
33380	637_4	7.5 µM	53	7	244	36
33380	637_5	7.5 µM	73	13	297	34
33380	637_6	7.5 µM	65	1	124	17
33380	637_7	7.5 µM	74	5	133	5
33380	637_8	7.5 µM	53	2	207	7
33380	637_9	7.5 µM	54	15	226	26
39806	638_1	7.5 µM	37	7	283	31
39806	638_2	7.5 µM	49	11	291	30
39806	638_3	7.5 µM	41	1	270	20

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
39806	638_4	7.5 µM	42	13	267	9
39806	638_5	7.5 µM	50	1	184	5
39806	638_6	7.5 µM	38	1	276	15
39806	638_7	7.5 µM	56	1	292	4
39806	638_8	7.5 µM	41	4	267	11
39806	638_9	7.5 µM	41	4	218	33
39807	639_1	7.5 µM	48	15	293	30
39807	639_2	7.5 µM	38	3	269	2
39807	639_3	7.5 µM	72	5	167	3
39807	639_4	7.5 µM	69	38	242	36
39807	639_5	7.5 µM	47	6	303	36
39807	639_6	7.5 µM	53	6	179	5
39807	639_7	7.5 µM	51	3	189	8
39807	639_8	7.5 µM	42	3	185	19
39807	639_9	7.5 µM	45	3	202	15
39808	640_1	7.5 µM	39	5	265	7
39808	640_2	7.5 µM	37	4	272	56
39808	640_3	7.5 µM	38	3	260	17
39808	640_4	7.5 µM	33	4	255	2
39808	640_5	7.5 µM	38	3	253	3
39808	640_6	7.5 µM	40	8	216	10
39808	640_7	7.5 µM	39	8	310	7
39808	640_8	7.5 µM	41	6	282	21
39808	640_9	7.5 µM	40	5	269	12
44439	641_1	7.5 µM	35	6	336	32
44439	641_2	7.5 µM	67	20	161	6
44439	641_3	7.5 µM	34	9	317	30
44439	641_4	7.5 µM	62	18	193	9
44439	641_5	7.5 µM	34	4	280	3
44439	641_6	7.5 µM	43	1	315	45
44439	641_7	7.5 µM	45	17	307	53
44439	641_8	7.5 µM	41	0	294	41
44439	641_9	7.5 µM	37	2	334	43
44440	361_2	7.5 µM	36	1	303	15
44440	361_3	7.5 µM	32	3	315	12
44440	361_4	7.5 µM	41	1	299	7
44440	361_5	7.5 µM	40	5	295	6
44440	361_6	7.5 µM	40	2	296	30

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
44440	361_7	7.5 µM	39	1	300	55
44440	361_8	7.5 µM	45	6	285	45
44440	361_9	7.5 µM	44	6	321	26
44440	361_10	7.5 µM	46	7	290	18
44441	362_2	7.5 µM	50	4	277	4
44441	362_3	7.5 µM	40	6	296	8
44441	362_4	7.5 µM	37	5	340	18
44441	362_5	7.5 µM	45	2	266	21
44441	362_6	7.5 µM	39	7	263	0
44441	362_7	7.5 µM	41	12	262	36
44441	362_8	7.5 µM	35	13	313	6
44441	362_9	7.5 µM	36	8	300	20
44441	362_10	7.5 µM	48	10	293	1
46391	642_1	7.5 µM	51	25	278	6
46391	642_2	7.5 µM	46	2	303	4
46391	642_3	7.5 µM	48	3	297	11
46391	642_4	7.5 µM	45	11	320	37
46391	642_5	7.5 µM	71	32	303	40
46391	642_6	7.5 µM	47	15	298	16
46391	642_7	7.5 µM	38	6	277	5
46391	642_8	7.5 µM	38	3	280	20
46391	642_9	7.5 µM	51	20	285	16
46391	642_10	7.5 µM	32	7	293	20
46391	642_11	7.5 µM	42	2	291	2
46391	642_12	7.5 µM	40	3	317	19
46391	642_13	7.5 µM	39	11	295	5
46391	642_14	7.5 µM	52	20	295	16
46391	642_15	7.5 µM	39	8	316	38
46391	642_16	7.5 µM	35	2	294	30
46391	642_17	7.5 µM	51	5	292	8
46391	643_1	7.5 µM	39	4	276	16
46392	644_1	7.5 µM	39	0	321	7
46392	644_2	7.5 µM	46	4	308	4
46392	644_3	7.5 µM	44	1	317	3
46392	644_4	7.5 µM	38	6	315	11
46392	645_1	7.5 µM	46	5	342	42
46392	645_2	7.5 µM	37	5	292	25
46392	645_3	7.5 µM	46	16	317	30

(continued)

Start SEQ ID NO 1	CMP ID NO	Conc µM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
46392	645_4	7.5 µM	47	8	381	102
46392	645_5	7.5 µM	42	2	269	4
46393	646_1	7.5 µM	49	4	295	2
46393	646_2	7.5 µM	49	9	304	38
46393	646_3	7.5 µM	44	6	298	50
46393	646_4	7.5 µM	43	1	296	41
46393	646_5	7.5 µM	35	1	260	3
46393	646_6	7.5 µM	40	2	281	67
46393	646_7	7.5 µM	38	1	278	44
46393	646_8	7.5 µM	42	6	262	49
46393	646_9	7.5 µM	38	3	289	24
46393	646_10	7.5 µM	38	1	317	4
46393	646_11	7.5 µM	42	1	320	34
46393	646_12	7.5 µM	36	5	323	8
46393	646_13	7.5 µM	41	3	262	27
46393	646_14	7.5 µM	46	13	315	18
46393	646_15	7.5 µM	42	4	340	27
46393	646_16	7.5 µM	45	8	360	14
46393	646_17	7.5 µM	44	1	303	3
46393	646_18	7.5 µM	50	2	304	28
46393	646_19	7.5 µM	54	10	217	25
51241	425_2	7.5 µM	49	12	296	3
51241	425_3	7.5 µM	48	6	297	10
51241	425_4	7.5 µM	52	5	275	25
51241	425_5	7.5 µM	40	6	284	29
51241	425_6	7.5 µM	39	5	301	22
51241	425_7	7.5 µM	39	4	263	13
51241	425_8	7.5 µM	32	5	188	13
51241	425_9	7.5 µM	42	5	286	2
51241	425_10	7.5 µM	34	3	165	17

Example 6 -Activity of exon-exon spanning oligonucleotides

[0320] Oligonucleotides designed to be complementary across exon-exon junctions of SNHG14-023 (ENST00000554726) were tested for their ability to reduce the SNHG14 transcript in the region downstream of SNORD109B (also termed UBE3A suppressor or UBE3A-SUP in the data table). Furthermore, the ability to induce UBE3A mRNA re-expression was analyzed. The oligonucleotides primarily span exon2 and exon3 (i.e. are complementary to a region in exon2 and a region in exon 3).

[0321] The oligonucleotides were screened according to the protocol for screening oligonucleotides in human neuronal cell cultures described in the section Example 5.

[0322] The results are shown in table 9.

Table 9: Oligonucleotide activity in patient derived human neuronal cell cultures.

CMP ID NO	Conc μM	% of Mock UBE3A-SUP	sd	% of Mock UBE3A	sd
674_1	7.5 μM	47	2	214	12
675_1	7.5 μM	44	6	265	10
676_1	7.5 μM	44	3	284	16
677_1	7.5 μM	55	19	351	18
678_1	7.5 μM	41	11	257	1
656_1	7.5 μM	46	3	140	19
657_1	7.5 μM	35	7	218	27
658_1	7.5 μM	38	12	253	43
659_1	7.5 μM	39	7	274	6
660_1	7.5 μM	38	8	275	29
661_1	7.5 μM	43	13	246	21
662_1	7.5 μM	27	10	290	5
663_1	7.5 μM	28	0	287	23
664_1	7.5 μM	27	2	288	14
665_1	7.5 μM	37	9	321	47
666_1	7.5 μM	54	1	259	10
667_1	7.5 μM	47	8	236	2
647_1	7.5 μM	19	3	300	25
648_1	7.5 μM	22	7	320	3
649_1	7.5 μM	34	8	326	2
650_1	7.5 μM	44	4	292	7
651_1	7.5 μM	36	5	254	9
652_1	7.5 μM	21	2	314	18
653_1	7.5 μM	24	5	299	41
654_1	7.5 μM	31	2	344	41
655_1	7.5 μM	60	9	301	3
668_1	7.5 μM	21	3	297	11
669_1	7.5 μM	24	5	296	27
670_1	7.5 μM	30	3	274	55
671_1	7.5 μM	27	6	263	35
672_1	7.5 μM	27	6	280	50
673_1	7.5 μM	33	2	290	19

Example 7 - Testing in vitro efficacy and potency of selected oligonucleotides

[0323] Based on the screenings in examples 2 to 5 above 52 oligonucleotides were selected for potency and efficacy testing.

[0324] The oligonucleotides were screened in human AS patient derived cells as described in the Materials and Method section "Screening oligonucleotides in human neuronal cell cultures - 96 well system" with the following modifications: For UBE3a-Sense primer commercially available primers and probe from ThermoFisher:

Hs00166580_m1 amplifying a 94 bp sequence in position 838 of refseq ID NM_000462.3 were used.

[0325] Each plate include PBS controls (instead on a non-targeting oligonucleotide) and the positive control oligonucleotides CMP ID NO: 186_1 and 39_1 identified in previous screens were included. The additional control oligonucleotides described in the materials and method section were not included. Oligonucleotide test concentrations were from 31.6 μM to 1 nM using a 10 point half-log dilution. All oligonucleotides were tested in 5 independent experiments in 5 different weeks. In the data QC process some plates were removed from the analysis if these were obvious outliers e.g. no PCR product detected. After this filtration there is a minimum of three independent experiments behind each the reported valuess.

[0326] The EC50 (UBE3A mRNA re-expression) and IC50 (reduction of the SNHG14 transcript in the region downstream of SNORD109B, also termed UBE3A suppressor or UBE3A-SUP in the data table) were determined after curve fitting using a 4 parameter sigmoidal dose-response model. Fitting was executed using the fit engine available inside the Biobook software by IDBS (XLfit). From the curve-fitting the maximum obtainable up-regulation of UBE3A (UBE3A Max Up) and the maximum obtainable knockdown of UBE3A-SUP (UBE3A-SUP max Kd) were determined. Both are shown as % of control (PBS treated cells).The results are shown in table 10, values are reported as geometric means of each biological replicate.

Table 10: Oligonucleotide EC50 and IC 50 values and maximum UBE3A upregulation and UBE3A suppressor knock down.

CMP ID NO	EC50 ↑ UBE3A	Sd	IC50 ↓ UBE3A-SUP	Sd	UBE3A Max Kd	Sd	UBE3A-SUP max Kd	Sd
586_9	0,02	0,02	0,01	0,00	329,4	25,5	33,5	3,8
585_1	0,03	0,01	0,03	0,02	301,6	18,3	31,0	5,3
572_7	0,03	0,00	0,01	0,03	294,1	30,4	31,3	3,5
591_1	0,03	0,02	0,01	0,00	387,3	46,0	41,4	2,8
585_8	0,04	0,02	0,02	0,01	312,3	23,1	35,2	3,3
626_7	0,04	0,02	0,02	0,00	362,5	44,6	38,7	3,3
621_2	0,04	0,03	0,02	0,01	264,5	19,6	24,7	3,9
624_3	0,04	0,03	0,04	0,03	288,1	19,2	29,7	5,2
169_52	0,04	0,04	0,02	0,01	303,4	23,1	27,3	1,8
624_5	0,04	0,07	0,01	0,01	249,2	16,3	16,4	1,4
586_5	0,04	0,01	0,01	0,00	364,4	43,9	30,4	3,3
626_8	0,04	0,03	0,01	0,01	338,7	24,0	39,1	2,6
169_50	0,05	0,02	0,02	0,02	280,3	23,0	28,3	2,4
572_6	0,05	0,01	0,01	0,02	298,5	22,4	36,3	4,0
639_5	0,05	0,03	0,01	0,00	327,7	22,0	38,2	3,6
592_2	0,05	0,03	0,02	0,05	364,9	27,1	36,4	3,6
586_8	0,05	0,03	0,02	0,01	366,6	35,1	38,0	3,9
625_6	0,06	0,03	0,01	0,00	335,5	34,7	32,5	1,9
644_3	0,06	0,04	0,01	0,02	298,5	22,0	25,3	1,6
586_4	0,06	0,03	0,01	0,01	354,3	31,5	33,0	2,3
642_12	0,06	0,05	0,02	0,01	289,2	14,8	24,7	3,0
572_5	0,07	0,09	0,02	0,00	312,7	25,9	31,5	3,0
592_4	0,07	0,06	0,03	0,01	341,1	31,9	35,7	1,8
622_3	0,07	0,04	0,02	0,01	300,9	21,0	27,6	3,6
622_5	0,07	0,01	0,02	0,01	306,2	13,5	24,4	4,0

(continued)

CMP ID NO	EC50↑ UBE3A	Sd	IC50↓ UBE3A-SUP	Sd	UBE3A Max Kd	Sd	UBE3A-SUP max Kd	Sd
616_4	0,07	0,04	0,03	0,02	293,8	17,9	29,1	5,0
304_6	0,08	0,08	0,02	0,00	318,1	39,2	43,8	3,9
638_8	0,08	0,01	0,01	0,01	354,8	30,6	42,4	4,1
622_4	0,08	0,07	0,02	0,01	330,3	24,8	29,5	2,4
642_13	0,08	0,07	0,04	0,03	268,4	21,0	26,8	2,5
573_8	0,08	0,01	0,04	0,02	320,1	34,4	34,3	3,4
241_9	0,09	0,04	0,04	0,03	352,6	26,4	34,1	2,3
304_10	0,09	0,07	0,03	0,01	289,5	19,9	28,3	2,8
636_8	0,10	0,08	0,03	0,04	330,8	34,1	53,9	13,4
598_4	0,11	0,06	0,03	0,04	295,0	15,1	41,3	2,2
586_6	0,11	0,10	0,02	0,02	316,2	21,2	23,8	3,5
621_1	0,11	0,21	0,02	0,01	311,9	19,2	27,5	5,2
331_1	0,12	0,02	0,03	0,02	293,6	49,0	25,1	5,4
626_9	0,13	0,12	0,02	0,03	302,2	32,6	34,4	2,2
169_56	0,14	0,18	0,02	0,01	356,5	22,3	26,8	2,2
631_6	0,14	0,30	0,04	0,00	292,9	25,1	33,5	4,9
186_1	0,16	0,02	0,04	0,05	371,7	70,1	32,5	5,5
611_7	0,16	0,15	0,02	0,01	369,2	29,3	37,2	3,9
165_1	0,17	0,02	0,07	0,12	266,3	NA	26,7	NA
646_16	0,18	0,15	0,03	0,02	306,0	9,0	30,6	2,9
640_4	0,20	0,10	0,02	0,01	328,4	31,0	40,4	7,0
631_1	0,22	0,07	0,07	0,02	324,6	1,6	47,5	8,1
590_13	0,23	0,59	0,02	0,02	353,4	22,3	31,8	2,2
172_1	0,24	0,10	0,11	0,14	254,2	NA	34,2	NA
35_2	0,26	0,02	0,06	0,09	257,9	NA	22,3	NA
425_5	0,26	0,14	0,08	0,08	317,3	33,9	32,9	2,4
359_1	0,27	0,03	0,03	0,08	260,5	NA	31,3	NA
209_1	0,28	0,08	0,03	0,03	339,9	30,6	48,2	11,6
123_1	0,28	0,13	0,26	0,08	235,9	NA	51,8	NA
361_1	0,29	0,10	0,06	0,02	331,9	17,2	30,7	6,3
602_1	0,31	0,33	0,15	0,20	340,3	21,7	42,2	5,0
NA	0,44	0,12	0,15	0,18	251,3	NA	24,6	NA
287_1	0,45	0,09	0,04	0,02	318,1	45,2	28,8	9,3
303_1	0,46	0,05	0,09	0,15	259,9	NA	30,9	NA
379_1	0,47	0,02	0,08	0,16	247,2	NA	22,5	NA
405_1	0,48	0,42	0,04	0,01	323,0	56,2	32,5	11,9

(continued)

CMP ID NO	EC50↑ UBE3A	Sd	IC50↓ UBE3A-SUP	Sd	UBE3A Max Kd	Sd	UBE3A-SUP max Kd	Sd
39_1	0,51	0,20	0,06	0,06	341,2	30,3	40,4	4,7
206_1	0,52	0,07	0,14	0,31	262,9	NA	30,5	NA
155_1	0,53	0,10	NA	0,53	260,8	NA	26,7	NA
362_1	0,57	0,25	0,09	0,02	328,1	57,3	27,4	8,6
178_1	0,58	0,35	0,11	0,04	334,3	50,8	26,6	8,0
48_1	0,59	0,02	0,07	0,56	262,7	NA	27,2	NA
200_1	0,62	0,51	0,15	0,06	331,0	54,3	33,1	6,2
361_5	0,67	0,18	0,07	0,00	307,1	22,9	32,1	4,5
597_4	0,67	0,51	0,10	0,06	325,3	17,3	35,3	2,7
85_1	0,68	0,06	0,28	0,41	255,5	NA	35,1	NA
278_1	0,69	0,67	0,08	0,09	313,8	33,4	27,2	4,6
271_1	0,69	0,00	0,03	0,65	247,3	NA	24,0	NA
403_1	0,77	0,57	0,11	0,09	296,4	55,0	28,8	7,0
204_1	0,78	0,59	0,05	0,05	316,1	35,5	36,3	7,9
116_1	0,91	0,05	0,09	0,43	240,6	NA	31,6	NA
124_1	0,92	0,29	0,55	0,94	190,0	NA	43,9	NA
237_8	0,93	0,66	0,05	0,03	376,2	32,8	33,6	3,7
378_1	0,95	0,64	0,13	0,09	317,7	30,1	48,5	6,1
126_2	0,95	0,05	0,12	0,70	219,7	NA	45,0	NA
373_1	1,03	0,63	0,13	0,08	321,7	38,6	27,5	4,8
641_5	1,16	1,36	0,07	0,06	335,1	28,9	26,6	5,1
207_1	1,18	0,58	0,18	0,06	318,5	42,9	44,0	7,2
19_1	1,50	0,19	0,24	1,07	261,7	NA	28,4	NA
175_1	1,51	0,42	0,17	0,11	333,5	23,8	29,2	5,2
304_1	1,55	0,09	0,08	0,11	297,8	26,2	32,5	5,7
399_1	1,86	2,50	0,44	0,26	340,1	52,2	39,6	4,3
38_1	2,12	0,10	0,34	0,43	257,3	NA	45,1	NA
222_1	2,29	0,75	0,28	0,12	298,2	34,9	26,8	5,6
187_1	2,30	1,39	1,00	0,91	315,3	38,4	28,6	6,2
272_1	2,32	1,39	0,24	0,16	330,4	41,2	37,1	6,1
18_1	2,42	0,21	0,24	2,00	271,0	NA	29,3	NA
118_1	2,78	0,30	0,31	0,07	205,4	NA	40,4	NA
35_1	2,93	4,94	3,61	1,52	258,4	NA	48,2	NA
233_1	3,14	1,68	0,35	0,16	330,3	20,1	29,3	5,2
220_1	3,47	0,99	1,02	0,48	315,5	27,4	29,6	7,6
33_1	3,97	0,41	1,07	NA	265,7	NA	32,2	NA

(continued)

CMP ID NO	EC50 ↑ UBE3A	Sd	IC50 ↓ UBE3A-SUP	Sd	UBE3A Max Kd	Sd	UBE3A-SUP max Kd	Sd
109_1	4,06	1,45	1,33	0,67	231,7	44,7	39,6	3,9
40_1	4,17	0,05	0,12	3,74	263,6	NA	38,3	NA
115_1	4,98	0,15	0,25	NA	184,2	NA	47,0	NA
161_1	6,55	3,20	1,25	1,24	294,0	24,8	32,1	7,4
105_4	6,61	1,62	1,38	4,20	NA	NA	50,6	NA
19_2	6,66	1,17	3,17	1,52	201,7	NA	57,7	NA
104_1	7,75	6,77	1,67	1,05	267,9	25,5	42,5	4,1
18_2	20,00	1,67	3,50	NA	245,9	NA	46,4	NA
108_1	20,00	0,61	1,27	NA	219,6	NA	51,2	NA
129_2	20,00	0,08	1,10	NA	165,8	NA	56,5	NA
141_1	20,00	0,03	0,15	NA	159,0	NA	64,1	NA
142_1	20,00	1,04	1,12	NA	133,1	NA	57,6	NA
145_1	20,00	1,30	1,81	NA	139,0	NA	56,9	NA

Claims

1. An antisense oligonucleotide for use in the treatment or prevention of Angelman syndrome in a subject, wherein the antisense oligonucleotide comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length with 100% complementarity to position 25278410 to 25419462 on human chromosome 15 (SEQ ID NO:1), wherein the antisense oligonucleotide is capable of inducing human paternal UBE3A expression.

2. A conjugate for use in the treatment or prevention of Angelman syndrome in a subject, the conjugate comprising an antisense oligonucleotide and at least one conjugate moiety covalently attached to the oligonucleotide, wherein the antisense oligonucleotide comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length with 100% complementarity to position 25278410 to 25419462 on human chromosome 15 (SEQ ID NO:1), wherein the antisense oligonucleotide is capable of inducing human paternal UBE3A expression.

3. A pharmaceutical composition for use in the treatment or prevention of Angelman syndrome in a subject, the pharmaceutical composition comprising

   (a) an antisense oligonucleotide comprising a contiguous nucleotide sequence of 10 to 30 nucleotides in length with 100% complementarity to position 25278410 to 25419462 on human chromosome 15 (SEQ ID NO:1), wherein the antisense oligonucleotide is capable of inducing human paternal UBE3A expression; or
   (b) a conjugate comprising the antisense oligonucleotide of (a) and at least one conjugate moiety covalently attached to the oligonucleotide;

   and a pharmaceutically acceptable diluent, solvent, carrier, salt and/or adjuvant.

4. An *in vitro* method for inducing UBE3A expression in a target cell where expression of paternal UBE3A is suppressed, said method comprising administering in an effective amount to said cell

   (a) an antisense oligonucleotide comprising a contiguous nucleotide sequence of 10 to 30 nucleotides in length with 100% complementarity to position 25278410 to 25419462 on human chromosome 15 (SEQ ID NO:1), wherein the antisense oligonucleotide is capable of inducing human paternal UBE3A expression; or
   (b) a conjugate comprising the antisense oligonucleotide of (a) and at least one conjugate moiety covalently attached to the oligonucleotide; or

(c) a pharmaceutical composition comprising the antisense oligonucleotide of (a) or the conjugate of (b), and a pharmaceutically acceptable diluent, solvent, carrier, salt and/or adjuvant.

5. The oligonucleotide for use of claim 1, the conjugate for use of claim 2, the pharmaceutical composition for use of claim 3, or the method of claim 4, wherein the contiguous nucleotide sequence is complementary to a region of the target nucleic acid of SEQ ID NO: 1.

6. The oligonucleotide for use of claim 1 or claim 5, the conjugate for use of claim 2 or claim 5, the pharmaceutical composition for use of claim 3 or claim 5, or the method of claim 4 or claim 5, wherein the contiguous nucleotide sequence is 100% complementary to a region of the target nucleic acid of position 1 to 55318 of SEQ ID NO: 1.

7. The oligonucleotide for use of any one of claims 1, 5 and 6, the conjugate for use of any one of claims 2, 5 and 6, the pharmaceutical composition for use of any one of claims 3, 5 and 6, or the method of any one of claims 4 to 6, wherein the contiguous nucleotide sequence is complementary to a sub-sequence of the target nucleic acid, wherein the sub-sequence is selected from the group consisting of the regions indicated in table 1 or 2.

8. The oligonucleotide for use of any one of claims 1 and 5 to 7, the conjugate for use of any one of claims 2 and 5 to 7, the pharmaceutical composition for use of any one of claims 3 and 5 to 7, or the method of any one of claims 4 to 7, wherein the oligonucleotide comprises or consists of either 17 to 22 nucleotides in length or 15 to 20 nucleotides in length.

9. The oligonucleotide for use of any one of claims 1 and 5 to 8, the conjugate for use of any one of claims 2 and 5 to 8, the pharmaceutical composition for use of any one of claims 3 and 5 to 8, or the method of any one of claims 4 to 8, wherein the oligonucleotide consists of 20 nucleotides in length.

10. The oligonucleotide for use of any one of claims 1 and 5 to 9, the conjugate for use of any one of claims 2 and 5 to 9, the pharmaceutical composition for use of any one of claims 3 and 5 to 9, or the method of any one of claims 4 to 9, wherein the oligonucleotide comprises one or more modified nucleosides.

11. The oligonucleotide for use of any one of claims 1 and 5 to 10, the conjugate for use of any one of claims 2 and 5 to 10, the pharmaceutical composition for use of any one of claims 3 and 5 to 10, or the method of any one of claims 4 to 10, wherein 5-methyl cytosine is used in place of cytosine in the oligonucleotide.

12. The oligonucleotide for use, the conjugate for use, the pharmaceutical composition for use, or the method of claim 10 or claim 11, wherein the one or more modified nucleosides is a 2' sugar modified nucleoside.

13. The oligonucleotide for use, the conjugate for use, the pharmaceutical composition for use, or the method of claim 12, wherein the one or more 2' sugar modified nucleoside is independently selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA, 2'-amino-DNA, 2'-fluoro-DNA, arabino nucleic acid (ANA), 2'-fluoro-ANA and LNA nucleosides.

14. The oligonucleotide for use, the conjugate for use, the pharmaceutical composition for use, or the method of any one of claims 10 to 13, wherein the one or more modified nucleoside is a 2'-O-methoxyethyl-RNA nucleoside.

15. The oligonucleotide for use of any one of claims 1 and 5 to 14, the conjugate for use of any one of claims 2 and 5 to 14, the pharmaceutical composition for use of any one of claims 3 and 5 to 14, or the method of any one of claims 4 to 14, wherein the oligonucleotide comprises at least one modified internucleoside linkage.

16. The oligonucleotide for use, the conjugate for use, the pharmaceutical composition for use, or the method of claim 15, wherein the modified internucleoside linkage is a phosphorothioate internucleoside linkage.

17. The oligonucleotide for use, the conjugate for use, the pharmaceutical composition for use, or the method of claim 16, wherein at least 60% of the internucleoside linkages in the oligonucleotide are phosphorothioate internucleoside linkages.

18. The oligonucleotide for use of any one of claims 1 and 5 to 17, the conjugate for use of any one of claims 2 and 5 to 17, the pharmaceutical composition for use of any one of claims 3 and 5 to 17, or the method of any one of claims 4 to 17, wherein the oligonucleotide is capable of recruiting RNase H.

19. The oligonucleotide for use, the conjugate for use, the pharmaceutical composition for use, or the method of claim 18, wherein the oligonucleotide is a gapmer.

20. The oligonucleotide for use, the conjugate for use, the pharmaceutical composition for use, or the method of claim 18 or claim 19, wherein the oligonucleotide is a gapmer of formula 5'-F-G-F'-3', where region F and F' independently comprise 1 to 7 modified nucleosides and G is a region between 6 and 16 nucleosides which are capable of recruiting RNaseH.

21. The oligonucleotide for use, the conjugate for use, the pharmaceutical composition for use, or the method of claim 20, wherein the modified nucleosides are 2' sugar modified nucleosides independently selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA, 2'-amino-DNA, 2'-fluoro-DNA, arabino nucleic acid (ANA), 2'-fluoro-ANA and LNA nucleosides.

22. The oligonucleotide for use of any one of claims 1 and 5 to 21, the conjugate for use of any one of claims 2 and 5 to 21, the pharmaceutical composition for use of any one of claims 3 and 5 to 21, or the method of any one of claims 4 to 21, wherein the oligonucleotide is a gapmer of the formula F-G-F' wherein each of regions F and F' independently consists of 2, 3, 4 or 5 modified nucleoside units and region G consists of 9, 10, 11, 12, 13, 14 or 15 nucleoside units.

23. The oligonucleotide for use of any one of claims 1 and 5 to 20, the conjugate for use of any one of claims 2 and 5 to 22, the pharmaceutical composition for use of any one of claims 3 and 5 to 22, or the method of any one of claims 4 to 22, wherein the oligonucleotide is a gapmer of the formula F-G-F' wherein each of regions F and F' independently consists of 2, 3, 4 or 5 2'-O-methoxyethyl-ribose sugar (2'-MOE) units, and region G consists of 9, 10, 11, 12, 13, 14 or 15 DNA units.

24. The oligonucleotide for use, the conjugate for use, the pharmaceutical composition for use, or the method of any one of claims 20 to 23, wherein each of regions F and F' independently consists of 5 2'-O-methoxyethyl-ribose sugar (2'-MOE) nucleoside units and region G consists of 10 DNA nucleoside units.

25. An antisense oligonucleotide capable of inducing human paternal UBE3A expression for use in the treatment or prevention of Angelman syndrome in a subject, wherein said antisense oligonucleotide comprises a contiguous nucleotide sequence that is 100% complementary to a region of the target nucleic acid of position 1 to 55318 of SEQ ID NO: 1, wherein the oligonucleotide is either 15 to 20 nucleotides in length or 17 to 22 nucleotides in length, wherein the oligonucleotide comprises one or more modified nucleosides, wherein the one or more modified nucleosides is a 2' sugar modified nucleoside, wherein the one or more 2' sugar modified nucleoside is independently selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA, 2'-amino-DNA, 2'-fluoro-DNA, arabino nucleic acid (ANA), 2'-fluoro-ANA and LNA nucleosides, wherein the oligonucleotide comprises at least one modified internucleoside linkage, wherein said modified internucleoside linkage is a phosphorothioate linkage, wherein the oligonucleotide is a gapmer of the formula F-G-F' wherein each of regions F and F' independently consists of 2, 3, 4 or 5 modified nucleoside units and region G consists of 9, 10, 11, 12, 13, 14 or 15 nucleoside units.

26. A conjugate for use in the treatment or prevention of Angelman syndrome in a subject, the conjugate comprising an antisense oligonucleotide and at least one conjugate moiety covalently attached to the oligonucleotide, wherein the antisense oligonucleotide comprises a contiguous nucleotide sequence that is 100% complementary to a region of the target nucleic acid of position 1 to 55318 of SEQ ID NO: 1, wherein the oligonucleotide is either 15 to 20 nucleotides in length or 17 to 22 nucleotides in length, wherein the oligonucleotide comprises one or more modified nucleosides, wherein the one or more modified nucleosides is a 2' sugar modified nucleoside, wherein the one or more 2' sugar modified nucleoside is independently selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA, 2'-amino-DNA, 2'-fluoro-DNA, arabino nucleic acid (ANA), 2'-fluoro-ANA and LNA nucleosides, wherein the oligonucleotide comprises at least one modified internucleoside linkage, wherein said modified internucleoside linkage is a phosphorothioate linkage, wherein the oligonucleotide is a gapmer of the formula F-G-F' wherein each of regions F and F' independently consists of 2, 3, 4 or 5 modified nucleoside units and region G consists of 9, 10, 11, 12, 13, 14 or 15 nucleoside units.

27. A pharmaceutical composition in the treatment or prevention of Angelman syndrome in a subject, the pharmaceutical composition comprising

(i) an antisense oligonucleotide comprising a contiguous nucleotide sequence that is 100% complementary to a region of the target nucleic acid of position 1 to 55318 of SEQ ID NO: 1, wherein the oligonucleotide is either 15 to 20 nucleotides in length or 17 to 22 nucleotides in length, wherein the oligonucleotide comprises one or more modified nucleosides, wherein the one or more modified nucleosides is a 2' sugar modified nucleoside, wherein the one or more 2' sugar modified nucleoside is independently selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA, 2'-amino-DNA, 2'-fluoro-DNA, arabino nucleic acid (ANA), 2'-fluoro-ANA and LNA nucleosides, wherein the oligonucleotide comprises at least one modified internucleoside linkage, wherein said modified internucleoside linkage is a phosphorothioate linkage, wherein the oligonucleotide is a gapmer of the formula F-G-F' wherein each of regions F and F' independently consists of 2, 3, 4 or 5 modified nucleoside units and region G consists of 9, 10, 11, 12, 13, 14 or 15 nucleoside units; or

(ii) a conjugate comprising the antisense oligonucleotide of (i) and at least one conjugate moiety covalently attached to the oligonucleotide;

and a pharmaceutically acceptable diluent, solvent, carrier, salt and/or adjuvant.

28. An *in vitro* method for inducing UBE3A expression in a target cell where expression of paternal UBE3A is suppressed, said method comprising administering in an effective amount to said cell

(i) an antisense oligonucleotide comprising a contiguous nucleotide sequence that is 100% complementary to a region of the target nucleic acid of position 1 to 55318 of SEQ ID NO: 1, wherein the oligonucleotide is either 15 to 20 nucleotides in length or 17 to 22 nucleotides in length, wherein the oligonucleotide comprises one or more modified nucleosides, wherein the one or more modified nucleosides is a 2' sugar modified nucleoside, wherein the one or more 2' sugar modified nucleoside is independently selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA, 2'-amino-DNA, 2'-fluoro-DNA, arabino nucleic acid (ANA), 2'-fluoro-ANA and LNA nucleosides, wherein the oligonucleotide comprises at least one modified internucleoside linkage, wherein said modified internucleoside linkage is a phosphorothioate linkage, wherein the oligonucleotide is a gapmer of the formula F-G-F' wherein each of regions F and F' independently consists of 2, 3, 4 or 5 modified nucleoside units and region G consists of 9, 10, 11, 12, 13, 14 or 15 nucleoside units; or

(ii) a conjugate comprising the antisense oligonucleotide of (i) and at least one conjugate moiety covalently attached to the oligonucleotide; or

(iii) a pharmaceutical composition comprising the antisense oligonucleotide of (i) or the conjugate of (ii), and a pharmaceutically acceptable diluent, solvent, carrier, salt and/or adjuvant.

29. The method according to any one of claims 4 to 24 and 28, wherein the expression of UBE3A is increased by at least 40% compared to a control.

30. The method according to any one of claims 4 to 24, 28 and 29, wherein the level of the SNHG14 transcript downstream of SNORD109B is reduced by at least 30% compared to a control.

31. The method according to any one of claims 4 to 24 and 28 to 30, wherein the target cell is a neuronal cell.

32. The method according to any one of claims 4 to 24 and 28 to 31, wherein the expression of SNORD115 is not significantly affected compared to a control.

Patentansprüche

1. Antisense-Oligonukleotid zur Verwendung bei der Behandlung oder Prävention des Angelman-Syndroms in einem Subjekt, wobei das Antisense-Oligonukleotid eine zusammenhängende Nukleotidsequenz mit einer Länge von 10 bis 30 Nukleotiden mit 100%iger Komplementarität zur Position 25278410 bis 25419462 auf dem menschlichen Chromosom 15 (SEQ ID NO:1) umfasst,
wobei das Antisense-Oligonukleotid in der Lage ist, die menschliche paternale UBE3A-Expression zu induzieren.

2. Konjugat zur Verwendung bei der Behandlung oder Prävention des Angelman-Syndroms in einem Subjekt, wobei das Konjugat ein Antisense-Oligonukleotid und mindestens eine kovalent an das Oligonukleotid gebundene Konjugateinheit umfasst, wobei das Antisense-Oligonukleotid eine zusammenhängende Nukleotidsequenz mit einer Länge von 10 bis 30 Nukleotiden mit 100%iger Komplementarität zur Position 25278410 bis 25419462 auf dem menschlichen Chromosom 15 (SEQ ID NO:1) umfasst, wobei das Antisense-Oligonukleotid in der Lage ist, die menschliche paternale UBE3A-Expression zu induzieren.

3. Pharmazeutische Zusammensetzung zur Verwendung bei der Behandlung oder Prävention des Angelman-Syndroms bei einem Subjekt, wobei die pharmazeutische Zusammensetzung umfasst

(a) ein Antisense-Oligonukleotid, umfassend eine zusammenhängende Nukleotidsequenz von 10 bis 30 Nukleotiden Länge mit 100%iger Komplementarität zur Position 25278410 bis 25419462 auf dem menschlichen Chromosom 15 (SEQ ID NO:1),
wobei das Antisense-Oligonukleotid in der Lage ist, die menschliche paternale UBE3A-Expression zu induzieren; oder
(b) ein Konjugat, umfassend das Antisense-Oligonukleotid von (a) und mindestens eine konjugierte Einheit, die kovalent an das Oligonukleotid gebunden ist;
und ein pharmazeutisch akzeptables Verdünnungsmittel, Lösungsmittel, einen Träger, ein Salz und/oder ein Adjuvans.

4. In-vitro-Verfahren zur Induktion der UBE3A-Expression in einer Zielzelle, in der die Expression von paternaler UBE3A unterdrückt ist, wobei das Verfahren die Verabreichung einer wirksamen Menge an die Zelle umfasst von

(a) ein Antisense-Oligonukleotid, umfassend eine zusammenhängende Nukleotidsequenz von 10 bis 30 Nukleotiden Länge mit 100%iger Komplementarität zur Position 25278410 bis 25419462 auf dem menschlichen Chromosom 15 (SEQ ID NO:1),
wobei das Antisense-Oligonukleotid in der Lage ist, die menschliche paternale UBE3A-Expression zu induzieren; oder
(b) einem Konjugat, umfassend das Antisense-Oligonukleotid von (a) und mindestens eine konjugierte Einheit, die kovalent an das Oligonukleotid gebunden ist; oder
(c) einer pharmazeutischen Zusammensetzung, umfassend das Antisense-Oligonukleotid von (a) oder das Konjugat von (b) und ein pharmazeutisch akzeptables Verdünnungsmittel, Lösungsmittel, einen Träger, ein Salz und/oder ein Adjuvans.

5. Oligonukleotid zur Verwendung nach Anspruch 1, das Konjugat zur Verwendung nach Anspruch 2, die pharmazeutische Zusammensetzung zur Verwendung nach Anspruch 3 oder das Verfahren nach Anspruch 4, wobei die zusammenhängende Nukleotidsequenz komplementär zu einer Region der Ziel-Nukleinsäure von SEQ ID NO: 1.

6. Oligonukleotid zur Verwendung nach Anspruch 1 oder Anspruch 5, Konjugat zur Verwendung nach Anspruch 2 oder Anspruch 5, pharmazeutische Zusammensetzung zur Verwendung nach Anspruch 3 oder Anspruch 5 oder Verfahren nach Anspruch 4 oder Anspruch 5, wobei die zusammenhängende Nukleotidsequenz zu 100 % komplementär zu einer Region der Ziel-Nukleinsäure der Position 1 bis 55318 von SEQ ID NO: 1.

7. Oligonukleotid zur Verwendung nach einem der Ansprüche 1, 5 und 6, Konjugat zur Verwendung nach einem der Ansprüche 2, 5 und 6, pharmazeutische Zusammensetzung zur Verwendung nach einem der Ansprüche 3, 5 und 6 oder Verfahren nach einem der Ansprüche 4 bis 6, wobei die zusammenhängende Nukleotidsequenz komplementär zu einer Untersequenz der Zielnukleinsäure ist, wobei die Untersequenz aus der Gruppe ausgewählt ist, bestehend aus den in Tabelle 1 oder 2 angegebenen Regionen.

8. Oligonukleotid zur Verwendung nach einem der Ansprüche 1 und 5 bis 7, Konjugat zur Verwendung nach einem der Ansprüche 2 und 5 bis 7, pharmazeutische Zusammensetzung zur Verwendung nach einem der Ansprüche 3 und 5 bis 7 oder Verfahren nach einem der Ansprüche 4 bis 7, wobei das Oligonukleotid in der Länge entweder 17 bis 22 Nukleotide oder 15 bis 20 Nukleotide umfasst oder daraus besteht.

9. Oligonukleotid zur Verwendung nach einem der Ansprüche 1 und 5 bis 8, Konjugat zur Verwendung nach einem der Ansprüche 2 und 5 bis 8, pharmazeutische Zusammensetzung zur Verwendung nach einem der Ansprüche 3 und 5 bis 8 oder Verfahren nach einem der Ansprüche 4 bis 8, wobei das Oligonukleotid in der Länge aus 20 Nukleotiden besteht.

10. Oligonukleotid zur Verwendung nach einem der Ansprüche 1 und 5 bis 9, Konjugat zur Verwendung nach einem der Ansprüche 2 und 5 bis 9, pharmazeutische Zusammensetzung zur Verwendung nach einem der Ansprüche 3 und 5 bis 9 oder Verfahren nach einem der Ansprüche 4 bis 9, wobei das Oligonukleotid ein oder mehrere modifizierte

Nukleoside umfasst.

11. Oligonukleotid zur Verwendung nach einem der Ansprüche 1 und 5 bis 10, Konjugat zur Verwendung nach einem der Ansprüche 2 und 5 bis 10, pharmazeutische Zusammensetzung zur Verwendung nach einem der Ansprüche 3 und 5 bis 10 oder Verfahren nach einem der Ansprüche 4 bis 10, wobei 5-Methylcytosin anstelle von Cytosin in dem Oligonukleotid verwendet wird.

12. Oligonukleotid zur Verwendung, Konjugat zur Verwendung, pharmazeutische Zusammensetzung zur Verwendung oder Verfahren nach Anspruch 10 oder Anspruch 11, wobei das eine oder die mehreren modifizierten Nukleoside ein 2'-Zucker-modifiziertes Nukleosid sind.

13. Oligonukleotid zur Verwendung, Konjugat zur Verwendung, pharmazeutische Zusammensetzung zur Verwendung oder Verfahren nach Anspruch 12, wobei das eine oder mehrere 2'-Zucker-modifizierte Nukleosid unabhängig aus der Gruppe ausgewählt sind, bestehend aus 2'-O-Alkyl-RNA, 2'-O-Methyl-RNA, 2'-Alkoxy-RNA, 2'-O-Methoxyethyl-RNA, 2'-Amino-DNA, 2'-Fluor-DNA, Arabino-Nucleinsäure (ANA), 2'-Fluor-ANA und LNA-Nucleosiden.

14. Oligonukleotid zur Verwendung, Konjugat zur Verwendung, pharmazeutische Zusammensetzung zur Verwendung oder Verfahren nach einem der Ansprüche 10 bis 13, wobei das eine oder die mehreren modifizierten Nukleoside ein 2'-O-Methoxyethyl-RNA-Nukleosid sind.

15. Oligonukleotid zur Verwendung nach einem der Ansprüche 1 und 5 bis 14, Konjugat zur Verwendung nach einem der Ansprüche 2 und 5 bis 14, pharmazeutische Zusammensetzung zur Verwendung nach einem der Ansprüche 3 und 5 bis 14 oder Verfahren nach einem der Ansprüche 4 bis 14, wobei das Oligonukleotid mindestens eine modifizierte Internukleosid-Bindung umfasst.

16. Oligonukleotid zur Verwendung, Konjugat zur Verwendung, pharmazeutische Zusammensetzung zur Verwendung oder Verfahren nach Anspruch 15, wobei die modifizierte Internukleosid-Bindung eine Phosphorothioat-Internukleosid-Bindung ist.

17. Oligonukleotid zur Verwendung, Konjugat zur Verwendung, pharmazeutische Zusammensetzung zur Verwendung oder Verfahren nach Anspruch 16, wobei mindestens 60 % der Internukleosidbindungen in dem Oligonukleotid Phosphorothioat-Internukleosidbindungen sind.

18. Oligonukleotid zur Verwendung nach einem der Ansprüche 1 und 5 bis 17, Konjugat zur Verwendung nach einem der Ansprüche 2 und 5 bis 17, pharmazeutische Zusammensetzung zur Verwendung nach einem der Ansprüche 3 und 5 bis 17 oder Verfahren nach einem der Ansprüche 4 bis 17, wobei das Oligonukleotid in der Lage ist, RNase H zu rekrutieren.

19. Oligonukleotid zur Verwendung, Konjugat zur Verwendung, pharmazeutische Zusammensetzung zur Verwendung oder Verfahren nach Anspruch 18, wobei das Oligonukleotid ein Gapmer ist.

20. Oligonukleotid zur Verwendung, Konjugat zur Verwendung, pharmazeutische Zusammensetzung zur Verwendung oder Verfahren nach Anspruch 18 oder Anspruch 19, wobei das Oligonukleotid ein Gapmer der Formel 5'-F-G-F'-3' ist, wobei die Regionen F und F' unabhängig voneinander 1 bis 7 modifizierte Nukleoside umfassen und G eine Region zwischen 6 und 16 Nukleosiden ist, die in der Lage sind, RNaseH zu rekrutieren.

21. Oligonukleotid zur Verwendung, Konjugat zur Verwendung, pharmazeutische Zusammensetzung zur Verwendung oder Verfahren nach Anspruch 20, wobei die modifizierten Nukleoside 2'-Zucker-modifizierte Nukleoside sind, die unabhängig voneinander aus der Gruppe ausgewählt sind, bestehend aus 2'-O-Alkyl-RNA, 2'-O-Methyl-RNA, 2'-Alkoxy-RNA, 2'-O-Methoxyethyl-RNA, 2'-Amino-DNA, 2'-Fluor-DNA, Arabino-Nukleinsäure (ANA), 2'-Fluor-ANA und LNA-Nukleosiden.

22. Oligonukleotid zur Verwendung nach einem der Ansprüche 1 und 5 bis 21, Konjugat zur Verwendung nach einem der Ansprüche 2 und 5 bis 21, pharmazeutische Zusammensetzung zur Verwendung nach einem der Ansprüche 3 und 5 bis 21 oder Verfahren nach einem der Ansprüche 4 bis 21, wobei das Oligonukleotid ein Gapmer der Formel F-G-F' ist, wobei jede der Regionen F und F' unabhängig voneinander aus 2, 3, 4 oder 5 modifizierten Nukleosideinheiten besteht und die Region G aus 9, 10, 11, 12, 13, 14 oder 15 Nukleosideinheiten besteht.

23. Oligonukleotid zur Verwendung nach einem der Ansprüche 1 und 5 bis 20, Konjugat zur Verwendung nach einem der Ansprüche 2 und 5 bis 22, pharmazeutische Zusammensetzung zur Verwendung nach einem der Ansprüche 3 und 5 bis 22 oder Verfahren nach einem der Ansprüche 4 bis 22, wobei das Oligonukleotid ein Gapmer der Formel F-G-F' ist, wobei jede der Regionen F und F' unabhängig voneinander aus 2, 3, 4 oder 5 2'-O-Methoxyethyl-RiboseZucker (2'-MOE)-Einheiten besteht, und die Region G aus 9, 10, 11, 12, 13, 14 oder 15 DNA-Einheiten besteht.

24. Oligonukleotid zur Verwendung, Konjugat zur Verwendung, pharmazeutische Zusammensetzung zur Verwendung oder Verfahren nach einem der Ansprüche 20 bis 23, wobei jede der Regionen F und F' unabhängig voneinander aus 5 2'-O-Methoxyethyl-Ribosezucker (2'-MOE)-Nukleosideinheiten besteht und die Region G aus 10 DNA-Nukleosideinheiten besteht.

25. Antisense-Oligonukleotid, das in der Lage ist, die menschliche paternale UBE3A-Expression zu induzieren, zur Verwendung bei der Behandlung oder Prävention des Angelman-Syndroms in einem Subjekt,
wobei das Antisense-Oligonukleotid eine zusammenhängende Nukleotidsequenz umfasst, die zu 100 % komplementär ist zu einer Region der Ziel-Nukleinsäure von Position 1 bis 55318 der SEQ ID NO: 1, wobei das Oligonukleotid entweder eine Länge von 15 bis 20 Nukleotiden oder eine Länge von 17 bis 22 Nukleotiden aufweist, wobei das Oligonukleotid ein oder mehrere modifizierte Nukleoside umfasst, wobei das eine oder die mehreren modifizierten Nukleoside ein 2'-Zucker-modifiziertes Nukleosid ist, wobei das eine oder die mehreren 2'-Zucker-modifizierten Nukleoside unabhängig voneinander ausgewählt sind aus der Gruppe bestehend aus 2'-O-Alkyl-RNA, 2'-O-Methyl-RNA, 2'-Alkoxy-RNA, 2'-O-Methoxyethyl-RNA, 2'-Amino-DNA, 2'-Fluor-DNA, Arabino-Nukleinsäure (ANA), 2'-Fluor-ANA und LNA-Nukleoside, wobei das Oligonukleotid mindestens eine modifizierte Internukleosid-Bindung umfasst, wobei die modifizierte Internukleosid-Bindung eine Phosphorothioat-Bindung ist, wobei das Oligonukleotid ein Gapmer der Formel F-G-F' ist, wobei jede der Regionen F und F' unabhängig voneinander aus 2, 3, 4 oder 5 modifizierten Nukleosideinheiten besteht und die Region G aus 9, 10, 11, 12, 13, 14 oder 15 Nukleosideinheiten besteht.

26. Konjugat zur Verwendung bei der Behandlung oder Prävention des Angelman-Syndroms in einem Subjekt, wobei das Konjugat ein Antisense-Oligonukleotid und mindestens eine kovalent an das Oligonukleotid gebundene Konjugateinheit umfasst, wobei das Antisense-Oligonukleotid eine zusammenhängende Nukleotidsequenz umfasst, die zu 100 % komplementär ist zu einer Region der Zielnukleinsäure der Position 1 bis 55318 von SEQ ID NO: 1, wobei das Oligonukleotid entweder eine Länge von 15 bis 20 Nukleotiden oder eine Länge von 17 bis 22 Nukleotiden aufweist, wobei das Oligonukleotid ein oder mehrere modifizierte Nukleoside umfasst, wobei das eine oder die mehreren modifizierten Nukleoside ein 2'-Zucker-modifiziertes Nukleosid ist, wobei das eine oder die mehreren 2'-Zucker-modifizierten Nukleoside unabhängig voneinander ausgewählt sind aus der Gruppe bestehend aus 2'-O-Alkyl-RNA, 2'-O-Methyl-RNA, 2'-Alkoxy-RNA, 2'-O-Methoxyethyl-RNA, 2'-Amino-DNA, 2'-Fluor-DNA, Arabino-Nukleinsäure (ANA), 2'-Fluor-ANA und LNA-Nukleoside, wobei das Oligonukleotid mindestens eine modifizierte Internukleosid-Bindung umfasst, wobei die modifizierte Internukleosid-Bindung eine Phosphorothioat-Bindung ist, wobei das Oligonukleotid ein Gapmer der Formel F-G-F' ist, wobei jede der Regionen F und F' unabhängig voneinander aus 2, 3, 4 oder 5 modifizierten Nukleosideinheiten besteht und die Region G aus 9, 10, 11, 12, 13, 14 oder 15 Nukleosideinheiten besteht.

27. Pharmazeutische Zusammensetzung für die Behandlung oder Prävention des Angelman-Syndroms in einem Subjekt, wobei die pharmazeutische Zusammensetzung umfasst (i) ein Antisense-Oligonukleotid, das eine zusammenhängende Nukleotidsequenz umfasst, die zu 100 % komplementär ist zu einer Region des Zielwertes der Nukleinsäure an den Positionen 1 bis 55318 der SEQ ID NO: 1, wobei das Oligonukleotid entweder eine Länge von 15 bis 20 Nukleotiden oder eine Länge von 17 bis 22 Nukleotiden aufweist, wobei das Oligonukleotid ein oder mehrere modifizierte Nukleoside umfasst, wobei das eine oder die mehreren modifizierten Nukleoside ein 2'-Zucker-modifiziertes Nukleosid ist, wobei das eine oder die mehreren 2'-Zucker-modifizierten Nukleoside unabhängig voneinander ausgewählt sind aus der Gruppe bestehend aus 2'-O-Alkyl-RNA, 2'-O-Methyl-RNA, 2'-Alkoxy-RNA, 2'-O-Methoxyethyl-RNA, 2'-Amino-DNA, 2'-Fluor-DNA, Arabino-Nukleinsäure (ANA), 2'-Fluor-ANA und LNA-Nukleoside, wobei das Oligonukleotid mindestens eine modifizierte Internukleosid-Bindung umfasst, wobei die modifizierte Internukleosid-Bindung eine Phosphorothioat-Bindung ist, wobei das Oligonukleotid ein Gapmer der Formel F-G-F' ist, wobei jede der Regionen F und F' unabhängig voneinander aus 2, 3, 4 oder 5 modifizierten Nukleosideinheiten besteht und die Region G aus 9, 10, 11, 12, 13, 14 oder 15 Nukleosideinheiten besteht; oder (ii) ein Konjugat, umfassend das Antisense-Oligonukleotid von (i) und mindestens eine konjugierte Einheit, die kovalent an das Oligonukleotid gebunden ist; und ein pharmazeutisch akzeptables Verdünnungsmittel, Lösungsmittel, einen Träger, ein Salz und/oder ein Adjuvans.

28. In-vitro-Verfahren zur Induktion der UBE3A-Expression in einer Zielzelle, in der die Expression von paternaler

UBE3A unterdrückt ist, wobei das Verfahren die Verabreichung einer wirksamen Menge an die Zelle umfasst von

(i) ein Antisense-Oligonukleotid, das eine zusammenhängende Nukleotidsequenz umfasst, die zu 100 % komplementär ist zu einer Region des Zielwertes der Nukleinsäure an den Positionen 1 bis 55318 der SEQ ID NO: 1, wobei das Oligonukleotid entweder eine Länge von 15 bis 20 Nukleotiden oder eine Länge von 17 bis 22 Nukleotiden aufweist, wobei das Oligonukleotid ein oder mehrere modifizierte Nukleoside umfasst, wobei das eine oder die mehreren modifizierten Nukleoside ein 2'-Zucker-modifiziertes Nukleosid ist, wobei das eine oder die mehreren 2'-Zucker-modifizierten Nukleoside unabhängig voneinander ausgewählt sind aus der Gruppe bestehend aus 2'-O-Alkyl-RNA, 2'-O-Methyl-RNA, 2'-Alkoxy-RNA, 2'-O-Methoxyethyl-RNA, 2'-Amino-DNA, 2'-Fluor-DNA, Arabino-Nukleinsäure (ANA), 2'-Fluor-ANA und LNA-Nukleoside, wobei das Oligonukleotid mindestens eine modifizierte Internukleosid-Bindung umfasst, wobei die modifizierte Internukleosid-Bindung eine Phosphorothioat-Bindung ist, wobei das Oligonukleotid ein Gapmer der Formel F-G-F' ist, wobei jede der Regionen F und F' unabhängig voneinander aus 2, 3, 4 oder 5 modifizierten Nukleosideinheiten besteht und die Region G aus 9, 10, 11, 12, 13, 14 oder 15 Nukleosideinheiten besteht; oder
(ii) einem Konjugat, umfassend das Antisense-Oligonukleotid von (i) und mindestens eine konjugierte Einheit, die kovalent an das Oligonukleotid gebunden ist; oder
(iii) einer pharmazeutischen Zusammensetzung, umfassend das Antisense-Oligonukleotid von (i) oder das Konjugat von (ii) und ein pharmazeutisch akzeptables Verdünnungsmittel, Lösungsmittel, einen Träger, ein Salz und/oder ein Adjuvans.

29. Verfahren nach einem der Ansprüche 4 bis 24 und 28, wobei die Expression von UBE3A um mindestens 40 % im Vergleich zu einer Kontrolle erhöht ist.

30. Verfahren nach einem der Ansprüche 4 bis 24, 28 und 29, wobei der Spiegel des SNHG14-Transkripts stromabwärts von SNORD109B um mindestens 30 % im Vergleich zu einer Kontrolle reduziert wird.

31. Verfahren nach einem der Ansprüche 4 bis 24 und 28 bis 30, wobei die Zielzelle eine neuronale Zelle ist.

32. Verfahren nach einem der Ansprüche 4 bis 24 und 28 bis 31, wobei die Expression von SNORD115 im Vergleich zu einer Kontrolle nicht signifikant beeinflusst wird.

Revendications

1. Oligonucléotide antisens pour une utilisation dans le traitement ou la prévention du syndrome d'Angelman chez un sujet, dans lequel l'oligonucléotide antisens comprend une séquence nucléotidique contiguë de 10 à 30 nucléotides de longueur avec une complémentarité de 100 % par rapport à la position 25278410 à 25419462 sur le chromosome humain 15 (SEQ ID NO:1),
dans lequel l'oligonucléotide antisens est capable d'induire l'expression du UBE3A paternel humain.

2. Conjugué pour une utilisation dans le traitement ou la prévention du syndrome d'Angelman chez un sujet, le conjugué comprenant un oligonucléotide antisens et au moins un groupement conjugué lié de manière covalente à l'oligonucléotide, dans lequel l'oligonucléotide antisens comprend une séquence nucléotidique contiguë de 10 à 30 nucléotides de longueur avec 100 % de complémentarité par rapport à la position 25278410 à 25419462 sur le chromosome humain 15 (SEQ ID NO:1), dans lequel l'oligonucléotide antisens est capable d'induire l'expression du UBE3A paternel humain.

3. Composition pharmaceutique pour une utilisation dans le traitement ou la prévention du syndrome d'Angelman chez un sujet, la composition pharmaceutique comprenant

(a) un oligonucléotide antisens comprenant une séquence nucléotidique contiguë de 10 à 30 nucléotides de longueur avec une complémentarité de 100 % par rapport à la position 25278410 à 25419462 sur le chromosome humain 15 (SEQ ID NO:1),
dans laquelle l'oligonucléotide antisens est capable d'induire l'expression du UBE3A paternel humain ; ou
(b) un conjugué comprenant l'oligonucléotide antisens de (a) et au moins un groupement conjugué lié de manière covalente à l'oligonucléotide ;
et un diluant, solvant, support, sel et/ou adjuvant acceptable sur le plan pharmaceutique.

4. Procédé *in vitro* pour induire l'expression du UBE3A dans une cellule cible où l'expression du UBE3A paternel est supprimée, ledit procédé comprenant l'administration en une quantité efficace à ladite cellule

(a) d'un oligonucléotide antisens comprenant une séquence nucléotidique contiguë de 10 à 30 nucléotides de longueur avec une complémentarité de 100 % par rapport à la position 25278410 à 25419462 sur le chromosome humain 15 (SEQ ID NO:1),
dans lequel l'oligonucléotide antisens est capable d'induire l'expression du UBE3A paternel humain ; ou
(b) d'un conjugué comprenant l'oligonucléotide antisens de (a) et au moins un groupement conjugué lié de manière covalente à l'oligonucléotide ; ou
(c) d'une composition pharmaceutique comprenant l'oligonucléotide antisens de (a) ou le conjugué de (b), et un diluant, solvant, support, sel et/ou adjuvant acceptable sur le plan pharmaceutique.

5. Oligonucléotide pour une utilisation selon la revendication 1, conjugué pour une utilisation selon la revendication 2, composition pharmaceutique pour une utilisation selon la revendication 3, ou procédé selon la revendication 4, dans lequel/laquelle la séquence nucléotidique contiguë est complémentaire à une région de l'acide nucléique cible de SEQ ID NO: 1.

6. Oligonucléotide pour une utilisation selon la revendication 1 ou la revendication 5, conjugué pour une utilisation selon la revendication 2 ou la revendication 5, composition pharmaceutique pour une utilisation selon la revendication 3 ou la revendication 5, ou procédé selon la revendication 4 ou la revendication 5, dans lequel/laquelle la séquence nucléotidique contiguë est 100 % complémentaire à une région de l'acide nucléique cible de la position 1 à 55318 de SEQ ID NO : 1.

7. Oligonucléotide pour une utilisation selon l'une quelconque des revendications 1, 5 et 6, conjugué pour une utilisation selon l'une quelconque des revendications 2, 5 et 6, composition pharmaceutique pour une utilisation selon l'une quelconque des revendications 3, 5 et 6, ou procédé selon l'une quelconque des revendications 4 à 6, dans lequel/laquelle la séquence nucléotidique contiguë est complémentaire à une sous-séquence de l'acide nucléique cible, dans lequel/laquelle la sous-séquence est sélectionnée dans le groupe constitué par les régions indiquées dans le tableau 1 ou 2.

8. Oligonucléotide pour une utilisation selon l'une quelconque des revendications 1 et 5 à 7, conjugué pour une utilisation selon l'une quelconque des revendications 2 et 5 à 7, composition pharmaceutique pour une utilisation selon l'une quelconque des revendications 3 et 5 à 7, ou procédé selon l'une quelconque des revendications 4 à 7, dans lequel/laquelle l'oligonucléotide comprend ou est constitué de 17 à 22 nucléotides de longueur ou de 15 à 20 nucléotides de longueur.

9. Oligonucléotide pour une utilisation selon l'une quelconque des revendications 1 et 5 à 8, conjugué pour une utilisation selon l'une quelconque des revendications 2 et 5 à 8, composition pharmaceutique pour une utilisation selon l'une quelconque des revendications 3 et 5 à 8, ou procédé selon l'une quelconque des revendications 4 à 8, dans lequel/laquelle l'oligonucléotide est constitué de 20 nucléotides de longueur.

10. Oligonucléotide pour une utilisation selon l'une quelconque des revendications 1 et 5 à 9, conjugué pour une utilisation selon l'une quelconque des revendications 2 et 5 à 9, composition pharmaceutique pour une utilisation selon l'une quelconque des revendications 3 et 5 à 9, ou procédé selon l'une quelconque des revendications 4 à 9, dans lequel/laquelle l'oligonucléotide comprend un ou plusieurs nucléosides modifiés.

11. Oligonucléotide pour une utilisation selon l'une quelconque des revendications 1 et 5 à 10, conjugué pour une utilisation selon l'une quelconque des revendications 2 et 5 à 10, composition pharmaceutique pour une utilisation selon l'une quelconque des revendications 3 et 5 à 10, ou procédé selon l'une quelconque des revendications 4 à 10, dans lequel/laquelle la 5-méthyl-cytosine est utilisée à la place de la cytosine dans l'oligonucléotide.

12. Oligonucléotide pour une utilisation, conjugué pour une utilisation, composition pharmaceutique pour une utilisation, ou procédé selon la revendication 10 ou la revendication 11, dans lequel/laquelle le ou les nucléosides modifiés sont un nucléoside à sucre modifié en 2'.

13. Oligonucléotide pour une utilisation, conjugué pour une utilisation, composition pharmaceutique pour une utilisation ou procédé selon la revendication 12, dans lequel/laquelle le ou les nucléosides à sucre modifié en 2' sont sélectionnés indépendamment dans le groupe constitué par des nucléosides 2'-O-alkyl-ARN, 2'-O-méthyl-ARN, 2'-alcoxy-

ARN, 2'-O-méthoxyéthyl-ARN, 2'-amino-ADN, 2'-fluoro-ADN, acide arabino nucléique (ANA), 2'-fluoro-ANA et LNA.

14. Oligonucléotide pour une utilisation, conjugué pour une utilisation, composition pharmaceutique pour une utilisation ou procédé selon l'une quelconque des revendications 10 à 13, dans lequel/laquelle le ou les nucléosides modifiés sont un nucléoside 2'-O-méthoxyéthyl-ARN.

15. Oligonucléotide pour une utilisation selon l'une quelconque des revendications 1 et 5 à 14, conjugué pour une utilisation selon l'une quelconque des revendications 2 et 5 à 14, composition pharmaceutique pour une utilisation selon l'une quelconque des revendications 3 et 5 à 14, ou procédé selon l'une quelconque des revendications 4 à 14, dans lequel/laquelle l'oligonucléotide comprend au moins une liaison internucléosidique modifiée.

16. Oligonucléotide pour une utilisation, conjugué pour une utilisation, composition pharmaceutique pour une utilisation ou procédé selon la revendication 15, dans lequel/laquelle la liaison internucléosidique modifiée est une liaison internucléosidique phosphorothioate.

17. Oligonucléotide pour une utilisation, conjugué pour une utilisation, composition pharmaceutique pour une utilisation, ou procédé selon la revendication 16, dans lequel/laquelle au moins 60 % des liaisons internucléosides dans l'oligonucléotide sont des liaisons internucléosides phosphorothioate.

18. Oligonucléotide pour une utilisation selon l'une quelconque des revendications 1 et 5 à 17, conjugué pour une utilisation selon l'une quelconque des revendications 2 et 5 à 17, composition pharmaceutique pour une utilisation selon l'une quelconque des revendications 3 et 5 à 17, ou procédé selon l'une quelconque des revendications 4 à 17, dans lequel/laquelle l'oligonucléotide est capable de recruter la RNase H.

19. Oligonucléotide pour une utilisation, conjugué pour une utilisation, composition pharmaceutique pour une utilisation ou procédé selon la revendication 18, dans lequel/laquelle l'oligonucléotide est un gapmère.

20. Oligonucléotide pour une utilisation, conjugué pour une utilisation, composition pharmaceutique pour une utilisation, ou procédé selon la revendication 18 ou la revendication 19, dans lequel/laquelle l'oligonucléotide est un gapmère de formule 5'-F-G-F'-3', où les régions F et F' comprennent indépendamment 1 à 7 nucléosides modifiés et G est une région comprise entre 6 et 16 nucléosides qui sont capables de recruter la RNaseH.

21. Oligonucléotide pour une utilisation, conjugué pour une utilisation, composition pharmaceutique pour une utilisation ou procédé selon la revendication 20, dans lequel/laquelle les nucléosides modifiés sont des nucléosides à sucre modifié en 2', sélectionnés indépendamment dans le groupe constitué par des nucléosides 2'-O-alkyl-ARN, 2'-O-méthyl-ARN, 2'-alcoxy-ARN, 2'-O-méthoxyéthyl-ARN, 2'-amino-ADN, 2'-fluoro-ADN, acide arabino nucléique (ANA), 2'-fluoro-ANA et LNA.

22. Oligonucléotide pour une utilisation selon l'une quelconque des revendications 1 et 5 à 21, conjugué pour une utilisation selon l'une quelconque des revendications 2 et 5 à 21, composition pharmaceutique pour une utilisation selon l'une quelconque des revendications 3 et 5 à 21, ou procédé selon l'une quelconque des revendications 4 à 21, dans lequel/laquelle l'oligonucléotide est un gapmère de la formule F-G-F' dans lequel chacune des régions F et F' est constituée indépendamment de 2, 3, 4 ou 5 unités nucléosides modifiées et la région G est constituée de 9, 10, 11, 12, 13, 14 ou 15 unités nucléosides.

23. Oligonucléotide pour une utilisation selon l'une quelconque des revendications 1 et 5 à 20, conjugué pour une utilisation selon l'une quelconque des revendications 2 et 5 à 22, composition pharmaceutique pour une utilisation selon l'une quelconque des revendications 3 et 5 à 22, ou procédé selon l'une quelconque des revendications 4 à 22, dans lequel/laquelle l'oligonucléotide est un gapmère de la formule F-G-F' dans lequel chacune des régions F et F' est constituée indépendamment de 2, 3, 4 ou 5 unités à sucre 2'-O-méthoxyéthyl-ribose (2'-MOE), et la région G est constituée de 9, 10, 11, 12, 13, 14 ou 15 unités d'ADN.

24. Oligonucléotide pour une utilisation, conjugué pour une utilisation, composition pharmaceutique pour une utilisation ou procédé selon l'une quelconque des revendications 20 à 23, dans lequel/laquelle chacune des régions F et F' est constituée indépendamment de 5 unités nucléosides à sucre 2'-O-méthoxyéthyl-ribose (2'-MOE) et la région G est constituée de 10 unités nucléosides d'ADN.

25. Oligonucléotide antisens capable d'induire l'expression du UBE3A paternel humain pour une utilisation dans le

traitement ou la prévention du syndrome d'Angelman chez un sujet,
dans lequel ledit oligonucléotide antisens comprend une séquence nucléotidique contiguë qui est 100 % complémentaire à une région de l'acide nucléique cible de la position 1 à 55318 de SEQ ID NO : 1, dans lequel l'oligonucléotide est soit de 15 à 20 nucléotides de longueur, soit de 17 à 22 nucléotides de longueur, dans lequel l'oligonucléotide comprend un ou plusieurs nucléosides modifiés, dans lequel le ou les nucléotides modifiés sont un nucléoside à sucre modifié en 2', dans lequel le ou les nucléosides à sucre modifié en 2' sont sélectionnés indépendamment dans le groupe constitué par des nucléosides 2'-O-alkyl-ARN, 2'-O-méthyl-ARN, 2'-alcoxy-ARN, 2'-O-méthoxyéthyl-ARN, 2'-amino-ADN, 2'-fluoro-ADN, acide arabino nucléique (ANA), 2'-fluoro-ANA et LNA, dans lequel l'oligonucléotide comprend au moins une liaison internucléosidique modifiée, dans lequel ladite liaison internucléosidique modifiée est une liaison phosphorothioate, dans lequel l'oligonucléotide est un gapmère de la formule F-G-F', dans lequel chacune des régions F et F' est constituée indépendamment de 2, 3, 4 ou 5 unités nucléosides modifiées et la région G est constituée de 9, 10, 11, 12, 13, 14 ou 15 unités nucléosides.

26. Conjugué pour une utilisation dans le traitement ou la prévention du syndrome d'Angelman chez un sujet, conjugué comprenant un oligonucléotide antisens et au moins un groupement conjugué lié de manière covalente à l'oligonucléotide, dans lequel l'oligonucléotide antisens comprend une séquence nucléotidique contiguë qui est 100 % complémentaire à une région de l'acide nucléique cible de la position 1 à 55318 de SEQ ID NO : 1, dans lequel l'oligonucléotide est soit de 15 à 20 nucléotides de longueur, soit de 17 à 22 nucléotides de longueur, dans lequel l'oligonucléotide comprend un ou plusieurs nucléosides modifiés, dans lequel le ou les nucléotides modifiés sont un nucléoside à sucre modifié en 2', dans lequel le ou les nucléosides à sucre modifié en 2' sont sélectionnés indépendamment dans le groupe constitué par des nucléosides 2'-O-alkyl-ARN, 2'-O-méthyl-ARN, 2'-alcoxy-ARN, 2'-O-méthoxyéthyl-ARN, 2'-amino-ADN, 2'-fluoro-ADN, acide arabino nucléique (ANA), 2'-fluoro-ANA et LNA, dans lequel l'oligonucléotide comprend au moins une liaison internucléosidique modifiée, dans lequel ladite liaison internucléosidique modifiée est une liaison phosphorothioate, dans lequel l'oligonucléotide est un gapmère de la formule F-G-F', dans lequel chacune des régions F et F' est constituée indépendamment de 2, 3, 4 ou 5 unités nucléosides modifiées et la région G est constituée de 9, 10, 11, 12, 13, 14 ou 15 unités nucléosides.

27. Composition pharmaceutique dans le traitement ou la prévention du syndrome d'Angelman chez un sujet, la composition pharmaceutique comprenant

(i) un oligonucléotide antisens comprenant une séquence nucléotidique contiguë qui est 100 % complémentaire à une région de l'acide nucléique cible de la position 1 à 55318 de SEQ ID NO: 1, dans laquelle l'oligonucléotide est soit de 15 à 20 nucléotides de longueur, soit de 17 à 22 nucléotides de longueur, dans laquelle l'oligonucléotide comprend un ou plusieurs nucléosides modifiés, dans laquelle le ou les nucléotides modifiés sont un nucléoside à sucre modifié en 2', dans laquelle le ou les nucléosides à sucre modifié en 2' sont sélectionnés indépendamment dans le groupe constitué par des nucléosides 2'-O-alkyl-ARN, 2'-O-méthyl-ARN, 2'-alcoxy-ARN, 2'-O-méthoxyéthyl-ARN, 2'-amino-ADN, 2'-fluoro-ADN, acide arabino nucléique (ANA), 2'-fluoro-ANA et LNA, dans laquelle l'oligonucléotide comprend au moins une liaison internucléosidique modifiée, dans laquelle ladite liaison internucléosidique modifiée est une liaison phosphorothioate, dans laquelle l'oligonucléotide est un gapmère de la formule F-G-F', dans laquelle chacune des régions F et F' est constituée indépendamment de 2, 3, 4 ou 5 unités nucléosides modifiées et la région G est constituée de 9, 10, 11, 12, 13, 14 ou 15 unités nucléosides ; ou
(ii) un conjugué comprenant l'oligonucléotide antisens de (i) et au moins un groupement conjugué lié de manière covalente à l'oligonucléotide ;

et un diluant, solvant, support, sel et/ou adjuvant acceptable sur le plan pharmaceutique.

28. Procédé *in vitro* pour induire l'expression du UBE3A dans une cellule cible où l'expression du UBE3A paternel est supprimée, ledit procédé comprenant l'administration en une quantité efficace à ladite cellule

(i) d'un oligonucléotide antisens comprenant une séquence nucléotidique contiguë qui est 100 % complémentaire à une région de l'acide nucléique cible de la position 1 à 55318 de SEQ ID NO: 1, dans lequel l'oligonucléotide est soit de 15 à 20 nucléotides de longueur, soit de 17 à 22 nucléotides de longueur, dans lequel l'oligonucléotide comprend un ou plusieurs nucléosides modifiés, dans lequel le ou les nucléotides modifiés sont un nucléoside à sucre modifié en 2', dans lequel le ou les nucléosides à sucre modifié en 2' sont sélectionnés indépendamment dans le groupe constitué par des nucléosides 2'-O-alkyl-ARN, 2'-O-méthyl-ARN, 2'-alcoxy-ARN, 2'-O-méthoxyéthyl-ARN, 2'-amino-ADN, 2'-fluoro-ADN, acide arabino nucléique (ANA), 2'-fluoro-ANA et LNA, dans lequel l'oligonucléotide comprend au moins une liaison internucléosidique modifiée, dans lequel ladite liaison internu-

cléosidique modifiée est une liaison phosphorothioate, dans lequel l'oligonucléotide est un gapmère de la formule F-G-F', dans lequel chacune des régions F et F' est constituée indépendamment de 2, 3, 4 ou 5 unités nucléosides modifiées et la région G est constituée de 9, 10, 11, 12, 13, 14 ou 15 unités nucléosides ; ou
(ii) d'un conjugué comprenant l'oligonucléotide antisens de (i) et au moins un groupement conjugué lié de manière covalente à l'oligonucléotide ; ou
(iii) d'une composition pharmaceutique comprenant l'oligonucléotide antisens de (i) ou le conjugué de (ii), et un diluant, solvant, support, sel et/ou adjuvant acceptable sur le plan pharmaceutique.

29. Procédé selon l'une quelconque des revendications 4 à 24 et 28, dans lequel l'expression du UBE3A est augmentée d'au moins 40 % par rapport à un témoin.

30. Procédé selon l'une quelconque des revendications 4 à 24, 28 et 29, dans lequel le niveau du transcript SNHG14 en aval de SNORD109B est réduit d'au moins 30 % par rapport à un témoin.

31. Procédé selon l'une quelconque des revendications 4 à 24 et 28 à 30, dans lequel la cellule cible est une cellule neuronale.

32. Procédé selon l'une quelconque des revendications 4 à 24 et 28 à 31, dans lequel l'expression de SNORD115 n'est pas significativement affectée par rapport à un témoin.

Figure 1

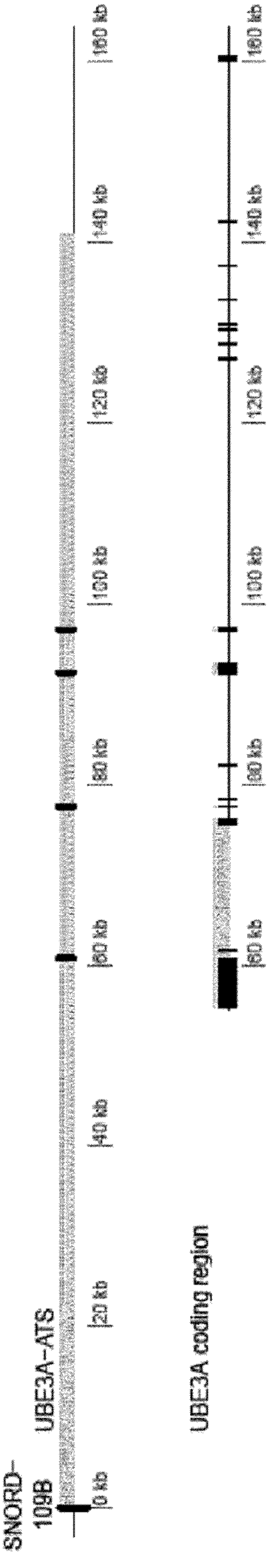
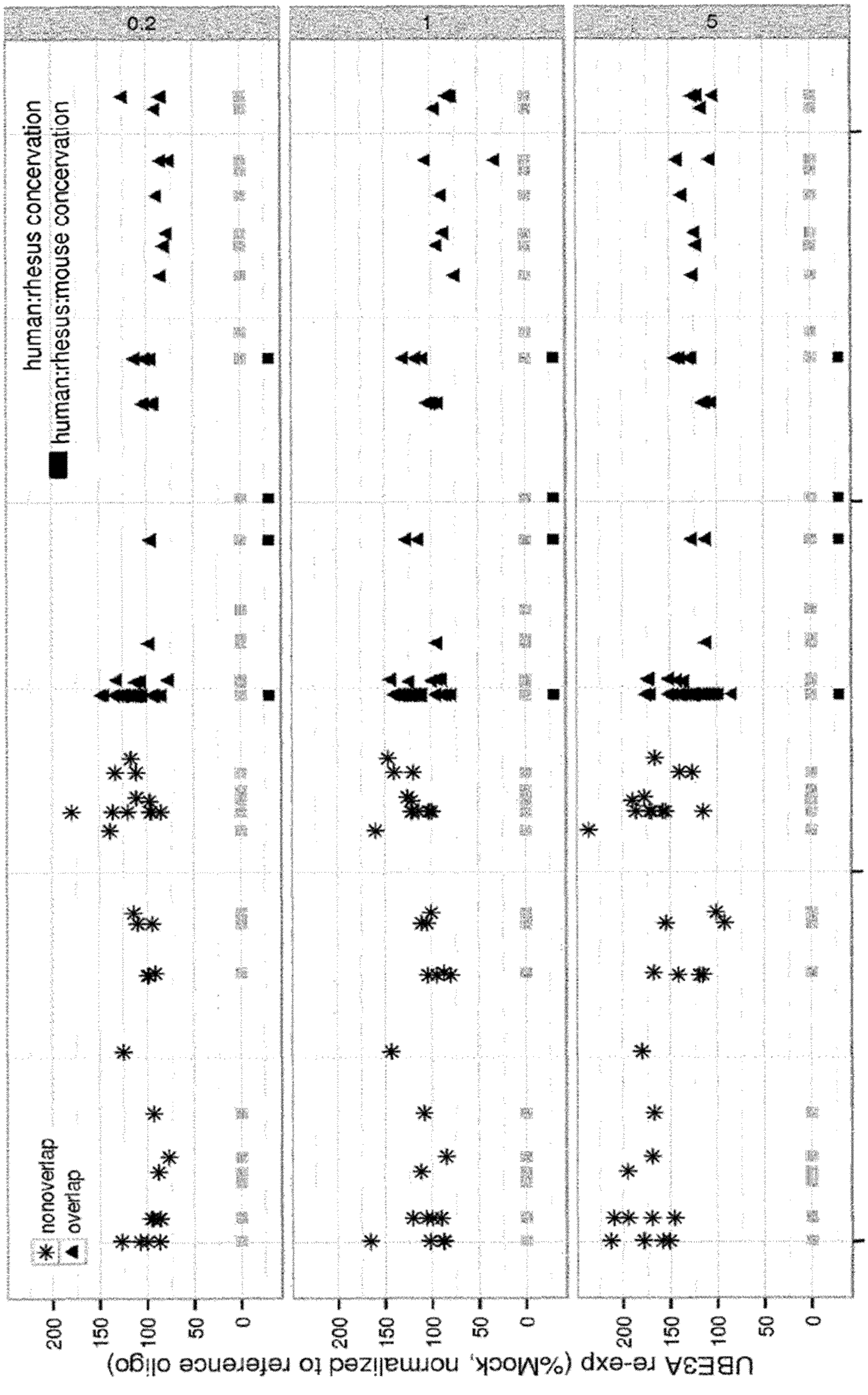

SNORD-
109B
UBE3A–ATS
UBE3A coding region
0 kb
20 kb
40 kb
60 kb
80 kb
100 kb
120 kb
140 kb
160 kb
60 kb
80 kb
100 kb
120 kb
140 kb
160 kb

Figure 2


nonoverlap
overlap
human:rhesus concervation
human:rhesus:mouse concervation
0.2
1
5
200
150
100
50
0
UBE3A re-exp (%Mock, normalized to reference oligo)
25280000
25320000
25360000
25400000
location on chromosome 15

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