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(54) **CONDITIONAL-SIRNAS AND USES THEREOF IN TREATING CARDIAC HYPERTROPHY**

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(57) **ABSTRACT**

Disclosed herein are conditional siRNAs activatable by pro-hypertrophic RNA sequences and use thereof for treating conditions such as cardiac hypertrophy. The conditional siRNAs target calcineurin or HDAC2.

21 Claims, 230 Drawing Sheets
(80 of 230 Drawing Sheet(s) Filed in Color)

Specification includes a Sequence Listing.

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FIG. 1

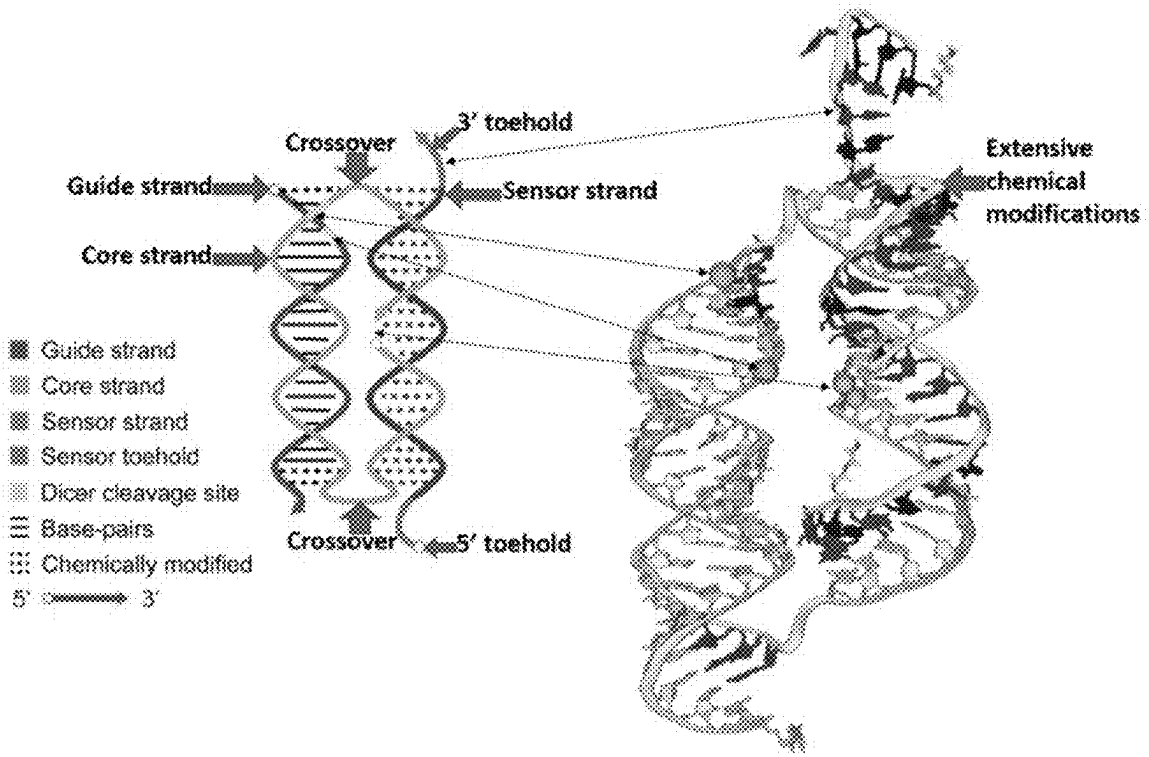

3' toehold
Crossover
Guide strand
Sensor strand
Core strand
Extensive chemical modifications
Guide strand
Core strand
Sensor strand
Sensor toehold
Dicer cleavage site
Base-pairs
Chemically modified
5' 3'
Crossover
5' toehold

FIG. 2

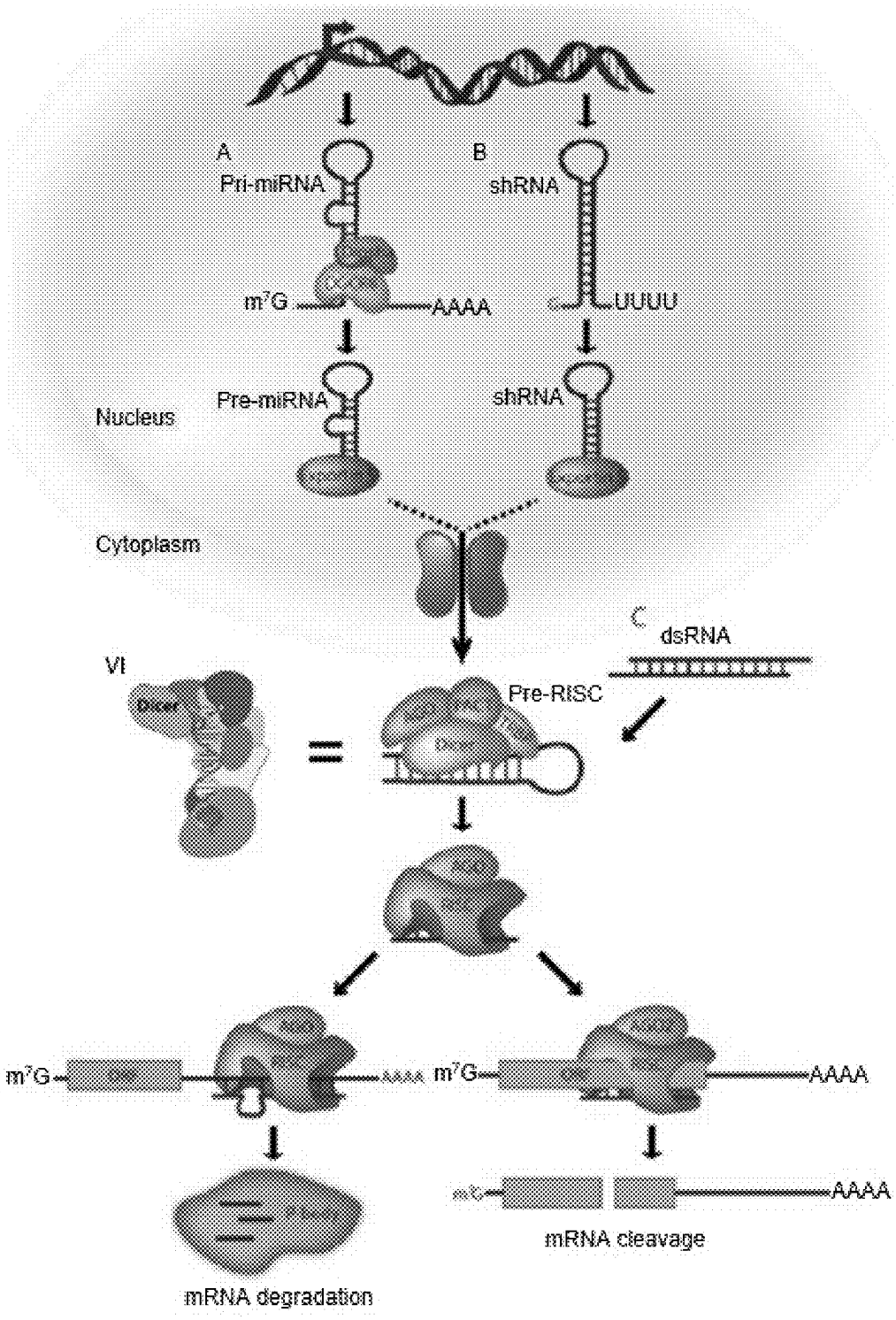

A
Pri-miRNA
B
shRNA
m7G
AAAA
UUUU
Pre-miRNA
shRNA
Nucleus
Cytoplasm
C
dsRNA
VI
Dicer
Pre-RISC
m7G
AAAA
m7G
AAAA
AAAA
mRNA degradation
mRNA cleavage

FIG. 3

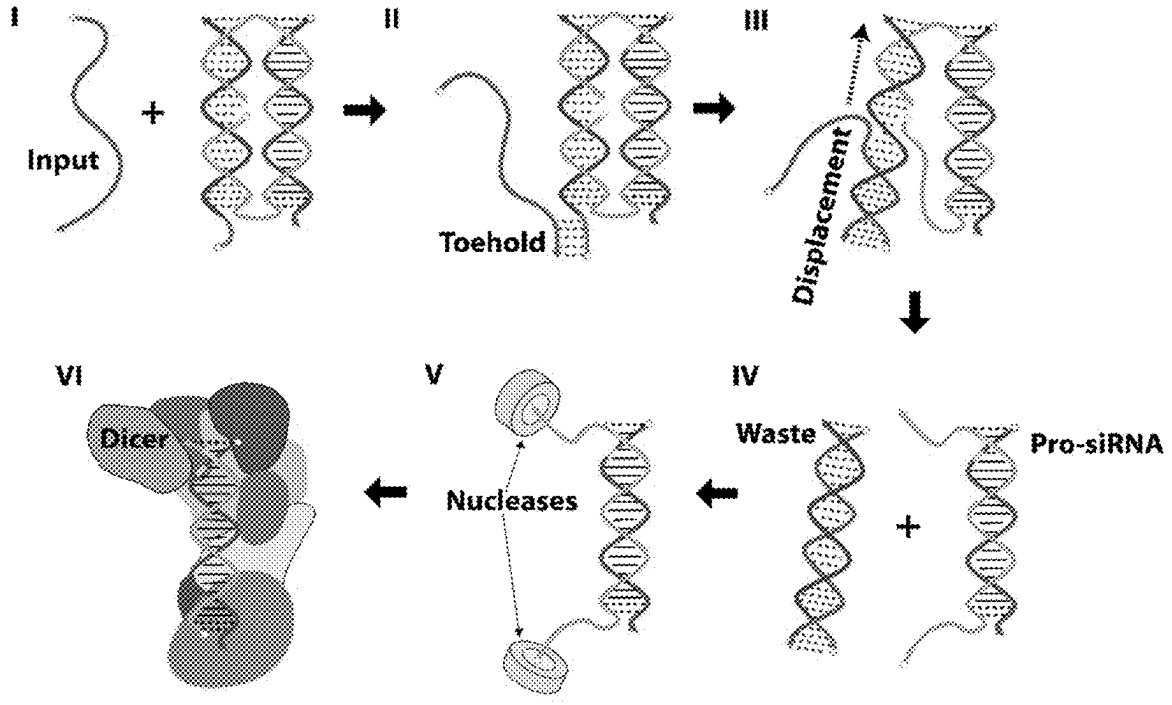

I
Input
+
II
Toehold
III
Displacement
IV
Waste
+
Pro-siRNA
V
Nucleases
VI
Dicer

FIG. 4A

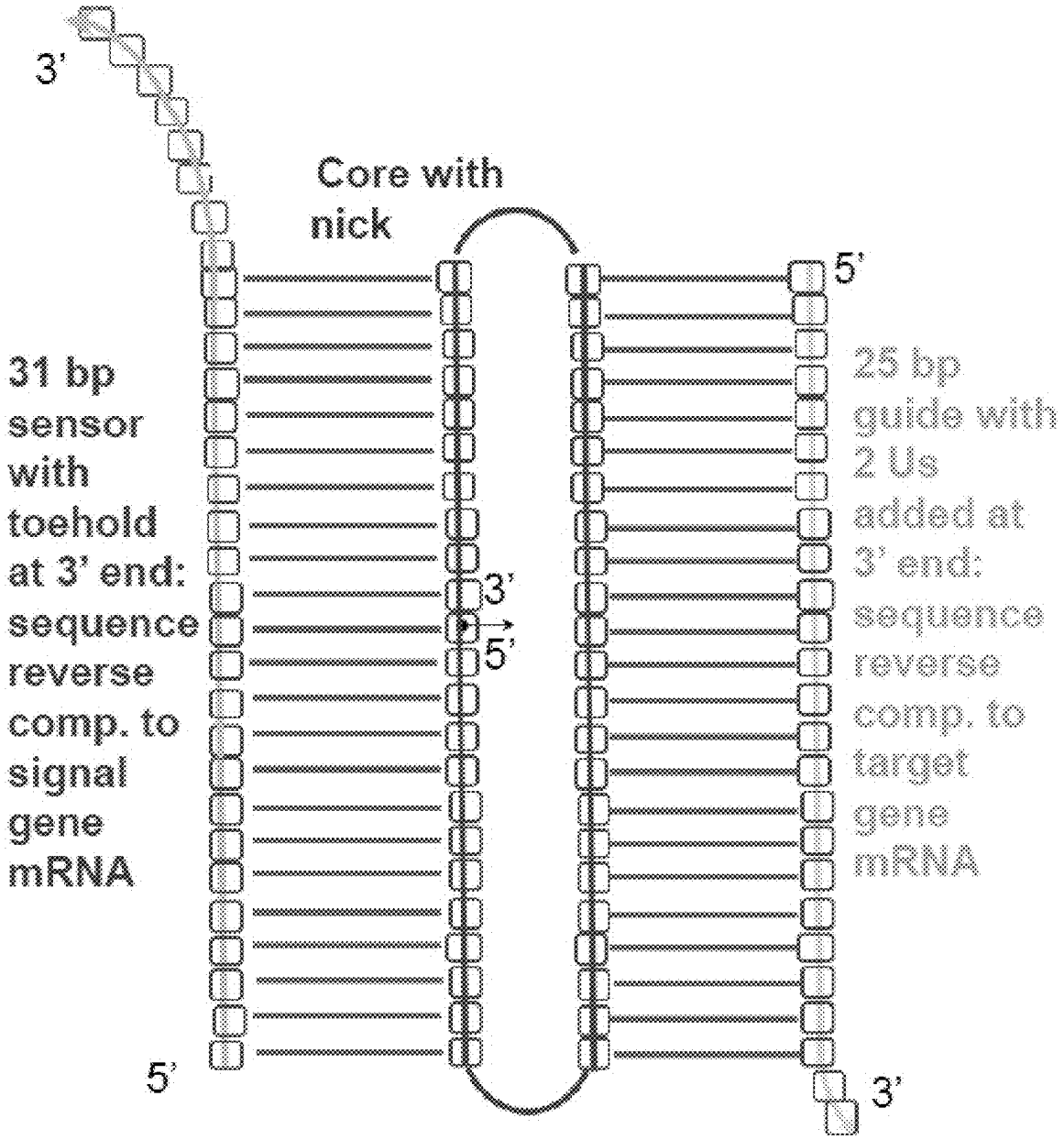

3'
Core with nick
5'
31 bp sensor with toehold at 3' end: sequence reverse comp. to signal gene mRNA
3'
5'
25 bp guide with 2 Us added at 3' end: sequence reverse comp. to target gene mRNA
5'
3'

FIG. 4B

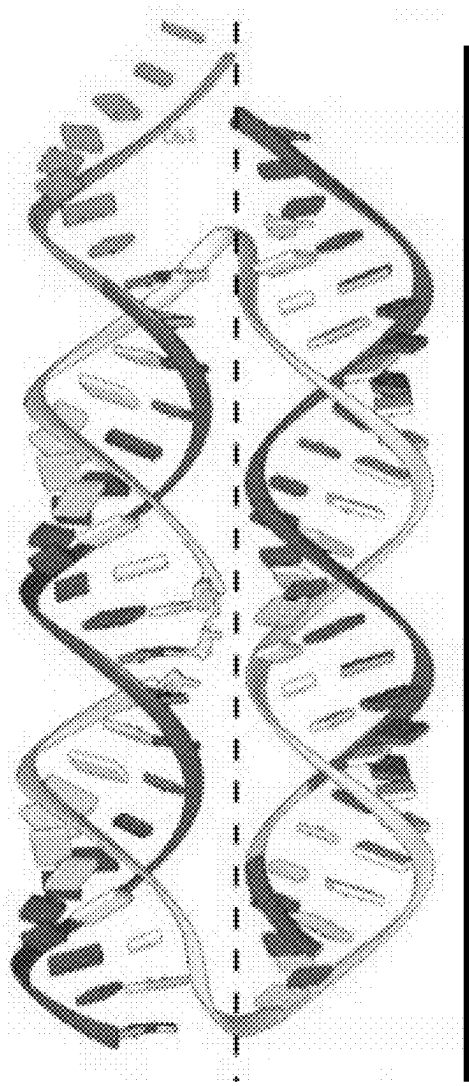


FIG. 4C

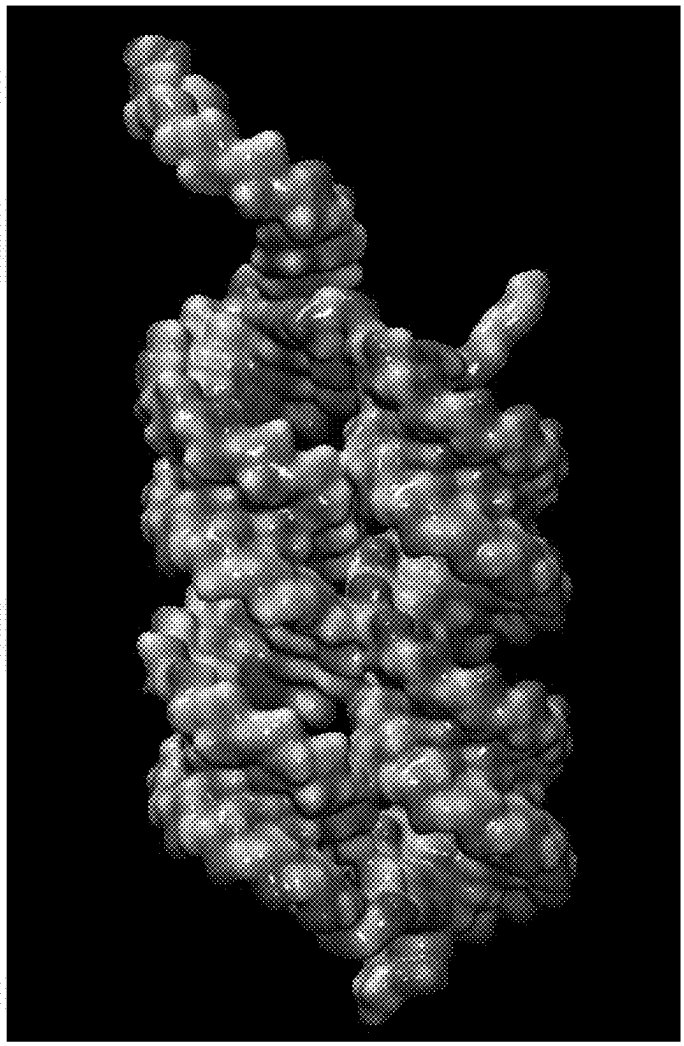


FIG. 5

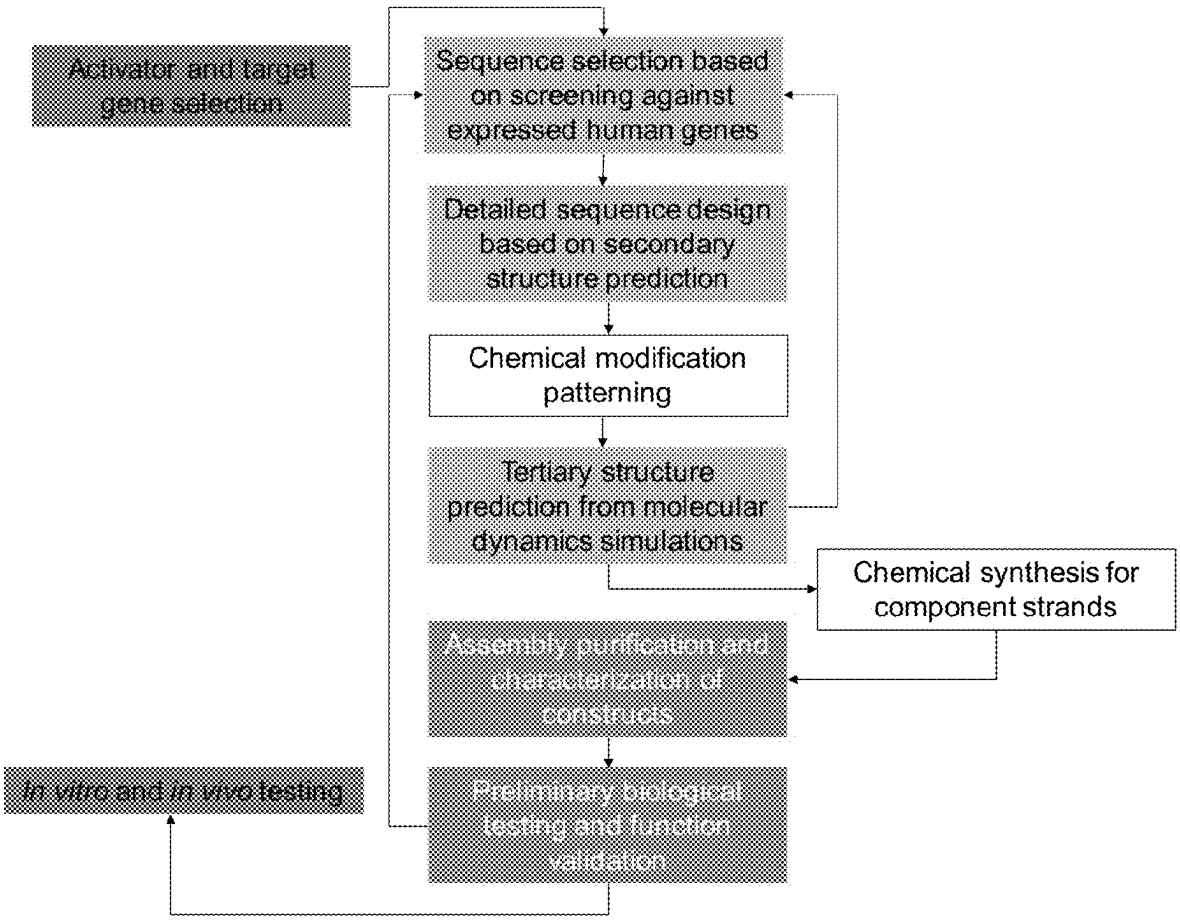

Activator and target gene selection
Sequence selection based on screening against expressed human genes
Detailed sequence design based on secondary structure prediction
Chemical modification patterning
Tertiary structure prediction from molecular dynamics simulations
Chemical synthesis for component strands
Assembly, purification and characterization of constructs
Preliminary biological testing and function validation
In vitro and in vivo testing

FIG. 6

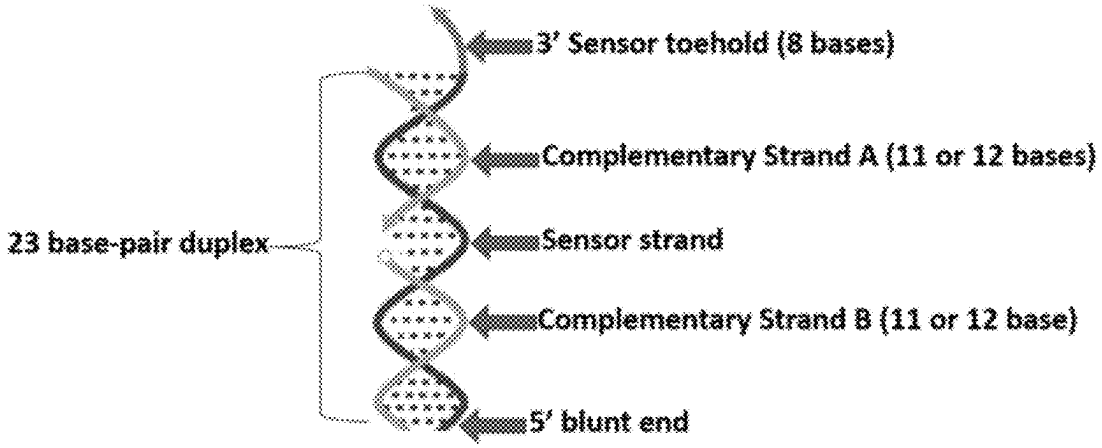

3' Sensor toehold (8 bases)
Complementary Strand A (11 or 12 bases)
23 base-pair duplex
Sensor strand
Complementary Strand B (11 or 12 base)
5' blunt end

FIG. 7

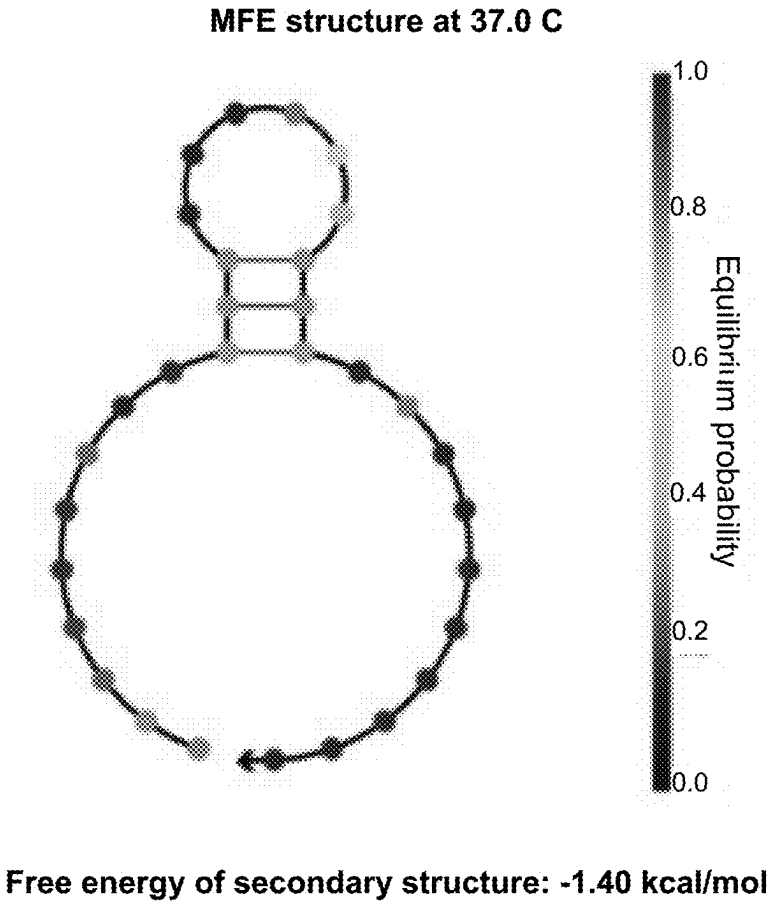

MFE structure at 37.0 C
1.0
0.8
0.6
0.4
0.2
0.0
Equilibrium probability
Free energy of secondary structure: -1.40 kcal/mol

FIG. 8

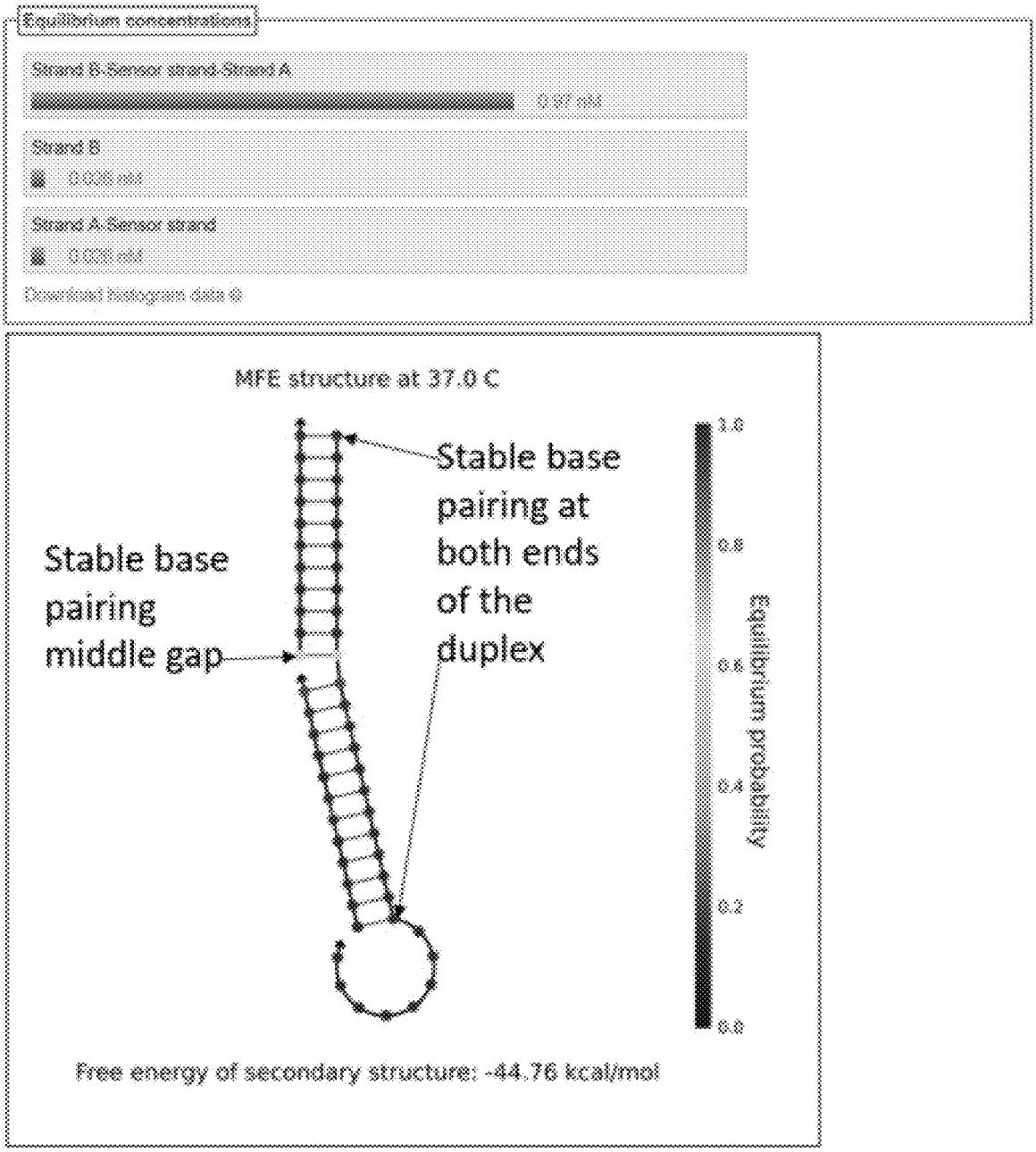

Equilibrium concentrations
Strand B-Sensor strand-Strand A
0.97 mM
Strand B
0.025 mM
Strand A-Sensor strand
0.025 mM
Download histogram data
MFE structure at 37.0 C
Stable base pairing at both ends of the duplex
Stable base pairing middle gap
1.0
0.8
0.6
0.4
0.2
0.0
Equilibrium probability
Free energy of secondary structure: -44.76 kcal/mol

FIG. 9

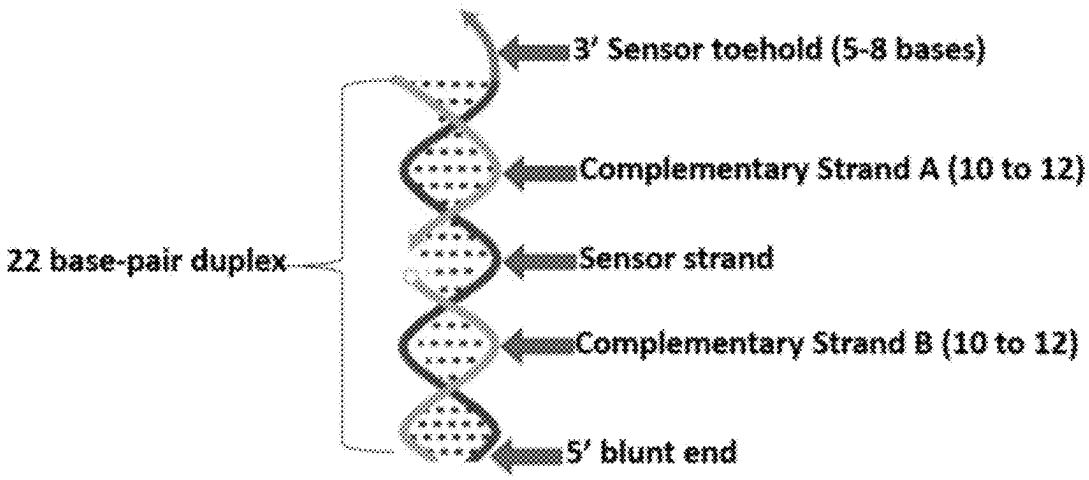
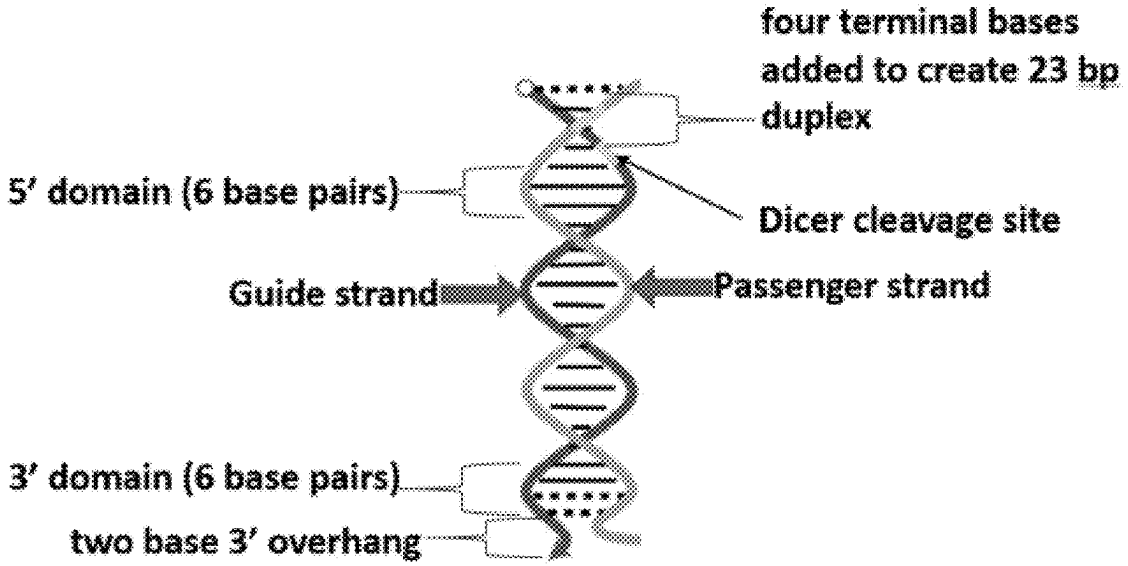

3′ Sensor toehold (5-8 bases)
Complementary Strand A (10 to 12)
22 base-pair duplex
Sensor strand
Complementary Strand B (10 to 12)
5′ blunt end

FIG. 10


four terminal bases added to create 23 bp duplex
5′ domain (6 base pairs)
Dicer cleavage site
Guide strand
Passenger strand
3′ domain (6 base pairs)
two base 3′ overhang

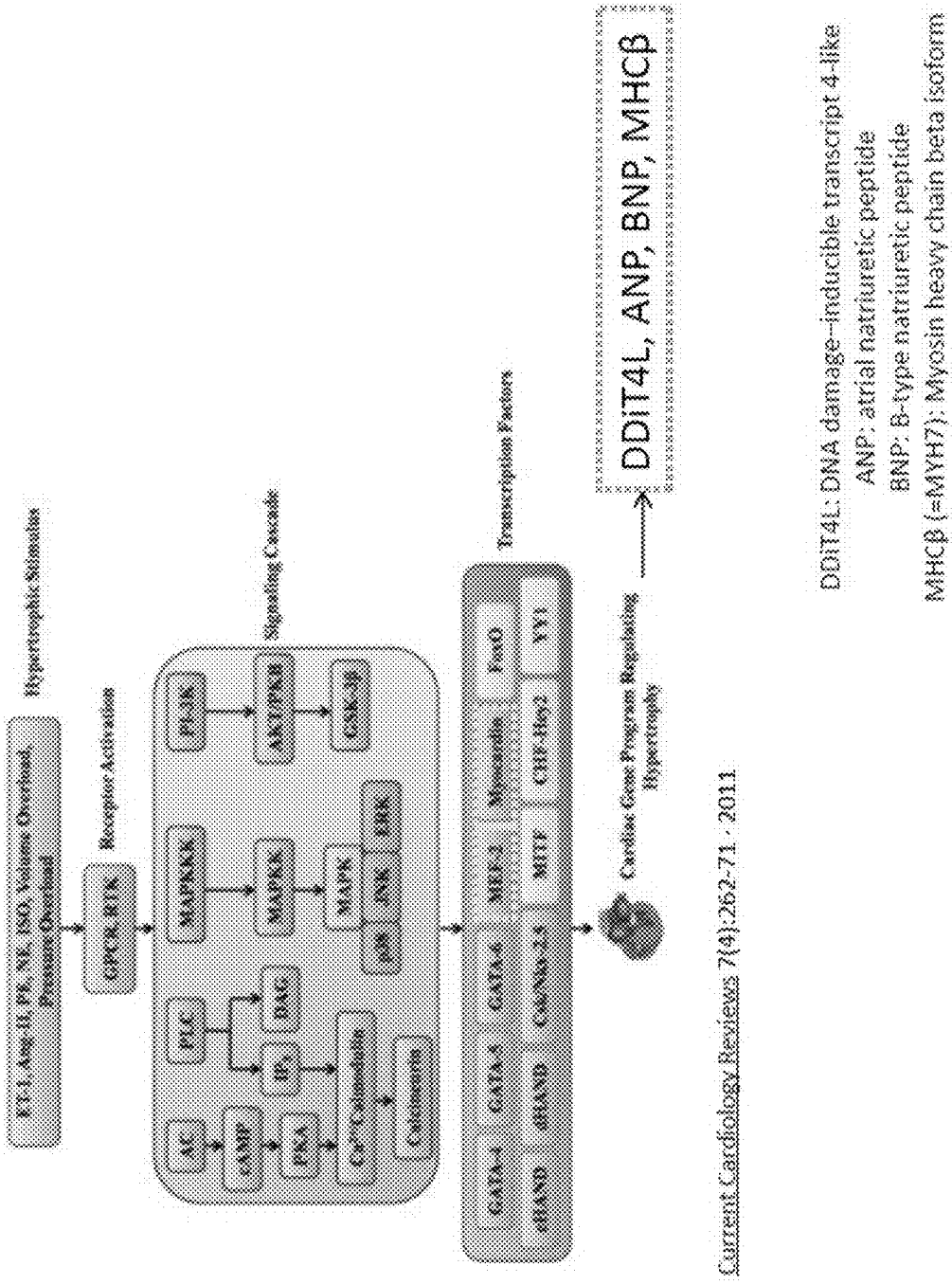

Hypertrophic Stimulus
Receptor Activation
Signaling Cascade
Transcription Factors
Cardiac Gene Program Regulating Hypertrophy
DDIT4L, ANP, BNP, MHCβ
DDIT4L: DNA damage–inducible transcript 4-like
ANP: atrial natriuretic peptide
BNP: B-type natriuretic peptide
MHCβ (=MYH7): Myosin heavy chain beta isoform
Current Cardiology Reviews 7(4):262-71 · 2011

FIG. 11

FIG. 12A

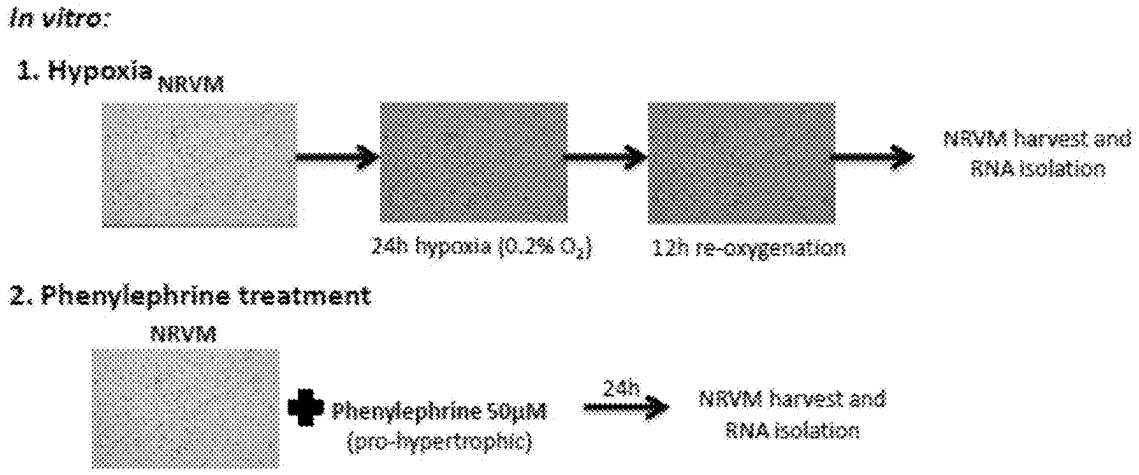


FIG. 12B

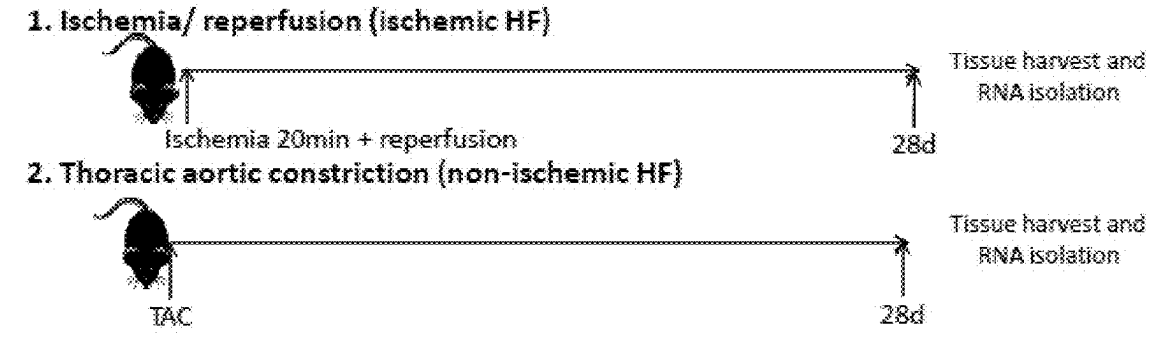


FIG. 13A

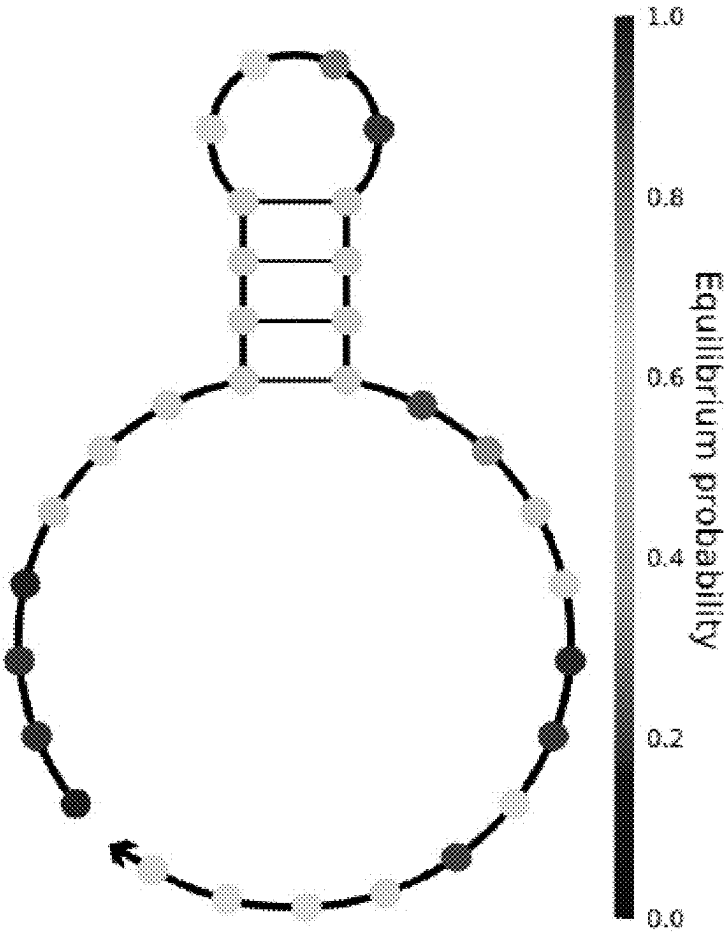


FIG. 13B

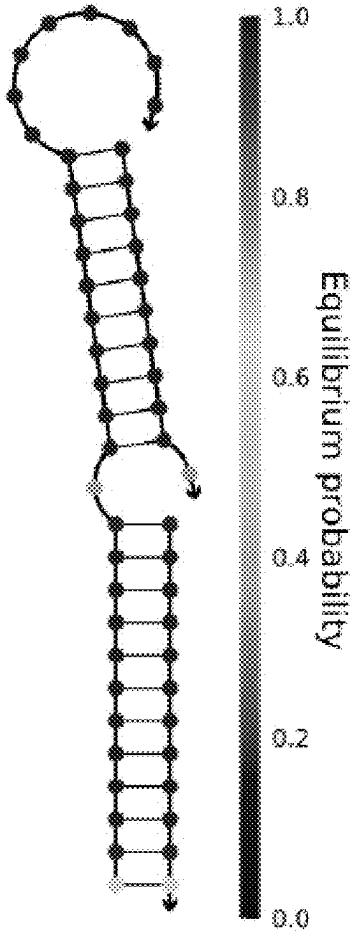


FIG. 14A

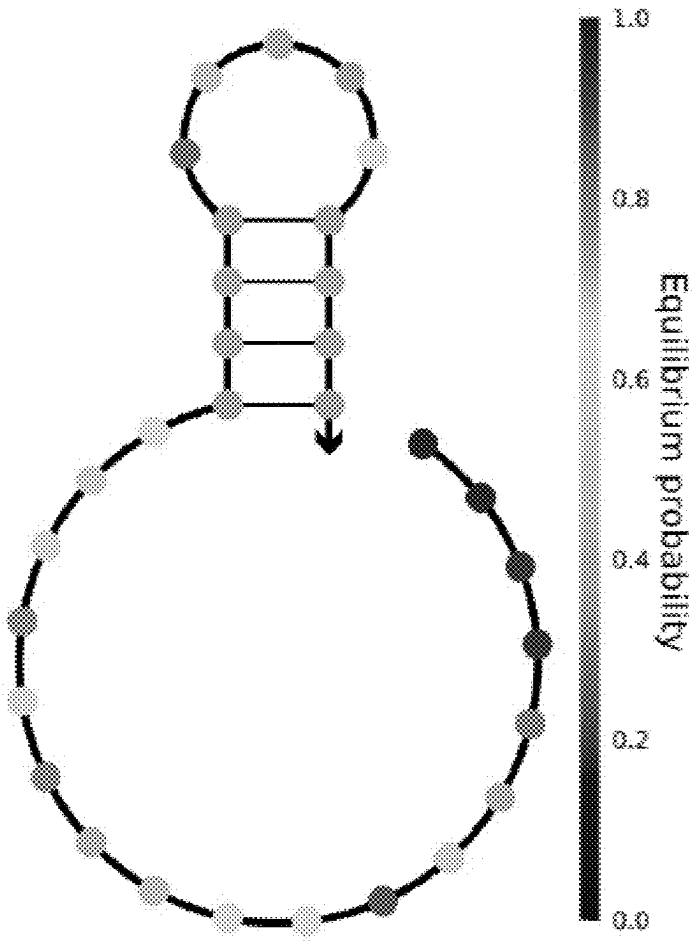


FIG. 14B

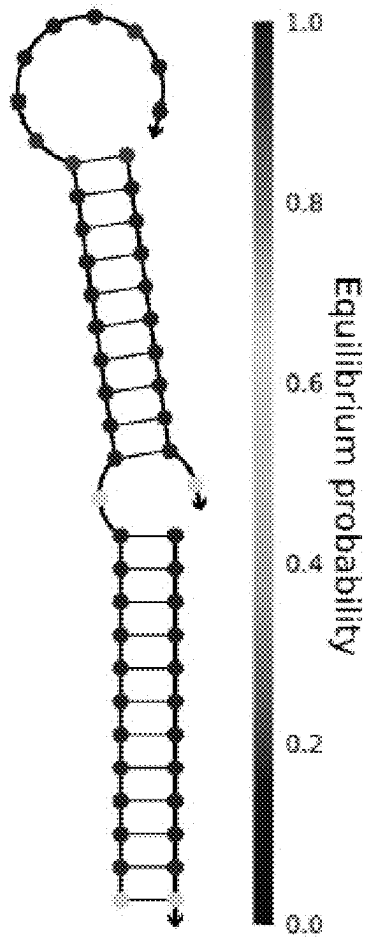


FIG. 15A

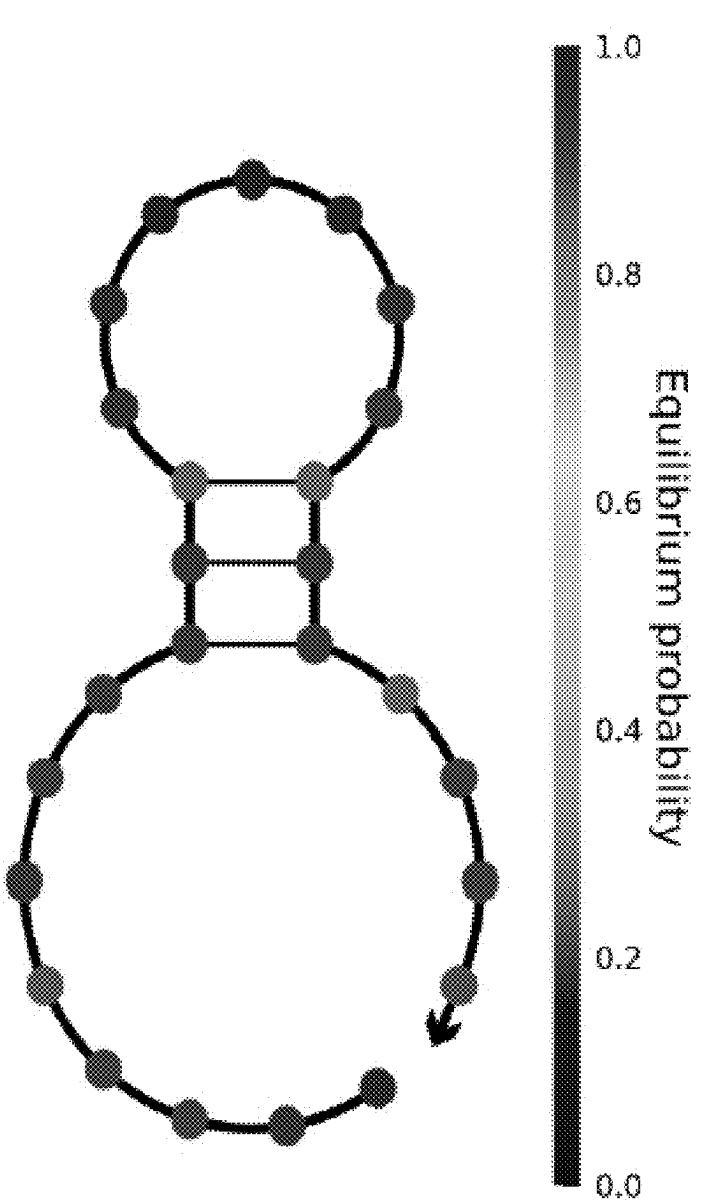


FIG. 15B

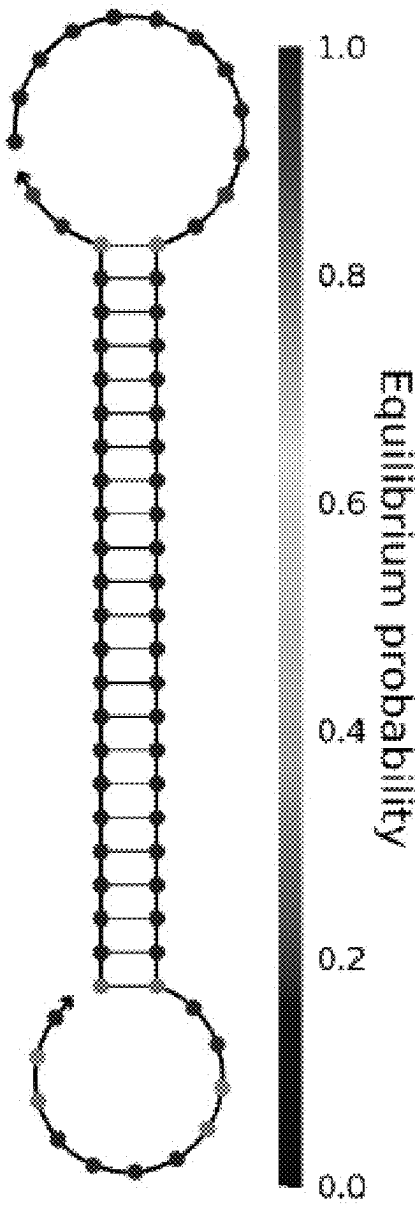


FIG. 16

Original ANP : Calcineurin

```
                                   SEQ ID NO:10
3'-NH2*A*A*C*C*A*G*C*G*U*A*A*C*G*G*T*G*A*C*U*C*U*C*C*A*C*C*A*C*U*T*C.Sp9-5'
ANP sensor strand          | | | | | | | | | | | | | | | | | | | | | | | | |
                          .A.U.U.G.C.C.A.C.U.G.A.G A.G.G.U.G.G.U.G.A.A.G.
                          C3                      3' 5'                  C3
Core strand               !G*C.U.C.A.C.A.A.C.A.A.A.C.C.G.A.A.A.A.G.G*A*C!SEQ ID NO:19
Calcineurin guide strand   | | | | | | | | | | | | | | | | | | | | | | | | |
                 5'-NH2.C*G.A.G.U.G.U.U.G.U.U.U.G.G.C.U.U.U.U.C.C.U.G.U.U-3'
                                 ↑        SEQ ID NO:12
```

New sensor with less PS and one more LNA (middle C) in toehold

```
                                   SEQ ID NO:10
3'-NH2*A*A*C*C*A*G*C*G*U.A.A.C.G.G.T.G.A.C.U.C.U.C.C.A.C.C.A.C.U.T.C.Sp9-5'
ANP sensor strand          | | | | | | | | | | | | | | | | | | | | | | | | |
                          .A.U.U.G.C.C.A.C.U.G.A.G A.G.G.U.G.G.U.G.A.A.G.
                          C3                      3' 5'                  C3
Core strand               !G*C.U.C.A.C.A.A.C.A.A.A.C.C.G.A.A.A.A.G.G*A*C!SEQ ID NO:19
Calcineurin guide strand   | | | | | | | | | | | | | | | | | | | | | | | | |
                 5'-NH2.C*G.A.G.U.G.U.U.G.U.U.U.G.G.C.U.U.U.U.C.C.U.G.U.U-3'
                                 ↑        SEQ ID NO:12
```

New sensor plus modified guide

```
                                   SEQ ID NO:10
3'-NH2*A*A*C*C*A*G*C*G*U.A.A.C.G.G.T.G.A.C.U.C.U.C.C.A.C.C.A.C.U.T.C.Sp9-5'
ANP sensor strand          | | | | | | | | | | | | | | | | | | | | | | | | |
                          .A.U.U.G.C.C.A.C.U.G.A.G A.G.G.U.G.G.U.G.A.A.G.
                          C3                      3' 5'                  C3
Core strand               !G*C.U.C.A.C.A.A.C.A.A.A.C.C.G.A.A.A.A.G.G*A*C!SEQ ID NO:19
Calcineurin guide strand   | | | | | | | | | | | | | | | | | | | | | | | | |
                 5'-NH2.C*G.A.G.U.G.U.U.G.U.U.U.G.G.C.U.U.U.U.C.C.U.G.U.U-3'
                                 ↑        SEQ ID NO:12
```

New sensor with Cholesterol*TEG, modified guide

```
                                   SEQ ID NO:10
3'-Chol*A*A*C*C*A*G*C*G*U.A.A.C.G.G.T.G.A.C.U.C.U.C.C.A.C.C.A.C.U.T.C.Sp9-5'
                           | | | | | | | | | | | | | | | | | | | | | | | | |
                          .A.U.U.G.C.C.A.C.U.G.A.G A.G.G.U.G.G.U.G.A.A.G.
                          C3                      3' 5'                  C3
                           .G*C.U.C.A.C.A.A.C.A.A.A.C.C.G.A.A.A.A.G.G*A*C.SEQ ID NO:19
                           | | | | | | | | | | | | | | | | | | | | | | | | |
                 5'-NH2.C*G.A.G.U.G.U.U.G.U.U.U.G.G.C.U.U.U.U.C.C.U.G.U.U-3'
                                   SEQ ID NO:12
```

▩ = LNA; ▩ = 2'-O-methyl; ▩ = RNA; . = phosphodiester; * = phosphorothioate; ↑ = Dicer cleavage site;
▒ = Exonuclease blocking domain; C3 = C_3 spacer; Sp9 = triethylene glycol; NH2 = primary amine linker

FIG. 17

Original mir-23a-3p : Calcineurin

SEQ ID NO:1

3'-NH2*T*A*G*T*G*U*A*A*C*G*G*U*C*C*C*U*A*A*A*G*G*C*A*A*G*A*A*G*C.Sp9-5'

mir-23a-3p sensor strand

.U.G.C.C.A.G.G.G.A.U.U U.C.C.G.U.U.C.U.U.C.G.

Core strand C3 3' 5' C3

!G*C.U.C.A.C.A.A.C.A.A.A.C.C.G.A.A.A.A.G.G*A*C! SEQ ID NO:41

Calcineurin guide strand

5'-NH2.C*G.A.G.U.G.U.U.G.U.U.U.G.G.C.U.U.U.U.C.C.U.G.U.U-3'

↑ SEQ ID NO:12

Updated with new sensor with no PS and different LNA pattern

SEQ ID NO:2

3'-NH2*U*A*G*T*G*T*A*A.C.G.G.T.C.C.C.U.A.A.A.G.G.C.A.A.G.A.A.G.C.Sp9-5'

mir-23a-3p sensor II

.U.G.C.C.A.G.G.G.A.U.U U.C.C.G.U.U.C.U.U.C.G.

Core strand C3 3' 5' C3

!G*C.U.C.A.C.A.A.C.A.A.A.C.C.G.A.A.A.A.G.G*A*C! SEQ ID NO:41

Calcineurin guide strand

5'-NH2.C*G.A.G.U.G.U.U.G.U.U.U.G.G.C.U.U.U.U.C.C.U.G.U.U-3'

↑ SEQ ID NO:12

Updated with new sensor and new guide

SEQ ID NO:2

3'-NH2*U*A*G*T*G*T*A*A.C.G.G.T.C.C.C.U.A.A.A.G.G.C.A.A.G.A.A.G.C.Sp9-5'

mir-23a-3p sensor II

.U.G.C.C.A.G.G.G.A.U.U U.C.C.G.U.U.C.U.U.C.G.

Core strand C3 3' 5' C3

!G*C.U.C.A.C.A.A.C.A.A.A.C.C.G.A.A.A.A.G.G*A*C! SEQ ID NO:41

Calcineurin guide strand

5'-NH2.C*G.A.G.U.G.U.U.G.U.U.U.G.G.C.U.U.U.U.C.C.U.G.U.U-3'

↑ SEQ ID NO:12

Updated with new sensor, guide, and cholesterol mod

SEQ ID NO:2

3'-Chol*U*A*G*T*G*T*A*A.C.G.G.T.C.C.C.U.A.A.A.G.G.C.A.A.G.A.A.G.C.Sp9-5'

mir-23a-3p sensor II

.U.G.C.C.A.G.G.G.A.U.U U.C.C.G.U.U.C.U.U.C.G.

Core strand C3 3' 5' C3

!G*C.U.C.A.C.A.A.C.A.A.A.C.C.G.A.A.A.A.G.G*A*C! SEQ ID NO:41

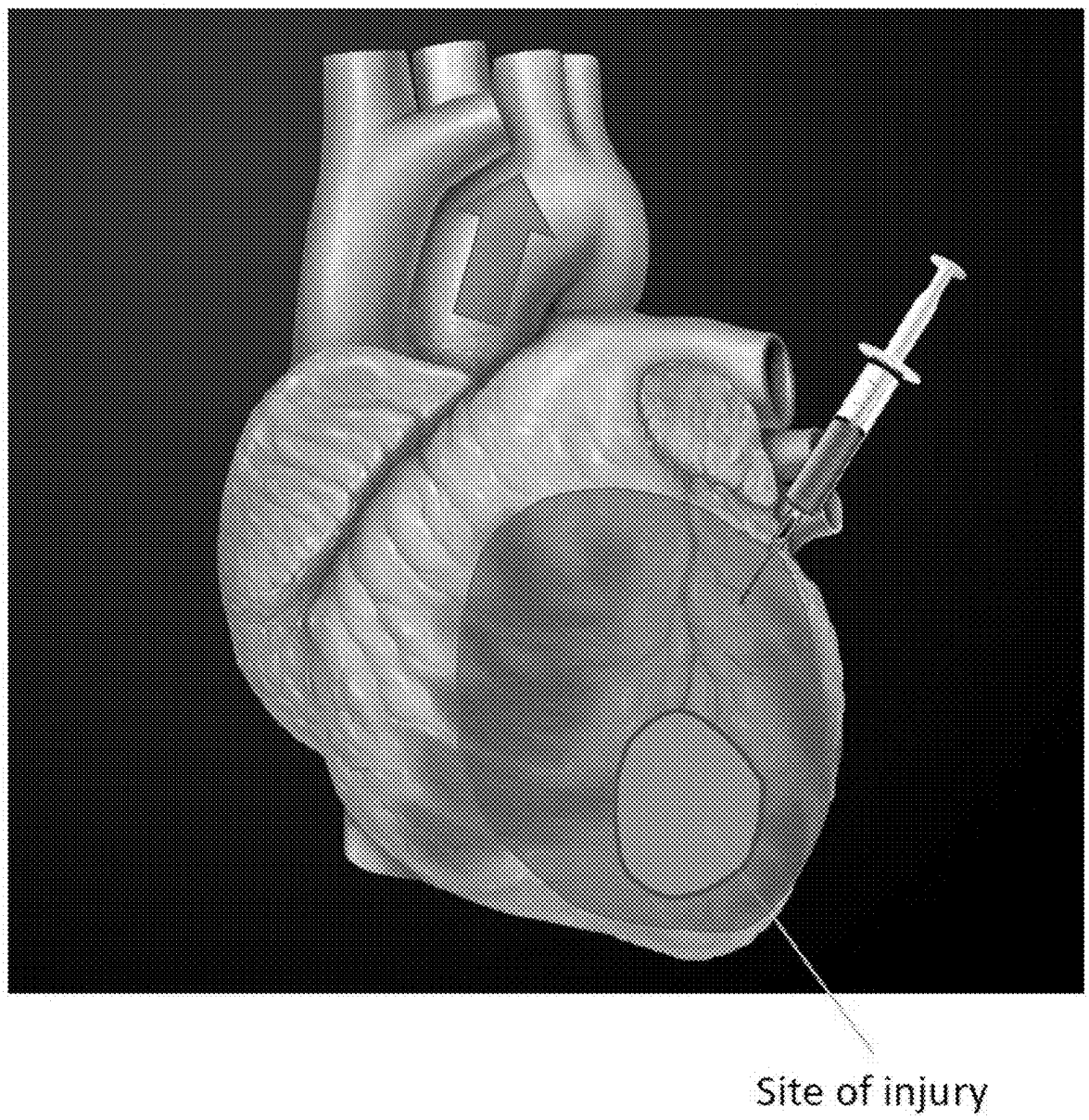
Calcineurin guide strand

5'-NH2.C*G.A.G.U.G.U.U.G.U.U.U.G.G.C.U.U.U.U.C.C.U.G.U.U-3'

↑ SEQ ID NO:12

= LNA; = 2'-O-methyl; = RNA; . = phosphodiester; * = phosphorothioate; ↑ = Dicer cleavage site;
= Exonuclease blocking domain; C3 = C_3 spacer; Sp9 = triethylene glycol; NH2 = primary amine linker

FIG. 18



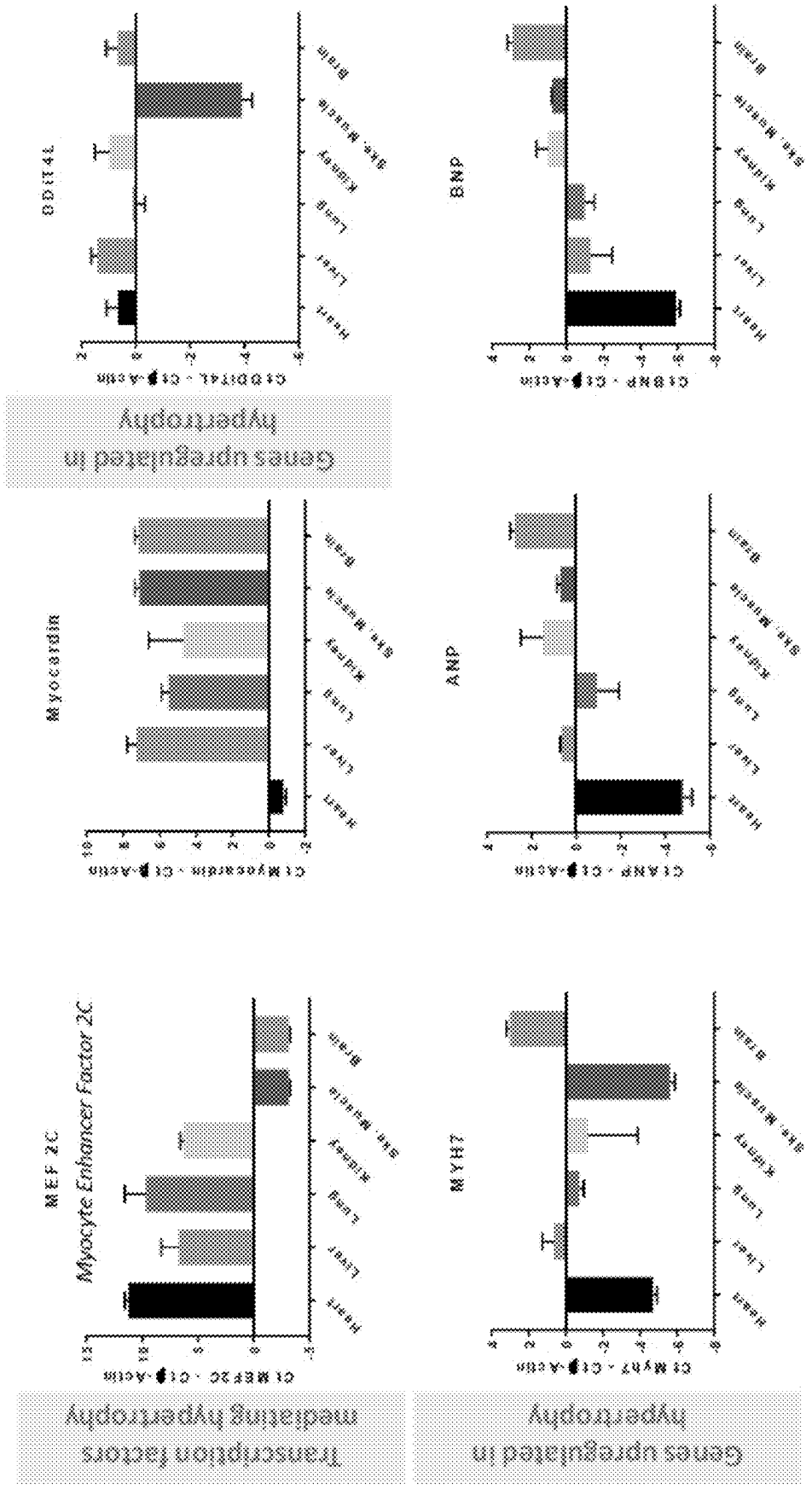

Transcription factors mediating hypertrophy
Genes upregulated in hypertrophy
Genes upregulated in hypertrophy
MEF 2C
Myocyte Enhancer Factor 2C
Myocardin
DDIT4L
MYH7
ANP
BNP
Heart
Liver
Lung
Kidney
Skm. Muscle
Brain

FIG. 19

FIG. 20

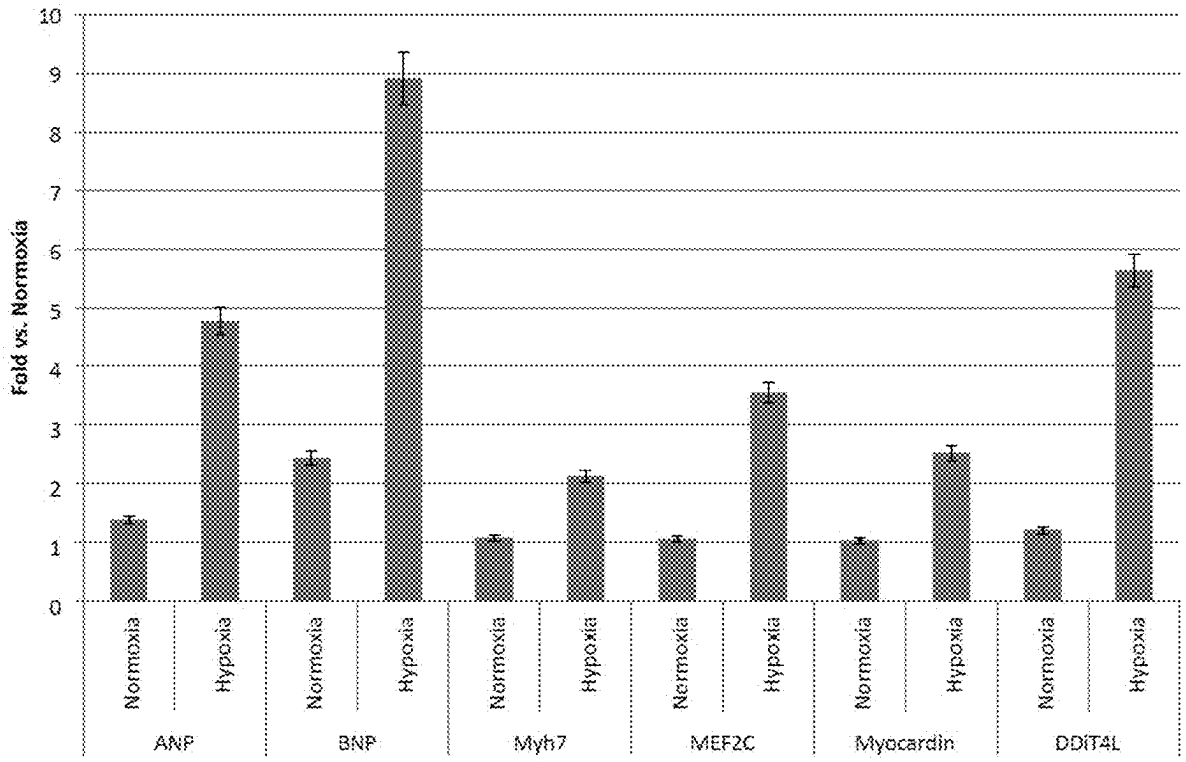

Fold vs. Normoxia
10
9
8
7
6
5
4
3
2
1
0
Normoxia
Hypoxia
ANP
BNP
Myh7
MEF2C
Myocardin
DDIT4L

FIG. 21

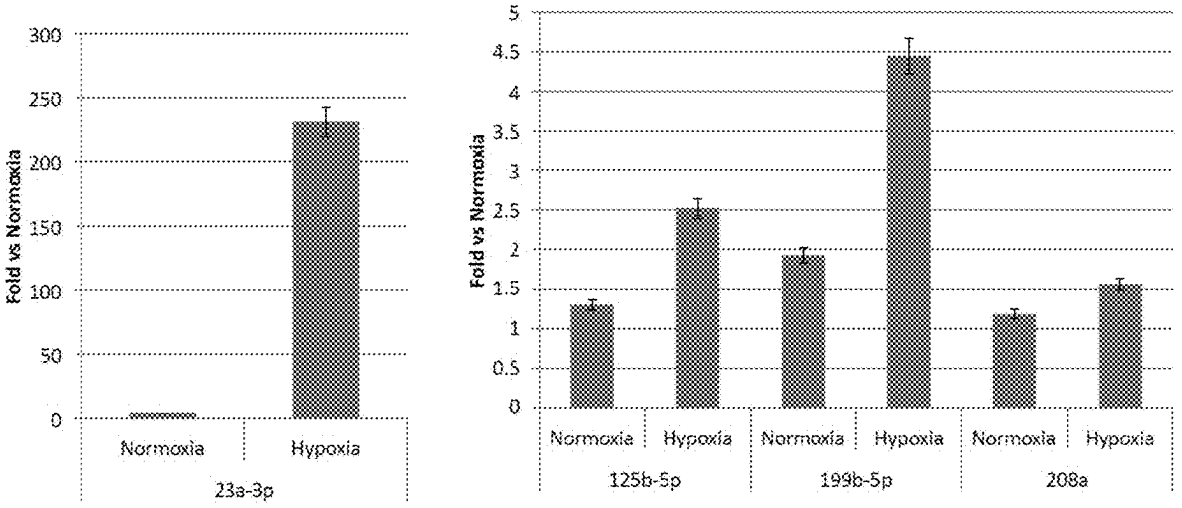
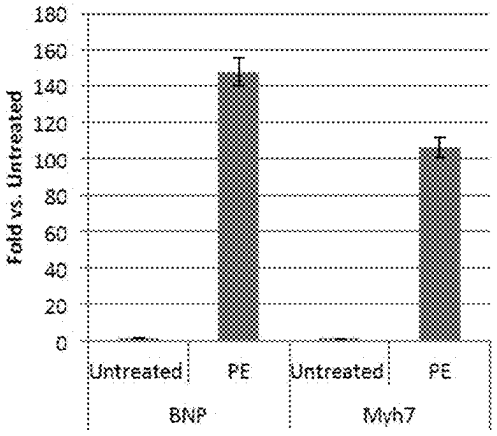
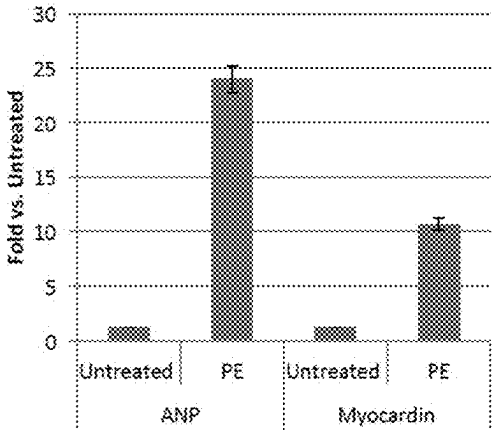

Fold vs Normoxia
300
250
200
150
100
50
0
Normoxia
Hypoxia
23a-3p
Fold vs Normoxia
5
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
Normoxia
Hypoxia
Normoxia
Hypoxia
Normoxia
Hypoxia
125b-5p
199b-5p
208a

FIG. 22


180
160
140
120
100
80
60
40
20
0
Fold vs. Untreated
Untreated
PE
Untreated
PE
BNP
Myh7


30
25
20
15
10
5
0
Fold vs. Untreated
Untreated
PE
Untreated
PE
ANP
Myocardin

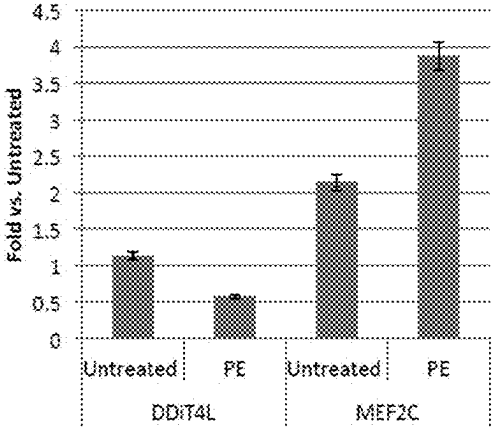

4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
Fold vs. Untreated
Untreated
PE
Untreated
PE
DDIT4L
MEF2C

FIG. 23

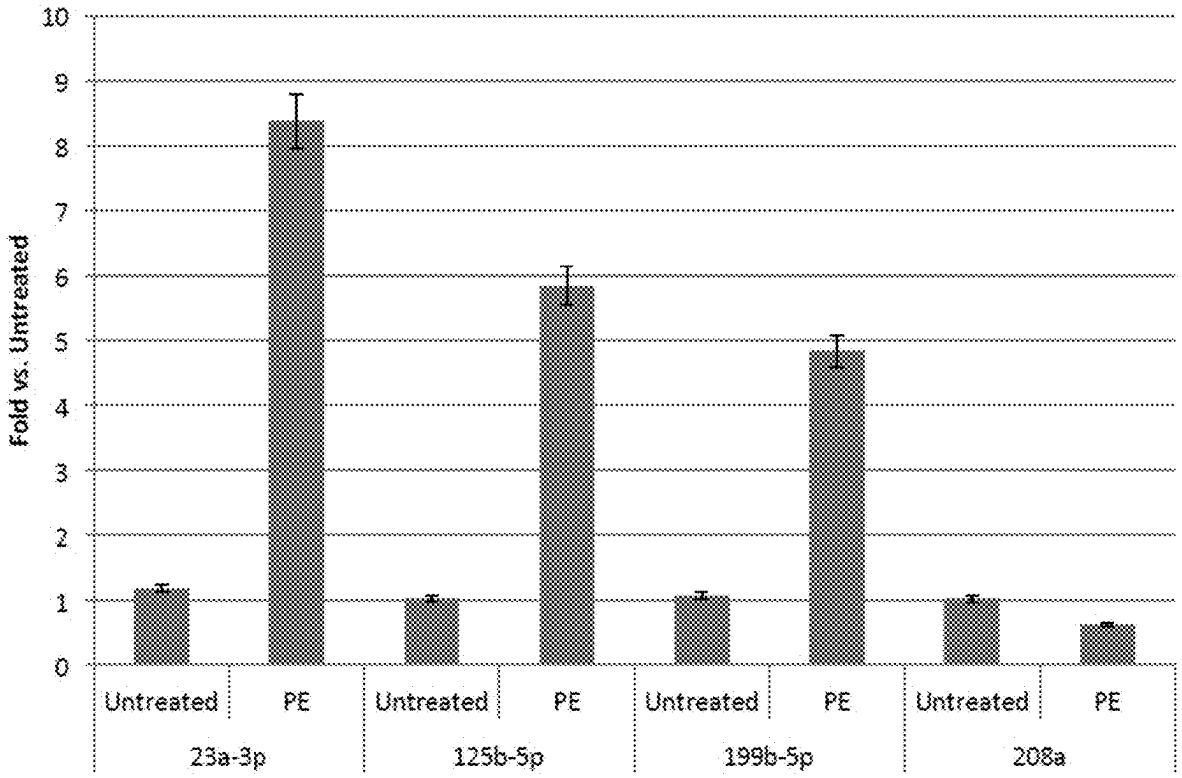

Fold vs. Untreated
10
9
8
7
6
5
4
3
2
1
0
Untreated
PE
Untreated
PE
Untreated
PE
Untreated
PE
23a-3p
125b-5p
199b-5p
208a

FIG. 24

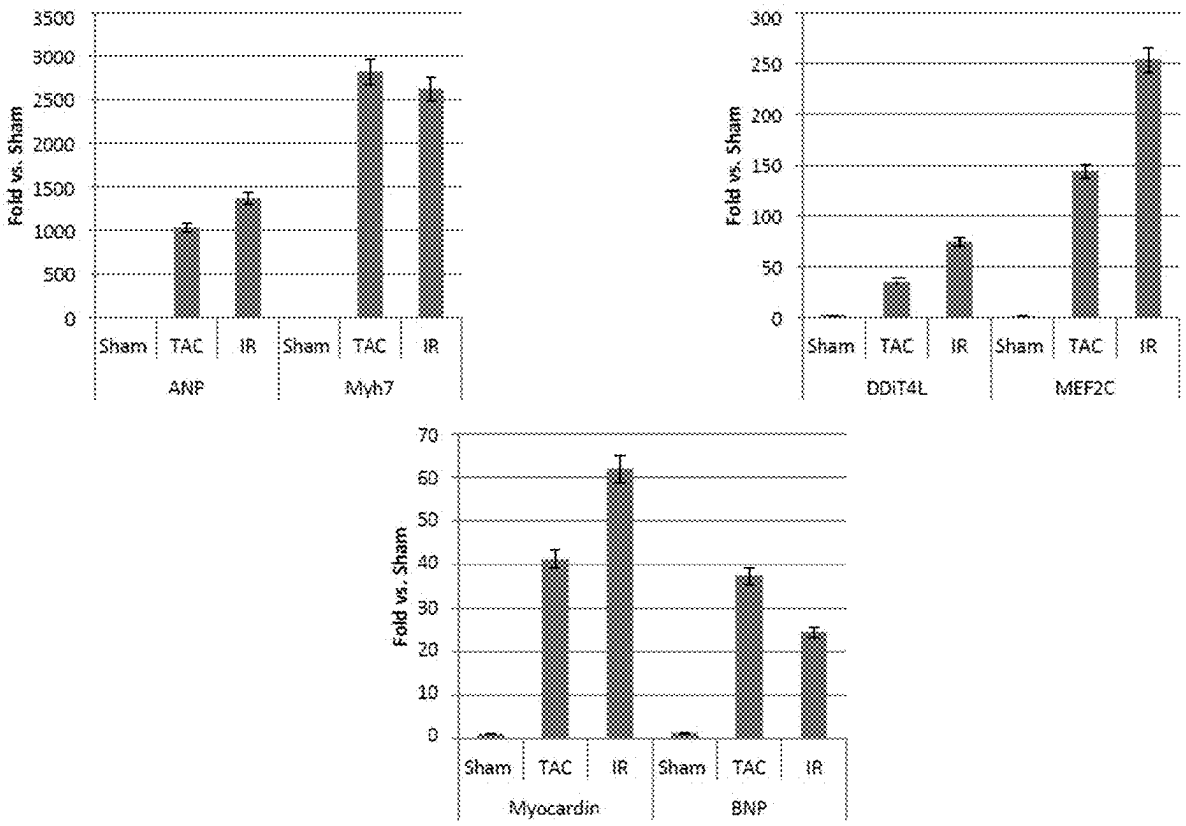

3500
3000
2500
2000
1500
1000
500
0
Fold vs. Sham
Sham
TAC
IR
Sham
TAC
IR
ANP
Myh7
300
250
200
150
100
50
0
Fold vs. Sham
Sham
TAC
IR
Sham
TAC
IR
DDIT4L
MEF2C
70
60
50
40
30
20
10
0
Fold vs. Sham
Sham
TAC
IR
Sham
TAC
IR
Myocardin
BNP

FIG. 25

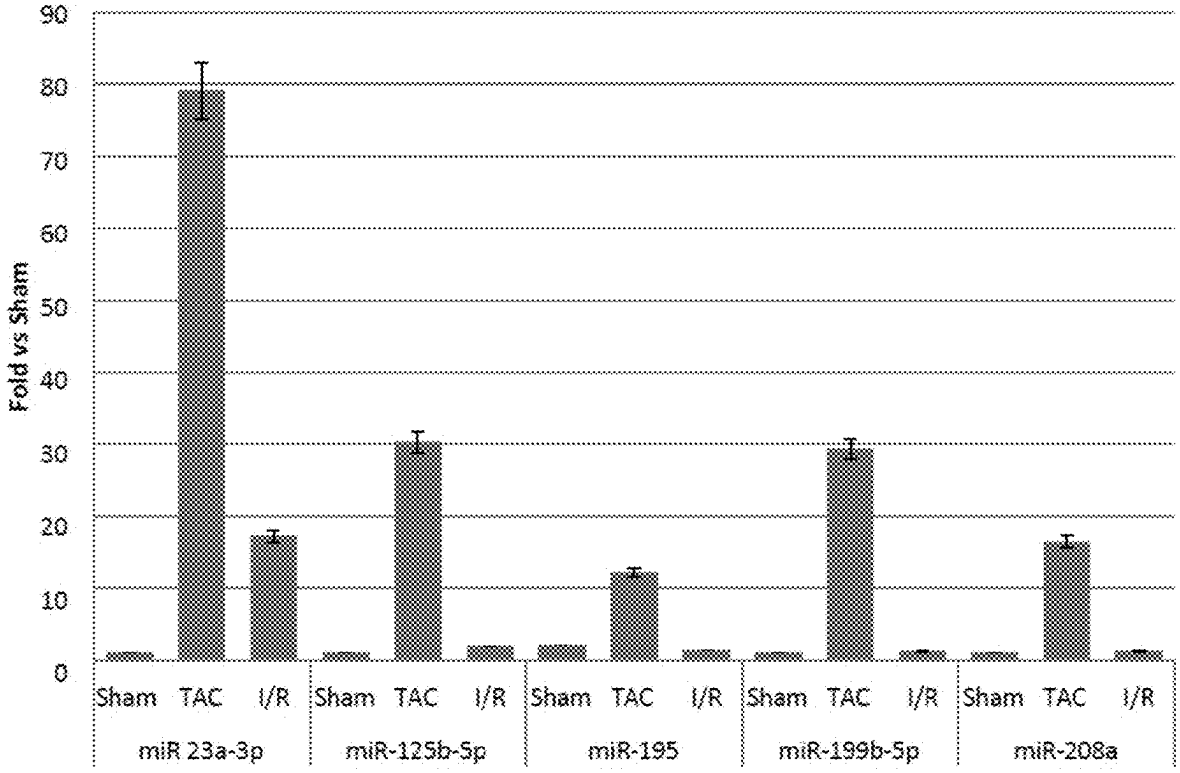

90
80
70
60
50
40
30
20
10
0
Fold vs Sham
Sham TAC I/R Sham TAC I/R Sham TAC I/R Sham TAC I/R Sham TAC I/R
miR 23a-3p
miR-12Sb-5p
miR-195
miR-199b-5p
miR-208a

FIG. 26

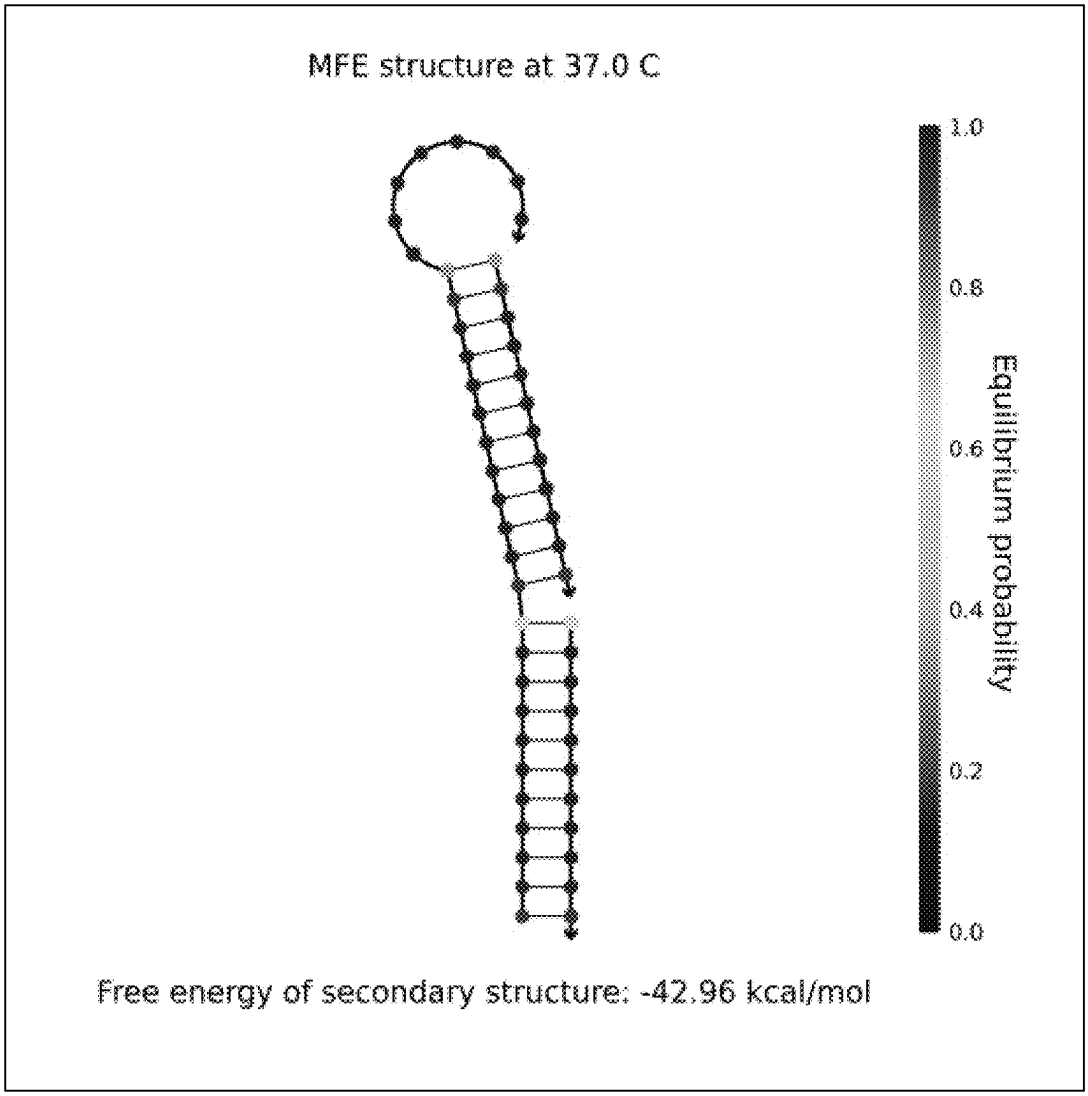

MFE structure at 37.0 C
1.0
0.8
0.6
0.4
0.2
0.0
Equilibrium probability
Free energy of secondary structure: -42.96 kcal/mol

FIG. 27

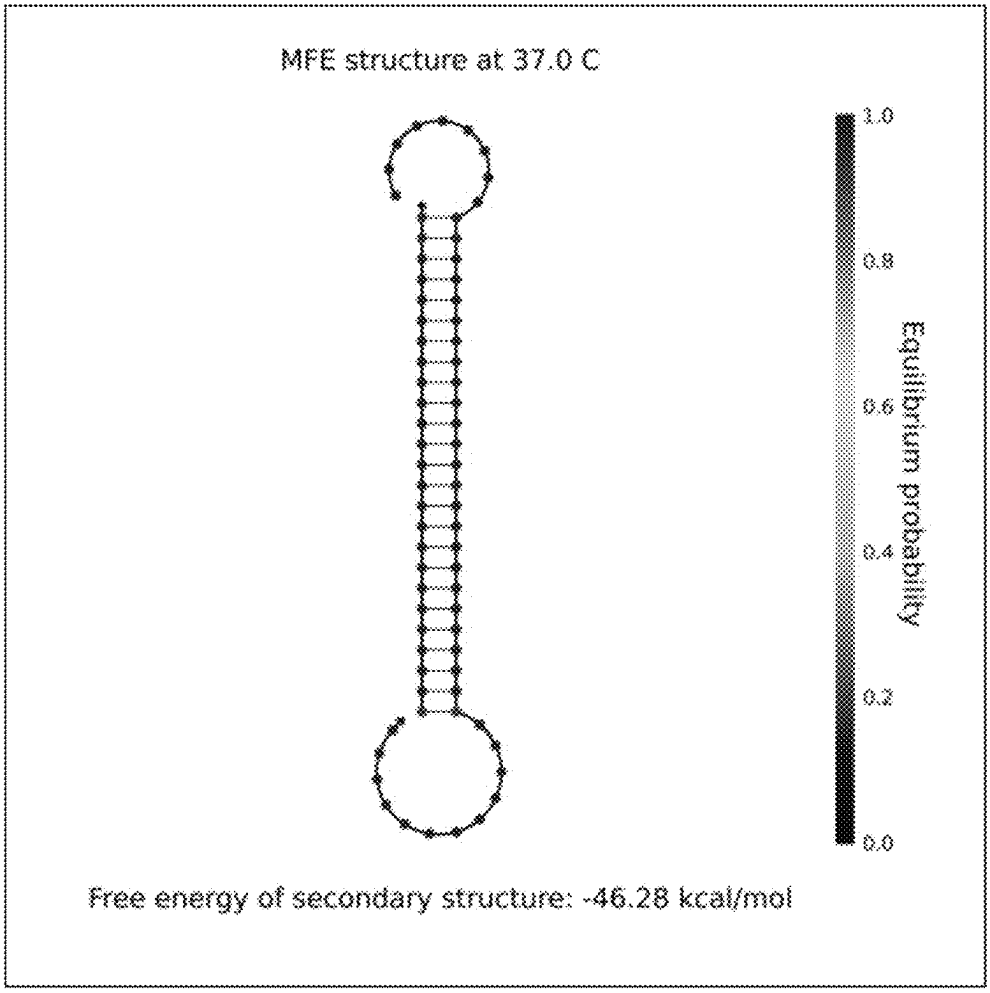

MFE structure at 37.0 C
1.0
0.8
0.6
0.4
0.2
0.0
Equilibrium probability
Free energy of secondary structure: -46.28 kcal/mol

FIG. 28

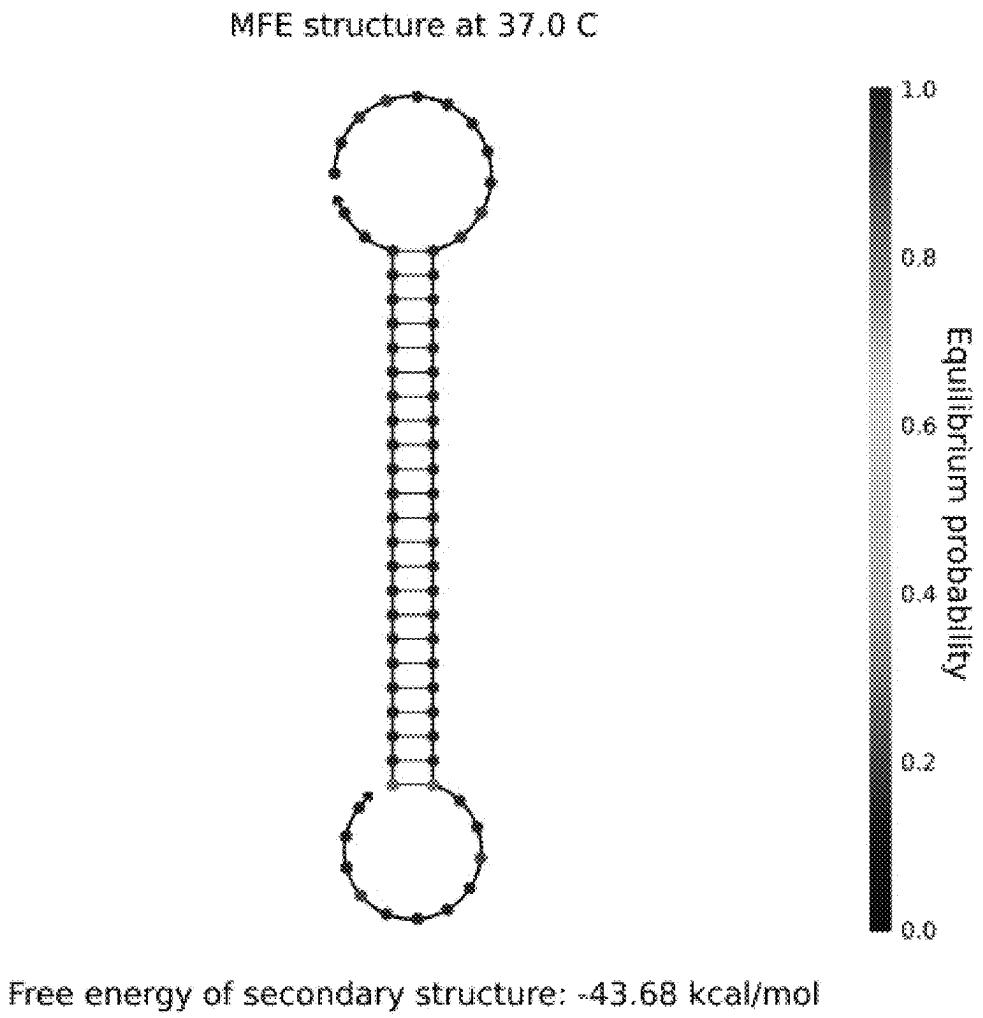

MFE structure at 37.0 C
1.0
0.8
0.6
0.4
0.2
0.0
Equilibrium probability
Free energy of secondary structure: -43.68 kcal/mol

FIG. 29

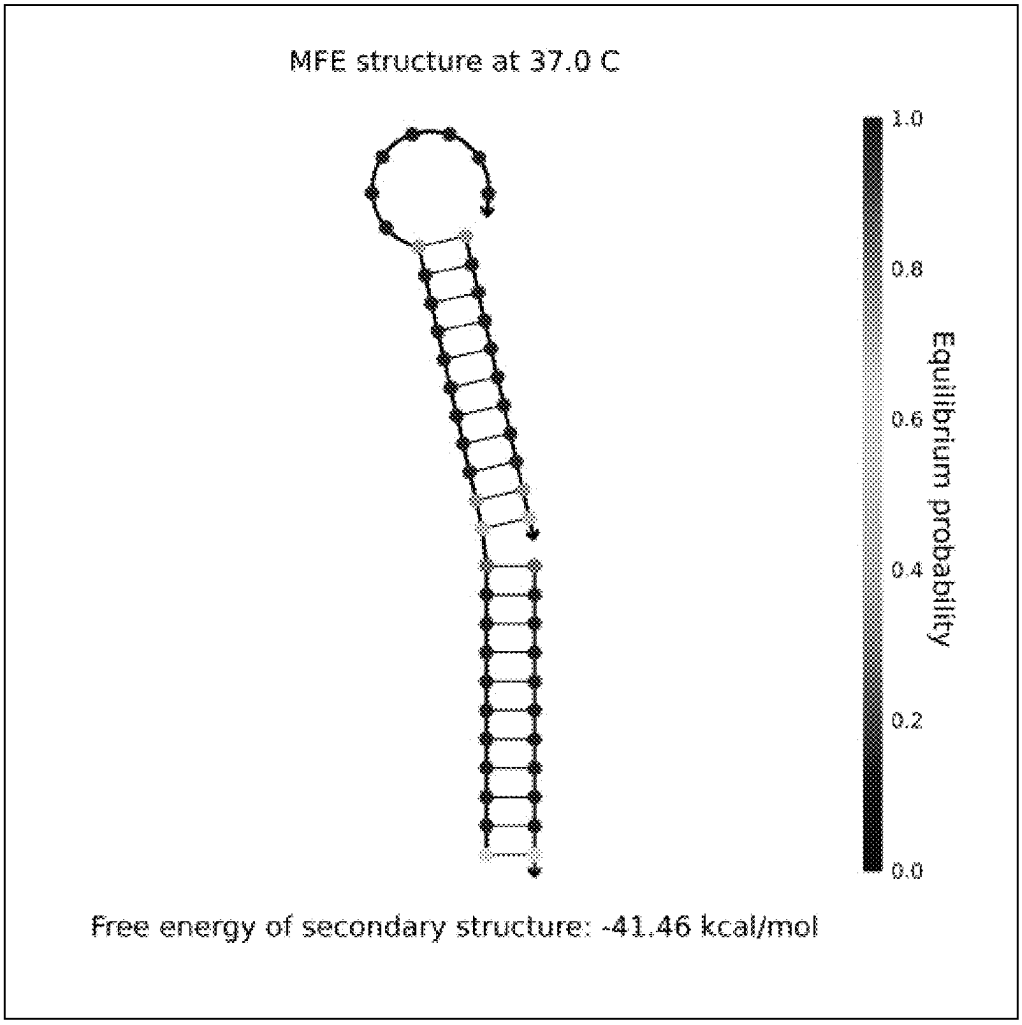

MFE structure at 37.0 C
1.0
0.8
0.6
0.4
0.2
0.0
Equilibrium probability
Free energy of secondary structure: -41.46 kcal/mol

FIG. 30

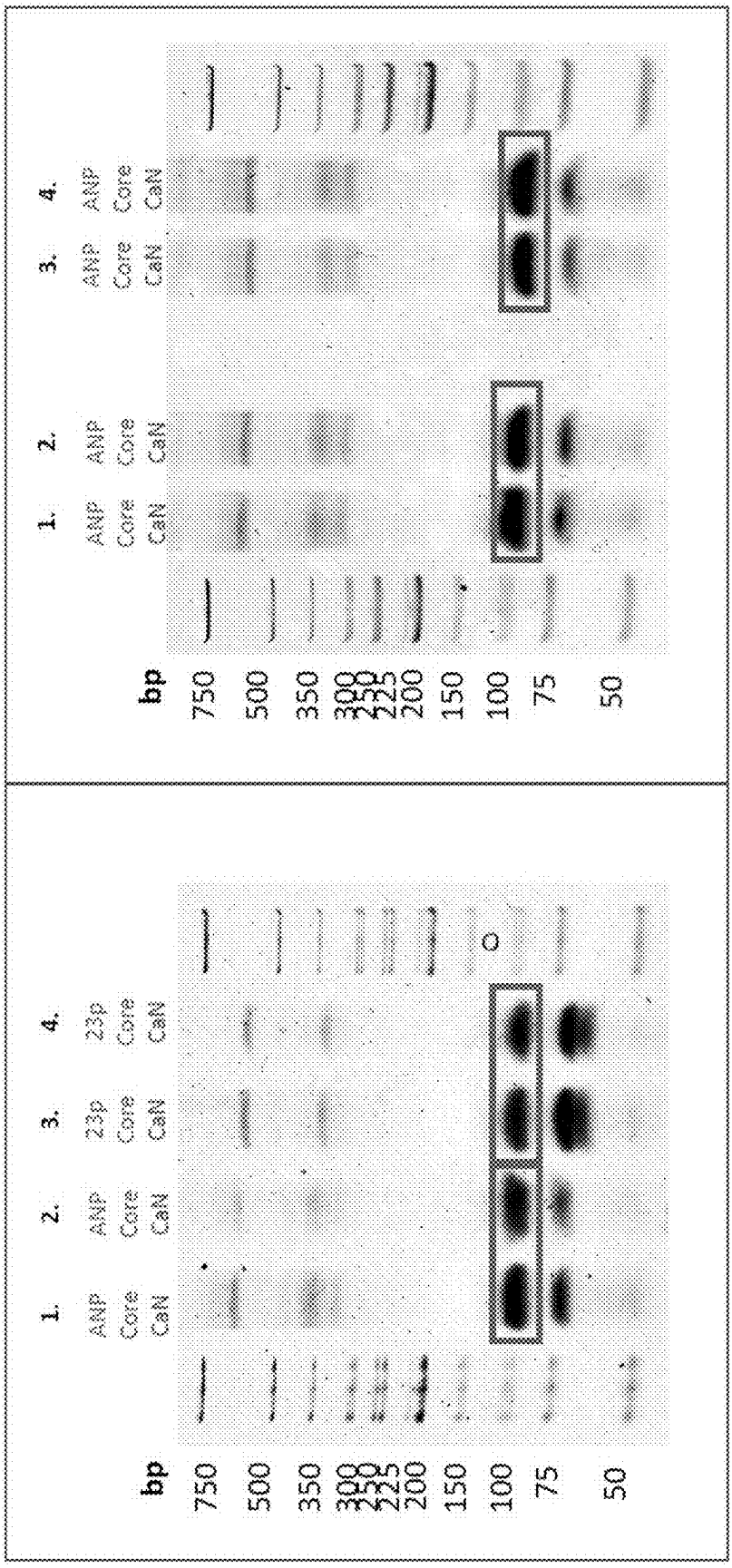

bp
750
500
350
300
250
225
200
150
100
75
50
1.
2.
3.
4.
ANP
Core
CaN
23p

FIG. 31

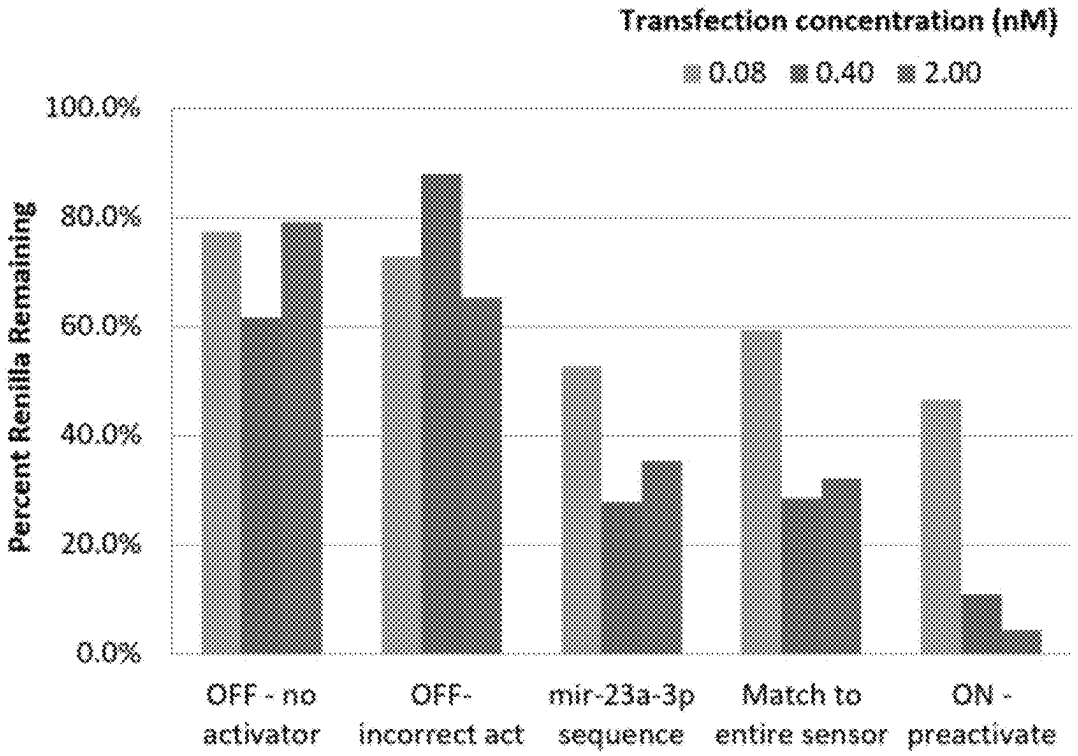

Transfection concentration (nM)
0.08
0.40
2.00
100.0%
80.0%
60.0%
40.0%
20.0%
0.0%
Percent Renilla Remaining
OFF - no activator
OFF- incorrect act
mir-23a-3p sequence
Match to entire sensor
ON - preactivate

FIG. 32

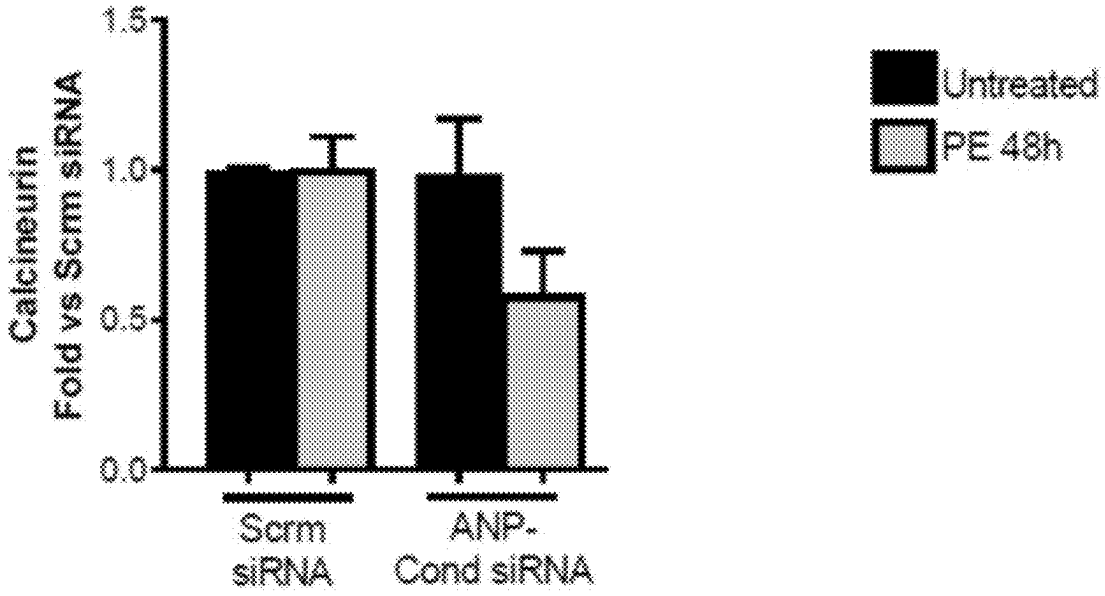

Calcineurin
Fold vs Scrm siRNA
1.5
1.0
0.5
0.0
Scrm siRNA
ANP-Cond siRNA
Untreated
PE 48h

FIG. 33

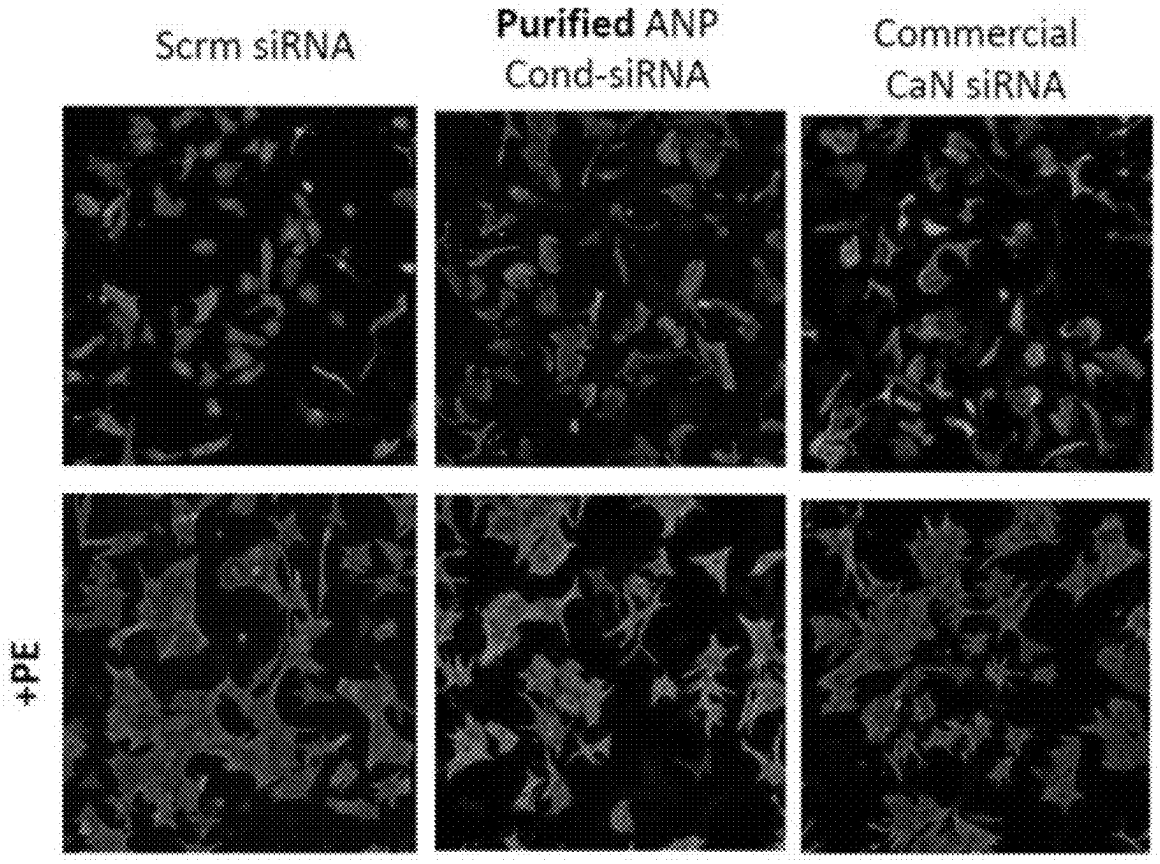


FIG. 34

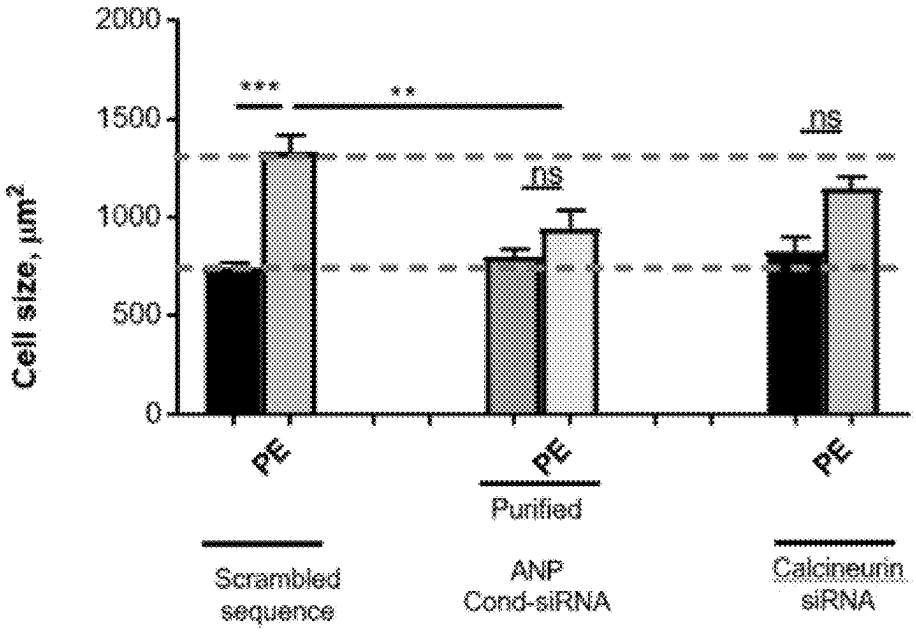

2000
1500
1000
500
0
Cell size, μm²
***
**
ns
ns
PE
PE
PE
Purified
Scrambled sequence
ANP Cond-siRNA
Calcineurin siRNA

FIG. 35A

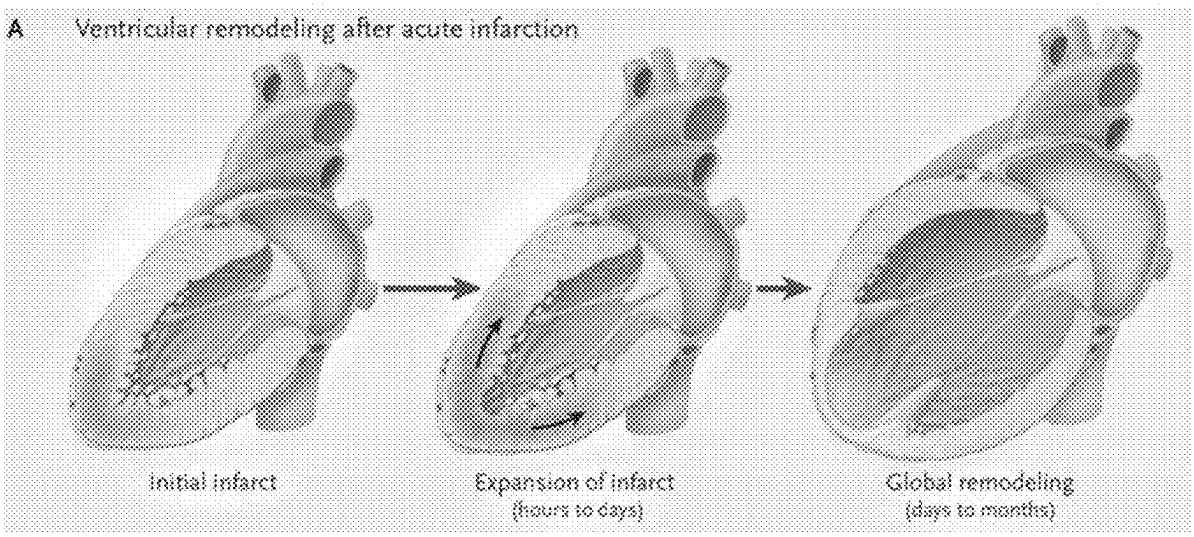

A
Ventricular remodeling after acute infarction
Initial infarct
Expansion of infarct
(hours to days)
Global remodeling
(days to months)

FIG. 35B

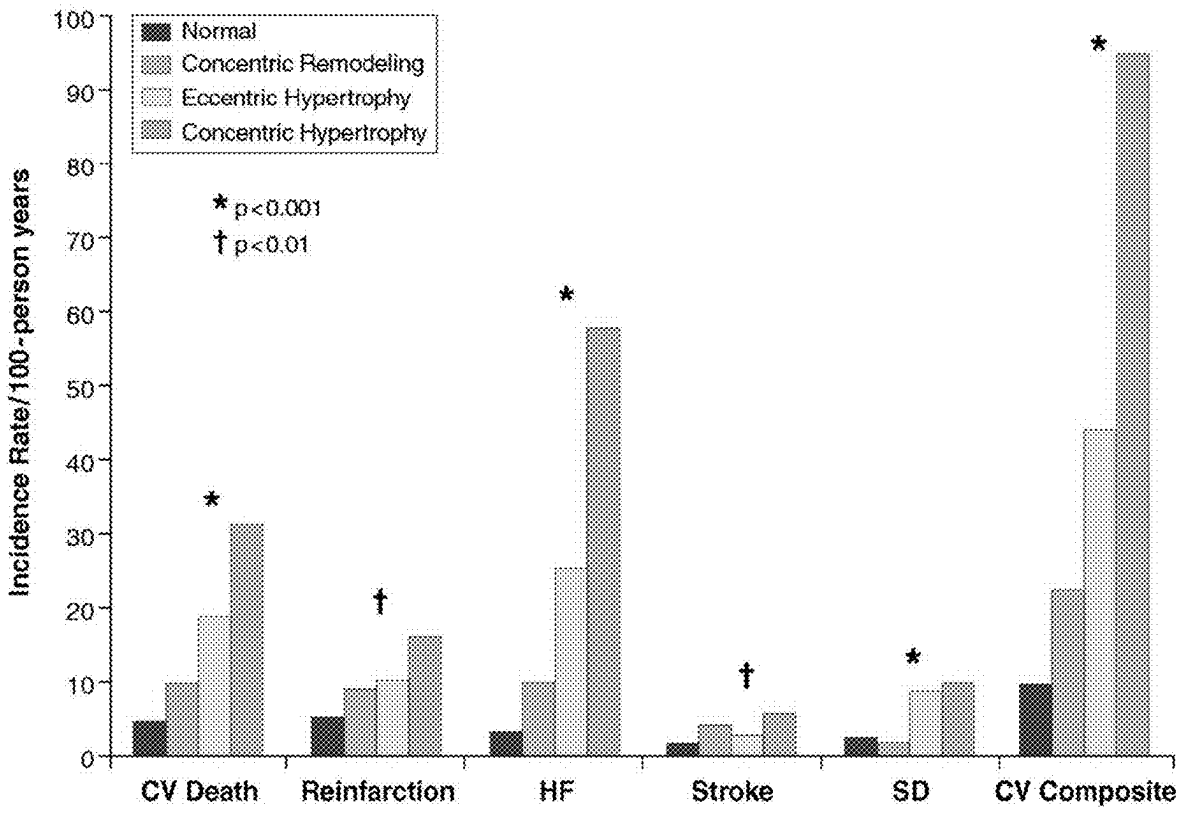

Normal
Concentric Remodeling
Eccentric Hypertrophy
Concentric Hypertrophy
* p<0.001
† p<0.01
Incidence Rate/100-person years
100
90
80
70
60
50
40
30
20
10
0
CV Death
Reinfarction
HF
Stroke
SD
CV Composite

FIG. 36

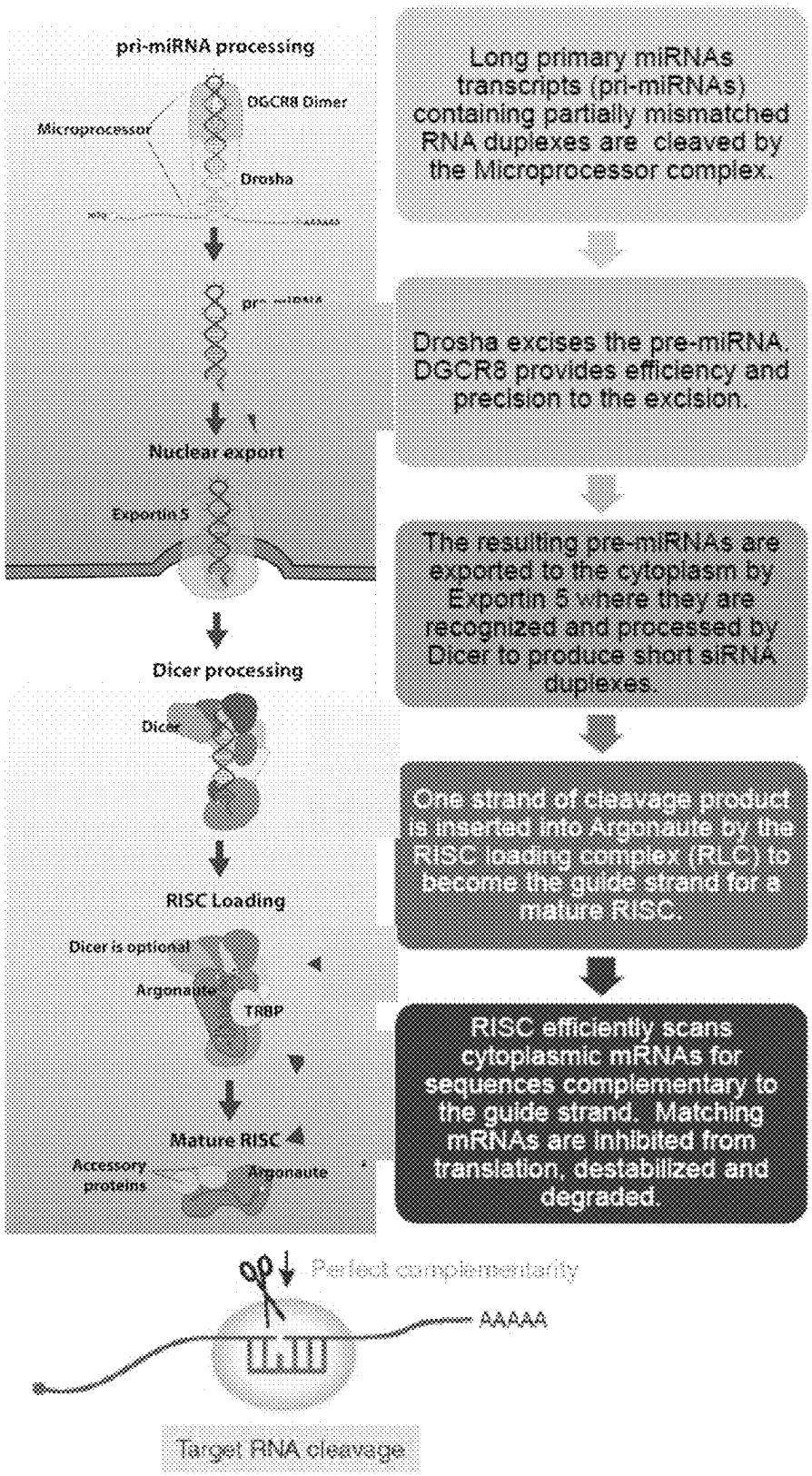
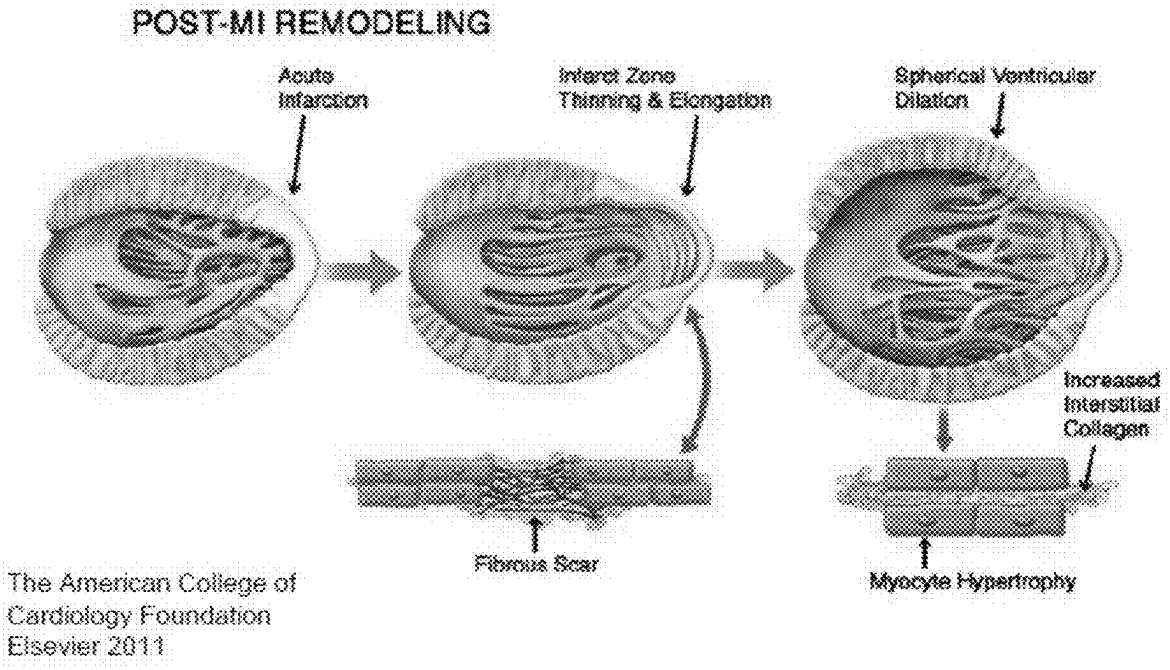

pri-miRNA processing
DGCR8 Dimer
Microprocessor
Drosha
Nuclear export
Exportin 5
Dicer processing
Dicer
RISC Loading
Dicer is optional
Argonaute
TRBP
Mature RISC
Accessory proteins
Argonaute
Long primary miRNAs transcripts (pri-miRNAs) containing partially mismatched RNA duplexes are cleaved by the Microprocessor complex.
Drosha excises the pre-miRNA. DGCR8 provides efficiency and precision to the excision.
The resulting pre-miRNAs are exported to the cytoplasm by Exportin 5 where they are recognized and processed by Dicer to produce short siRNA duplexes.
One strand of cleavage product is inserted into Argonaute by the RISC loading complex (RLC) to become the guide strand for a mature RISC.
RISC efficiently scans cytoplasmic mRNAs for sequences complementary to the guide strand. Matching mRNAs are inhibited from translation, destabilized and degraded.
Perfect complementarity
AAAAA
Target RNA cleavage

FIG. 37


POST-MI REMODELING
Acute Infarction
Infarct Zone Thinning & Elongation
Spherical Ventricular Dilation
Increased Interstitial Collagen
Fibrous Scar
Myocyte Hypertrophy
The American College of Cardiology Foundation Elsevier 2011

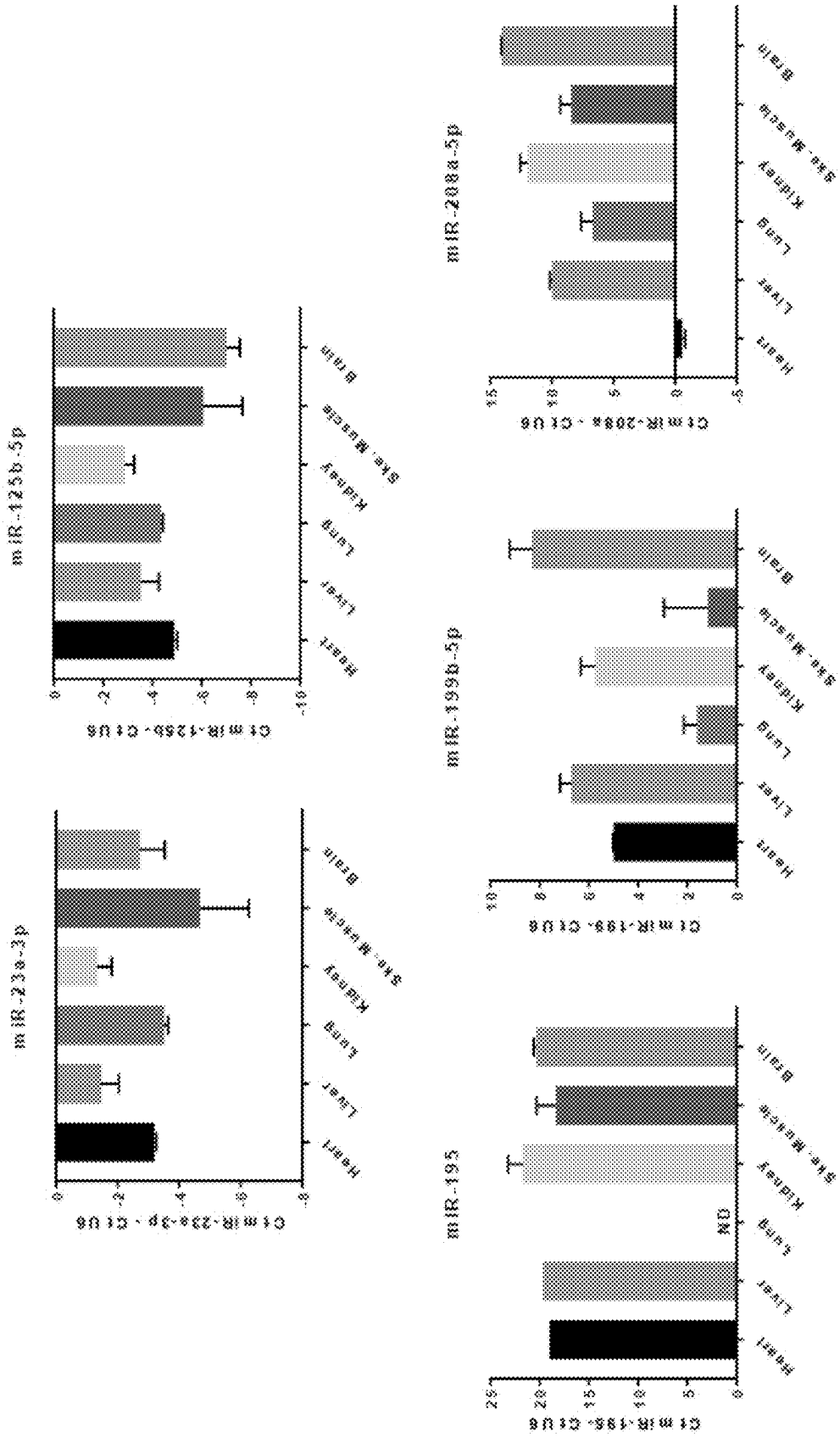

miR-23a-3p
Ct miR-23a-3p - Ct U6
miR-125b-5p
Ct miR-125b- Ct U6
miR-195
Ct miR-195- Ct U6
ND
miR-199b-5p
Ct miR-199- Ct U6
miR-208a-5p
Ct miR-208a - Ct U6
Heart
Liver
Lung
Kidney
Ske. Muscle
Brain

FIG. 38

FIG. 39

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CCAAGGAGCUGUUACAC AGGCUCCAGCAUGG' (SEQ ID NO:50)	[[], [], []]	0.580645	0.83871	0	37
'GGCUCCAGCAUGGGGC UUUGCUGGCACCUCC' (SEQ ID NO:168)	[[], ['GGG'], []]	0.677419	0.903226	1	55
'CCAGGGCUGAGCAGAUC AAGAUGUGGCAAAG' (SEQ ID NO:169)	[[], ['GGG'], []]	0.548387	0.870968	1	84
'CAGGGCUGAGCAGAUCA AGAUGUGGCAAAGC' (SEQ ID NO:170)	[[], ['GGG'], []]	0.548387	0.870968	1	85
'GCUGGCACCUCCAGGG CUGAGCAGAUCAAGA' (SEQ ID NO:171)	[[], ['GGG'], []]	0.612903	0.870968	1	74
'CAGGCUCCAGCAUGGG GCUUUGCUGGCACCU' (SEQ ID NO:172)	[[], ['GGG'], []]	0.645161	0.870968	1	53
'AGGCUCCAGCAUGGGG CUUUGCUGGCACCUC' (SEQ ID NO:173)	[[], ['GGG'], []]	0.645161	0.870968	1	54
'GCUCCAGCAUGGGGCU UUGCUGGCACCUCCA' (SEQ ID NO:174)	[[], ['GGG'], []]	0.645161	0.870968	1	56

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CUCCAGCAUGGGGCUUUGCUGGCACCUCCAG' (SEQ ID NO:175)	[[], ['GGG'], []]	0.645161	0.870968	1	57
'UCCAGCAUGGGGCUUUGCUGGCACCUCCAGG' (SEQ ID NO:176)	[[], ['GGG'], []]	0.645161	0.870968	1	58
'AUUCUGCUUCCUCCCAAGGAGCUGUUACACA' (SEQ ID NO:177)	[['CCC'], [], []]	0.483871	0.83871	1	24
'UCCAGGGCUGAGCAGAUCAAGAUGUGGCAAA' (SEQ ID NO:178)	[[], ['GGG'], []]	0.516129	0.83871	1	83
'UGUUACACAGGCUCCAGCAUGGGGCUUUGCU' (SEQ ID NO:179)	[[], ['GGG'], []]	0.548387	0.83871	1	46
'CUCCAGGGCUGAGCAGAUCAAGAUGUGGCAA' (SEQ ID NO:180)	[[], ['GGG'], []]	0.548387	0.83871	1	82
'CUCCCAAGGAGCUGUUACACAGGCUCCAGCA' (SEQ ID NO:181)	[['CCC'], [], []]	0.580645	0.83871	1	34
'CCCAAGGAGCUGUUACACAGGCUCCAGCAUG' (SEQ ID NO:182)	[['CCC'], [], []]	0.580645	0.83871	1	36

FIG. 39 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CAAGGAGCUGUUACACAGGCUCCAGCAUGGG' (SEQ ID NO:183)	[[], ['GGG'], []]	0.580645	0.83871	1	38
'AAGGAGCUGUUACACAGGCUCCAGCAUGGGG' (SEQ ID NO:184)	[[], ['GGG'], []]	0.580645	0.83871	1	39
'GCUGUUACACAGGCUCCAGCAUGGGGCUUUG' (SEQ ID NO:185)	[[], ['GGG'], []]	0.580645	0.83871	1	44
'CUGUUACACAGGCUCCAGCAUGGGGCUUUGC' (SEQ ID NO:186)	[[], ['GGG'], []]	0.580645	0.83871	1	45
'GUUACACAGGCUCCAGCAUGGGGCUUUGCUG' (SEQ ID NO:187)	[[], ['GGG'], []]	0.580645	0.83871	1	47
'UUACACAGGCUCCAGCAUGGGGCUUUGCUGG' (SEQ ID NO:188)	[[], ['GGG'], []]	0.580645	0.83871	1	48
'CUGGCACCUCCAGGGCUGAGCAGAUCAAGAU' (SEQ ID NO:189)	[[], ['GGG'], []]	0.580645	0.83871	1	75
'UGGCACCUCCAGGGCUGAGCAGAUCAAGAUG' (SEQ ID NO:190)	[[], ['GGG'], []]	0.580645	0.83871	1	76

FIG. 39 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GGCACCUCCAGGGCUGAGCAGAUCAAGAUGU' (SEQ ID NO:191)	[[], ['GGG'], []]	0.580645	0.83871	1	77
'GCACCUCCAGGGCUGAGCAGAUCAAGAUGUG' (SEQ ID NO:192)	[[], ['GGG'], []]	0.580645	0.83871	1	78
'CACCUCCAGGGCUGAGCAGAUCAAGAUGUGG' (SEQ ID NO:193)	[[], ['GGG'], []]	0.580645	0.83871	1	79
'ACCUCCAGGGCUGAGCAGAUCAAGAUGUGGC' (SEQ ID NO:194)	[[], ['GGG'], []]	0.580645	0.83871	1	80
'CCUCCAGGGCUGAGCAGAUCAAGAUGUGGCA' (SEQ ID NO:195)	[[], ['GGG'], []]	0.580645	0.83871	1	81
'CCUCCCAAGGAGCUGUUACACAGGCUCCAGC' (SEQ ID NO:196)	[['CCC'], [], []]	0.612903	0.83871	1	33
'AGGAGCUGUUACACAGGCUCCAGCAUGGGGC' (SEQ ID NO:197)	[[], ['GGG'], []]	0.612903	0.83871	1	40
'UACACAGGCUCCAGCAUGGGGCUUUGCUGGC' (SEQ ID NO:198)	[[], ['GGG'], []]	0.612903	0.83871	1	49

FIG. 39 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GCUUUGCUGGCACCUCCAGGGCUGAGCAGAU' (SEQ ID NO:199)	[[], ['GGG'], []]	0.612903	0.83871	1	69
'CUUUGCUGGCACCUCCAGGGCUGAGCAGAUC' (SEQ ID NO:200)	[[], ['GGG'], []]	0.612903	0.83871	1	70
'UGCUGGCACCUCCAGGGCUGAGCAGAUCAAG' (SEQ ID NO:201)	[[], ['GGG'], []]	0.612903	0.83871	1	73
'CACAGGCUCCAGCAUGGGGCUUUGCUGGCAC' (SEQ ID NO:202)	[[], ['GGG'], []]	0.645161	0.83871	1	51
'ACAGGCUCCAGCAUGGGGCUUUGCUGGCACC' (SEQ ID NO:203)	[[], ['GGG'], []]	0.645161	0.83871	1	52
'GGCUUUGCUGGCACCUCCAGGGCUGAGCAGA' (SEQ ID NO:204)	[[], ['GGG'], []]	0.645161	0.83871	1	68
'UUCUGCUUCCUCCCAAGGAGCUGUUACACAG' (SEQ ID NO:205)	[['CCC'], [], []]	0.516129	0.806452	1	25
'UCUGCUUCCUCCCAAGGAGCUGUUACACAGG' (SEQ ID NO:206)	[['CCC'], [], []]	0.548387	0.806452	1	26

FIG. 39 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UGCUUCCUCCCAAGGAG CUGUUACACAGGCU' (SEQ ID NO:207)	[['CCC'], [], []]	0.548387	0.806452	1	28
'UUCCUCCCAAGGAGCUG UUACACAGGCUCCA' (SEQ ID NO:208)	[['CCC'], [], []]	0.548387	0.806452	1	31
'UCCCAAGGAGCUGUUAC ACAGGCUCCAGCAU' (SEQ ID NO:209)	[['CCC'], [], []]	0.548387	0.806452	1	35
'AGCUGUUACACAGGCUC CAGCAUGGGGCUUU' (SEQ ID NO:210)	[[], ['GGG'], []]	0.548387	0.806452	1	43
'CUGCUUCCUCCCAAGGA GCUGUUACACAGGC' (SEQ ID NO:211)	[['CCC'], [], []]	0.580645	0.806452	1	27
'GCUUCCUCCCAAGGAGC UGUUACACAGGCUC' (SEQ ID NO:212)	[['CCC'], [], []]	0.580645	0.806452	1	29
'CUUCCUCCCAAGGAGCU GUUACACAGGCUCC' (SEQ ID NO:213)	[['CCC'], [], []]	0.580645	0.806452	1	30
'UCCUCCCAAGGAGCUGU UACACAGGCUCCAG' (SEQ ID NO:214)	[['CCC'], [], []]	0.580645	0.806452	1	32

FIG. 39 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GAGCUGUUACACAGGCUCCAGCAUGGGGCUU' (SEQ ID NO:215)	[[], ['GGG'], []]	0.580645	0.806452	1	42
'UUUGCUGGCACCUCCAGGGCUGAGCAGAUCA' (SEQ ID NO:216)	[[], ['GGG'], []]	0.580645	0.806452	1	71
'UUGCUGGCACCUCCAGGGCUGAGCAGAUCAA' (SEQ ID NO:217)	[[], ['GGG'], []]	0.580645	0.806452	1	72
'GGAGCUGUUACACAGGCUCCAGCAUGGGGCU' (SEQ ID NO:218)	[[], ['GGG'], []]	0.612903	0.806452	1	41
'ACACAGGCUCCAGCAUGGGGCUUUGCUGGCA' (SEQ ID NO:219)	[[], ['GGG'], []]	0.612903	0.806452	1	50
'GCAUGGGGCUUUGCUGGCACCUCCAGGGCUG' (SEQ ID NO:220)	[[], ['GGG', 'GGG'], []]	0.677419	0.903226	2	62
'UGGGGCUUUGCUGGCACCUCCAGGGCUGAGC' (SEQ ID NO:221)	[[], ['GGG', 'GGG'], []]	0.677419	0.903226	2	65
'CUUCAAGGAAAAUUGCUUUAUUCUGCUUCCU' (SEQ ID NO:222)	[[], [], ['AAAA', 'UUUA']]	0.354839	0.870968	2	5

FIG. 39 (Cont'd)

FIG. 39 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UUCAAGGAAAAUUGCUUUAUUCUGCUUCCUC' (SEQ ID NO:223)	[[], [], ['AAAA', 'UUUA']]	0.354839	0.870968	2	6
'UCAAGGAAAAUUGCUUUAUUCUGCUUCCUCC' (SEQ ID NO:224)	[[], [], ['AAAA', 'UUUA']]	0.387097	0.870968	2	7
'UUGCUUUAUUCUGCUUCCUCCCAAGGAGCUG' (SEQ ID NO:225)	[['CCC'], [], ['UUUA']]	0.483871	0.870968	2	17
'UGCUUUAUUCUGCUUCCUCCCAAGGAGCUGU' (SEQ ID NO:226)	[['CCC'], [], ['UUUA']]	0.483871	0.870968	2	18
'GCUUUAUUCUGCUUCCUCCCAAGGAGCUGUU' (SEQ ID NO:227)	[['CCC'], [], ['UUUA']]	0.483871	0.870968	2	19
'AGCAUGGGGCUUUGCUGGCACCUCCAGGGCU' (SEQ ID NO:228)	[[], ['GGG', 'GGG'], []]	0.645161	0.870968	2	61
'CAUGGGGCUUUGCUGGCACCUCCAGGGCUGA' (SEQ ID NO:229)	[[], ['GGG', 'GGG'], []]	0.645161	0.870968	2	63
'AUGGGGCUUUGCUGGCACCUCCAGGGCUGAG' (SEQ ID NO:230)	[[], ['GGG', 'GGG'], []]	0.645161	0.870968	2	64

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CCAGCAUGGGGCUUUG CUGGCACCUCCAGGG' (SEQ ID NO:231)	[[], ['GGG', 'GGG'], []]	0.677419	0.870968	2	59
'CAGCAUGGGGCUUUGC UGGCACCUCCAGGGC' (SEQ ID NO:232)	[[], ['GGG', 'GGG'], []]	0.677419	0.870968	2	60
'GGGGCUUUGCUGGCAC CUCCAGGGCUGAGCA' (SEQ ID NO:233)	[[], ['GGG', 'GGG'], []]	0.677419	0.870968	2	66
'GGGCUUUGCUGGCACC UCCAGGGCUGAGCAG' (SEQ ID NO:234)	[[], ['GGG', 'GGG'], []]	0.677419	0.870968	2	67
'GCUUCAAGGAAAAUUGC UUUAUUCUGCUUCC' (SEQ ID NO:235)	[[], [], ['AAAA', 'UUUA']]	0.387097	0.83871	2	4
'AUUGCUUUAUUCUGCUU CCUCCCAAGGAGCU' (SEQ ID NO:236)	[['CCC'], [], ['UUUA']]	0.451613	0.83871	2	16
'CUUUAUUCUGCUUCCUC CCAAGGAGCUGUUA' (SEQ ID NO:237)	[['CCC'], [], ['UUUA']]	0.451613	0.83871	2	20

FIG. 39 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UUUAUUCUGCUUCCUCCCAAGGAGCUGUUAC' (SEQ ID NO:238)	[['CCC'], [], ['UUUA']]	0.451613	0.83871	2	21
'UUAUUCUGCUUCCUCCCAAGGAGCUGUUACA' (SEQ ID NO:239)	[['CCC'], [], ['UUAU']]	0.451613	0.83871	2	22
'UAUUCUGCUUCCUCCCAAGGAGCUGUUACAC' (SEQ ID NO:240)	[['CCC'], [], ['UAUU']]	0.483871	0.83871	2	23
'UCGGCUUCAAGGAAAAUUGCUUUAUUCUGCU' (SEQ ID NO:241)	[[], [], ['AAAA', 'UUUA']]	0.387097	0.806452	2	1
'CGGCUUCAAGGAAAAUUGCUUUAUUCUGCUU' (SEQ ID NO:242)	[[], [], ['AAAA', 'UUUA']]	0.387097	0.806452	2	2
'GGCUUCAAGGAAAAUUGCUUUAUUCUGCUUC' (SEQ ID NO:243)	[[], [], ['AAAA', 'UUUA']]	0.387097	0.806452	2	3
'CUCGGCUUCAAGGAAAAUUGCUUUAUUCUGC' (SEQ ID NO:244)	[[], [], ['AAAA', 'UUUA']]	0.419355	0.806452	2	0
'AAGGAAAAUUGCUUUAUUCUGCUUCCUCCCA' (SEQ ID NO:245)	[['CCC'], [], ['AAAA', 'UUUA']]	0.387097	0.870968	3	9

FIG. 39 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AGGAAAAUUGCUUUAUUCUGCUUCCUCCCAA' (SEQ ID NO:246)	[['CCC'], [], ['AAAA', 'UUUA']]	0.387097	0.870968	3	10
'AAAAUUGCUUUAUUCUGCUUCCUCCCAAGGA' (SEQ ID NO:247)	[['CCC'], [], ['AAAA', 'UUUA']]	0.387097	0.870968	3	13
'CAAGGAAAAUUGCUUUAUUCUGCUUCCUCCC' (SEQ ID NO:248)	[['CCC'], [], ['AAAA', 'UUUA']]	0.419355	0.870968	3	8
'GGAAAAUUGCUUUAUUCUGCUUCCUCCCAAG' (SEQ ID NO:249)	[['CCC'], [], ['AAAA', 'UUUA']]	0.419355	0.83871	3	11
'GAAAAUUGCUUUAUUCUGCUUCCUCCCAAGG' (SEQ ID NO:250)	[['CCC'], [], ['AAAA', 'UUUA']]	0.419355	0.83871	3	12
'AAAUUGCUUUAUUCUGCUUCCUCCCAAGGAG' (SEQ ID NO:251)	[['CCC'], [], ['AAAU', 'UUUA']]	0.419355	0.83871	3	14

FIG. 39 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AAUUGCUUUAUUCUGCU UCCUCCCAAGGAGC' (SEQ ID NO:252)	[['CCC'], [], ['AAUU', 'UUUA']]	0.451613	0.83871	3	15

FIG. 39 (Cont'd)

FIG. 40

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GUGUUUCUGCCUAAGG UGCUGUUUCAAAGGC' (SEQ ID NO:253)	[[], [], []]	0.483871	0.83871	0	24
'GUUUCUGCCUAAGGUG CUGUUUCAAAGGCUC' (SEQ ID NO:254)	[[], [], []]	0.483871	0.83871	0	26
'UUUCUGCCUAAGGUGC UGUUUCAAAGGCUCC' (SEQ ID NO:255)	[[], [], []]	0.483871	0.83871	0	27
'UGUGUUUCUGCCUAAG GUGCUGUUUCAAAGG' (SEQ ID NO:256)	[[], [], []]	0.451613	0.83871	0	23
'UGUUUCUGCCUAAGGU GCUGUUUCAAAGGCU' (SEQ ID NO:257)	[[], [], []]	0.451613	0.83871	0	25
'UUGUGUUUCUGCCUAA GGUGCUGUUUCAAAG' (SEQ ID NO:258)	[[], [], []]	0.419355	0.83871	0	22
'AUUGUGUUUCUGCCUA AGGUGCUGUUUCAAA' (SEQ ID NO:259)	[[], [], []]	0.387097	0.83871	0	21
'CUGCCUAAGGUGCUGU UUCAAAGGCUCCAGG' (SEQ ID NO:260)	[[], [], []]	0.548387	0.806452	0	30

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GCCUAAGGUGCUGUUUCAAAGGCUCCAGGUC' (SEQ ID NO:261)	[[], [], []]	0.548387	0.806452	0	32
'AGGUGCUGUUUCAAAGGCUCCAGGUCUCAGG' (SEQ ID NO:262)	[[], [], []]	0.548387	0.806452	0	37
'UCUGCCUAAGGUGCUGUUUCAAAGGCUCCAG' (SEQ ID NO:263)	[[], [], []]	0.516129	0.806452	0	29
'UGCCUAAGGUGCUGUUUCAAAGGCUCCAGGU' (SEQ ID NO:264)	[[], [], []]	0.516129	0.806452	0	31
'CCUAAGGUGCUGUUUCAAAGGCUCCAGGUCU' (SEQ ID NO:265)	[[], [], []]	0.516129	0.806452	0	33
'CUAAGGUGCUGUUUCAAAGGCUCCAGGUCUC' (SEQ ID NO:266)	[[], [], []]	0.516129	0.806452	0	34
'UUCUGCCUAAGGUGCUGUUUCAAAGGCUCCA' (SEQ ID NO:267)	[[], [], []]	0.483871	0.806452	0	28
'AAGGUGCUGUUUCAAAGGCUCCAGGUCUCAG' (SEQ ID NO:268)	[[], [], []]	0.516129	0.774194	0	36

FIG. 40 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UAAGGUGCUGUUUCAAAGGCUCCAGGUCUCA' (SEQ ID NO:269)	[[], [], []]	0.483871	0.774194	0	35
'UUGCUUUAUUGUGUUUCUGCCUAAGGUGCUG' (SEQ ID NO:270)	[[], [], ['UUUA']]	0.419355	0.903226	1	14
'UGCUUUAUUGUGUUUCUGCCUAAGGUGCUGU' (SEQ ID NO:271)	[[], [], ['UUUA']]	0.419355	0.903226	1	15
'GCUUUAUUGUGUUUCUGCCUAAGGUGCUGUU' (SEQ ID NO:272)	[[], [], ['UUUA']]	0.419355	0.903226	1	16
'CUUUAUUGUGUUUCUGCCUAAGGUGCUGUUU' (SEQ ID NO:273)	[[], [], ['UUUA']]	0.387097	0.903226	1	17
'UUUAUUGUGUUUCUGCCUAAGGUGCUGUUUC' (SEQ ID NO:274)	[[], [], ['UUUA']]	0.387097	0.903226	1	18
'AUUGCUUUAUUGUGUUUCUGCCUAAGGUGCU' (SEQ ID NO:275)	[[], [], ['UUUA']]	0.387097	0.870968	1	13
'UUAUUGUGUUUCUGCCUAAGGUGCUGUUUCA' (SEQ ID NO:276)	[[], [], ['UUAU']]	0.387097	0.870968	1	19

FIG. 40 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GGCUCCAGGUCUCAGGGCUUCACAGGCAUCC' (SEQ ID NO:277)	[[], ['GGG'], []]	0.645161	0.83871	1	52
'CAAAGGCUCCAGGUCUCAGGGCUUCACAGGC' (SEQ ID NO:278)	[[], ['GGG'], []]	0.612903	0.83871	1	48
'GCUCCAGGUCUCAGGGCUUCACAGGCAUCCU' (SEQ ID NO:279)	[[], ['GGG'], []]	0.612903	0.83871	1	53
'GGUGCUGUUUCAAAGGCUCCAGGUCUCAGGG' (SEQ ID NO:280)	[[], ['GGG'], []]	0.580645	0.83871	1	38
'GUGCUGUUUCAAAGGCUCCAGGUCUCAGGGC' (SEQ ID NO:281)	[[], ['GGG'], []]	0.580645	0.83871	1	39
'AAAGGCUCCAGGUCUCAGGGCUUCACAGGCA' (SEQ ID NO:282)	[[], ['GGG'], []]	0.580645	0.83871	1	49
'CUCCAGGUCUCAGGGCUUCACAGGCAUCCUU' (SEQ ID NO:283)	[[], ['GGG'], []]	0.580645	0.83871	1	54
'UGCUGUUUCAAAGGCUCCAGGUCUCAGGGCU' (SEQ ID NO:284)	[[], ['GGG'], []]	0.548387	0.83871	1	40

FIG. 40 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GCUGUUUCAAAGGCUCCAGGUCUCAGGGCUU' (SEQ ID NO:285)	[[], ['GGG'], []]	0.548387	0.83871	1	41
'CUGUUUCAAAGGCUCCAGGUCUCAGGGCUUC' (SEQ ID NO:286)	[[], ['GGG'], []]	0.548387	0.83871	1	42
'UAUUGUGUUUCUGCCUAAGGUGCUGUUUCAA' (SEQ ID NO:287)	[[], [], ['UAUU']]	0.387097	0.83871	1	20
'AGGCUCCAGGUCUCAGGGCUUCACAGGCAUC' (SEQ ID NO:288)	[[], ['GGG'], []]	0.612903	0.806452	1	51
'UCAAAGGCUCCAGGUCUCAGGGCUUCACAGG' (SEQ ID NO:289)	[[], ['GGG'], []]	0.580645	0.806452	1	47
'AAGGCUCCAGGUCUCAGGGCUUCACAGGCAU' (SEQ ID NO:290)	[[], ['GGG'], []]	0.580645	0.806452	1	50
'CCAGGUCUCAGGGCUUCACAGGCAUCCUUAG' (SEQ ID NO:291)	[[], ['GGG'], []]	0.580645	0.806452	1	56
'CAGGUCUCAGGGCUUCACAGGCAUCCUUAGG' (SEQ ID NO:292)	[[], ['GGG'], []]	0.580645	0.806452	1	57

FIG. 40 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GUUUCAAAGGCUCCAG GUCUCAGGGCUUCAC' (SEQ ID NO:293)	[[], ['GGG'], []]	0.548387	0.806452	1	44
'UCCAGGUCUCAGGGCU UCACAGGCAUCCUUA' (SEQ ID NO:294)	[[], ['GGG'], []]	0.548387	0.806452	1	55
'UGUUUCAAAGGCUCCA GGUCUCAGGGCUUCA' (SEQ ID NO:295)	[[], ['GGG'], []]	0.516129	0.806452	1	43
'UUCAAAGGCUCCAGGU CUCAGGGCUUCACAG' (SEQ ID NO:296)	[[], ['GGG'], []]	0.548387	0.774194	1	46
'UUUCAAAGGCUCCAGG UCUCAGGGCUUCACA' (SEQ ID NO:297)	[[], ['GGG'], []]	0.516129	0.774194	1	45
'GGCUUGAAGGAAAAUU GCUUUAUUGUGUUUC' (SEQ ID NO:298)	[[], [], ['AAAA', 'UUUA']]	0.354839	0.903226	2	0
'GCUUGAAGGAAAAUUG CUUUAUUGUGUUUCU' (SEQ ID NO:299)	[[], [], ['AAAA', 'UUUA']]	0.322581	0.903226	2	1
'CUUGAAGGAAAAUUGC UUUAUUGUGUUUCUG' (SEQ ID NO:300)	[[], [], ['AAAA', 'UUUA']]	0.322581	0.903226	2	2

FIG. 40 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UUGAAGGAAAAUUGCU UUAUUGUGUUUCUGC' (SEQ ID NO:301)	[[], [], ['AAAA', 'UUUA']]	0.322581	0.903226	2	3
'UGAAGGAAAAUUGCUU UAUUGUGUUUCUGCC' (SEQ ID NO:302)	[[], [], ['AAAA', 'UUUA']]	0.354839	0.870968	2	4
'GAAGGAAAAUUGCUUU AUUGUGUUUCUGCCU' (SEQ ID NO:303)	[[], [], ['AAAA', 'UUUA']]	0.354839	0.870968	2	5
'GGAAAAUUGCUUUAUU GUGUUUCUGCCUAAG' (SEQ ID NO:304)	[[], [], ['AAAA', 'UUUA']]	0.354839	0.870968	2	8
'GAAAAUUGCUUUAUUG UGUUUCUGCCUAAGG' (SEQ ID NO:305)	[[], [], ['AAAA', 'UUUA']]	0.354839	0.870968	2	9
'AAAUUGCUUUAUUGUG UUUCUGCCUAAGGUG' (SEQ ID NO:306)	[[], [], ['AAAU', 'UUUA']]	0.354839	0.870968	2	11
'AAGGAAAAUUGCUUUAU UGUGUUUCUGCCUA' (SEQ ID NO:307)	[[], [], ['AAAA', 'UUUA']]	0.322581	0.870968	2	6
'AGGAAAAUUGCUUUAU UGUGUUUCUGCCUAA' (SEQ ID NO:308)	[[], [], ['AAAA', 'UUUA']]	0.322581	0.870968	2	7

FIG. 40 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AAAAUUGCUUUAUUGUGUUUCUGCCUAAGGU' (SEQ ID NO:309)	[[], [], ['AAAA', 'UUUA']]	0.322581	0.870968	2	10
'GGUCUCAGGGCUUCACAGGCAUCCUUAGGGU' (SEQ ID NO:310)	[[], ['GGG', 'GGG'], []]	0.580645	0.83871	2	59
'CUCAGGGCUUCACAGGCAUCCUUAGGGUUGG' (SEQ ID NO:311)	[[], ['GGG', 'GGG'], []]	0.580645	0.83871	2	62
'GGCUUCACAGGCAUCCUUAGGGUUGGGUAGC' (SEQ ID NO:312)	[[], ['GGG', 'GGG'], []]	0.580645	0.83871	2	67
'GUCUCAGGGCUUCACAGGCAUCCUUAGGGUU' (SEQ ID NO:313)	[[], ['GGG', 'GGG'], []]	0.548387	0.83871	2	60
'UCUCAGGGCUUCACAGGCAUCCUUAGGGUUG' (SEQ ID NO:314)	[[], ['GGG', 'GGG'], []]	0.548387	0.83871	2	61
'AAUUGCUUUAUUGUGUUUCUGCCUAAGGUGC' (SEQ ID NO:315)	[[], [], ['AAUU', 'UUUA']]	0.387097	0.83871	2	12
'AGGUCUCAGGGCUUCACAGGCAUCCUUAGGG' (SEQ ID NO:316)	[[], ['GGG', 'GGG'], []]	0.580645	0.806452	2	58

FIG. 40 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GCUUCACAGGCAUCCU UAGGGUUGGGUAGCA' (SEQ ID NO:317)	[[], ['GGG', 'GGG'], []]	0.548387	0.806452	2	68
'CUUCACAGGCAUCCUU AGGGUUGGGUAGCAC' (SEQ ID NO:318)	[[], ['GGG', 'GGG'], []]	0.548387	0.806452	2	69
'CACAGGCAUCCUUAGG GUUGGGUAGCACAAG' (SEQ ID NO:319)	[[], ['GGG', 'GGG'], []]	0.548387	0.806452	2	72
'ACAGGCAUCCUUAGGG UUGGGUAGCACAAGA' (SEQ ID NO:320)	[[], ['GGG', 'GGG'], []]	0.516129	0.806452	2	73
'CAGGCAUCCUUAGGGU UGGGUAGCACAAGAU' (SEQ ID NO:321)	[[], ['GGG', 'GGG'], []]	0.516129	0.806452	2	74
'UUCACAGGCAUCCUUA GGGUUGGGUAGCACA' (SEQ ID NO:322)	[[], ['GGG', 'GGG'], []]	0.516129	0.774194	2	70
'UCACAGGCAUCCUUAG GGUUGGGUAGCACAA' (SEQ ID NO:323)	[[], ['GGG', 'GGG'], []]	0.516129	0.774194	2	71
'UCAGGGCUUCACAGGC AUCCUUAGGGUUGGG' (SEQ ID NO:324)	[[], ['GGG', 'GGG', 'GGG'], []]	0.580645	0.83871	3	63

FIG. 40 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CAGGGCUUCACAGGCAUCCUUAGGGUUGGGU' (SEQ ID NO:325)	[[], ['GGG', 'GGG', 'GGG'], []]	0.580645	0.83871	3	64
'GGGCUUCACAGGCAUCCUUAGGGUUGGGUAG' (SEQ ID NO:326)	[[], ['GGG', 'GGG', 'GGG'], []]	0.580645	0.83871	3	66
'AGGGCUUCACAGGCAUCCUUAGGGUUGGGUA' (SEQ ID NO:327)	[[], ['GGG', 'GGG', 'GGG'], []]	0.548387	0.806452	3	65

FIG. 40 (Cont'd)

FIG. 41

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GGAGAGGCGAGGAAGU CACCAUCAAACCACU' (SEQ ID NO:328)	[[], [], []]	0.548387	0.903226	0	90
'AGAUGUGAGAAGUGUUG ACAGGAAGCUGCAG' (SEQ ID NO:329)	[[], [], []]	0.483871	0.903226	0	139
'UAAGAUGUGAGAAGUGU UGACAGGAAGCUGC' (SEQ ID NO:330)	[[], [], []]	0.451613	0.903226	0	137
'AAGAUGUGAGAAGUGUU GACAGGAAGCUGCA' (SEQ ID NO:331)	[[], [], []]	0.451613	0.903226	0	138
'AUUCACUUUCAAACCAC UUUCAGUAACAGGU' (SEQ ID NO:332)	[[], [], []]	0.354839	0.903226	0	26
'GAGAGGCGAGGAAGUCA CCAUCAAACCACUU' (SEQ ID NO:333)	[[], [], []]	0.516129	0.870968	0	91
'GAUGUGAGAAGUGUUGA CAGGAAGCUGCAGC' (SEQ ID NO:334)	[[], [], []]	0.516129	0.870968	0	140
'AUGUGAGAAGUGUUGAC AGGAAGCUGCAGCU' (SEQ ID NO:335)	[[], [], []]	0.483871	0.870968	0	141

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UGUGAGAAGUGUUGACAGGAAGCUGCAGCUU' (SEQ ID NO:336)	[[], [], []]	0.483871	0.870968	0	142
'GUGAGAAGUGUUGACAGGAAGCUGCAGCUUA' (SEQ ID NO:337)	[[], [], []]	0.483871	0.870968	0	143
'UGAGAAGUGUUGACAGGAAGCUGCAGCUUAG' (SEQ ID NO:338)	[[], [], []]	0.483871	0.870968	0	144
'GAGAAGUGUUGACAGGAAGCUGCAGCUUAGA' (SEQ ID NO:339)	[[], [], []]	0.483871	0.870968	0	145
'GAAGUGUUGACAGGAAGCUGCAGCUUAGAUG' (SEQ ID NO:340)	[[], [], []]	0.483871	0.870968	0	147
'AAGUGUUGACAGGAAGCUGCAGCUUAGAUGG' (SEQ ID NO:341)	[[], [], []]	0.483871	0.870968	0	148
'AGAAGUGUUGACAGGAAGCUGCAGCUUAGAU' (SEQ ID NO:342)	[[], [], []]	0.451613	0.870968	0	146
'GAUCACAACUCCAUGGCAACAAGAUGACACA' (SEQ ID NO:343)	[[], [], []]	0.451613	0.870968	0	182

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AUCACAACUCCAUGGCAACAAGAUGACACAA' (SEQ ID NO:344)	[[], [], []]	0.419355	0.870968	0	183
'UCACAACUCCAUGGCAACAAGAUGACACAAA' (SEQ ID NO:345)	[[], [], []]	0.419355	0.870968	0	184
'UUCACUUUCAAACCACUUUCAGUAACAGGUG' (SEQ ID NO:346)	[[], [], []]	0.387097	0.870968	0	27
'UCACUUUCAAACCACUUUCAGUAACAGGUGA' (SEQ ID NO:347)	[[], [], []]	0.387097	0.870968	0	28
'AGAGGCGAGGAAGUCACCAUCAAACCACUUU' (SEQ ID NO:348)	[[], [], []]	0.483871	0.83871	0	92
'GGAUGAUCACAACUCCAUGGCAACAAGAUGA' (SEQ ID NO:349)	[[], [], []]	0.451613	0.83871	0	178
'GAUGAUCACAACUCCAUGGCAACAAGAUGAC' (SEQ ID NO:350)	[[], [], []]	0.451613	0.83871	0	179
'UGAUCACAACUCCAUGGCAACAAGAUGACAC' (SEQ ID NO:351)	[[], [], []]	0.451613	0.83871	0	181

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CACUUUCAAACCACUUU CAGUAACAGGUGAG' (SEQ ID NO:352)	[[], [], []]	0.419355	0.83871	0	29
'AUGAUCACAACUCCAUG GCAACAAGAUGACA' (SEQ ID NO:353)	[[], [], []]	0.419355	0.83871	0	180
'AACCACUUUCAGUAACA GGUGAGGUUCUACC' (SEQ ID NO:354)	[[], [], []]	0.451613	0.806452	0	37
'ACCACUUUCAGUAACAG GUGAGGUUCUACCU' (SEQ ID NO:355)	[[], [], []]	0.451613	0.806452	0	38
'CCACUUUCAGUAACAGG UGAGGUUCUACCUU' (SEQ ID NO:356)	[[], [], []]	0.451613	0.806452	0	39
'ACUUUCAAACCACUUUC AGUAACAGGUGAGG' (SEQ ID NO:357)	[[], [], []]	0.419355	0.806452	0	30
'CUUUCAAACCACUUUCA GUAACAGGUGAGGU' (SEQ ID NO:358)	[[], [], []]	0.419355	0.806452	0	31
'UUCAAACCACUUUCAGU AACAGGUGAGGUUC' (SEQ ID NO:359)	[[], [], []]	0.419355	0.806452	0	33

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UCAAACCACUUUCAGUAACAGGUGAGGUUCU' (SEQ ID NO:360)	[[], [], []]	0.419355	0.806452	0	34
'CAAACCACUUUCAGUAACAGGUGAGGUUCUA' (SEQ ID NO:361)	[[], [], []]	0.419355	0.806452	0	35
'AAACCACUUUCAGUAACAGGUGAGGUUCUAC' (SEQ ID NO:362)	[[], [], []]	0.419355	0.806452	0	36
'CACUUUCAGUAACAGGUGAGGUUCUACCUUA' (SEQ ID NO:363)	[[], [], []]	0.419355	0.806452	0	40
'UUUCAAACCACUUUCAGUAACAGGUGAGGUU' (SEQ ID NO:364)	[[], [], []]	0.387097	0.806452	0	32
'UUUAUUCACUUUCAAACCACUUUCAGUAACA' (SEQ ID NO:365)	[[], [], ['UUUA']]	0.290323	0.967742	1	23
'GGGAGAGGCGAGGAAGUCACCAUCAAACCAC' (SEQ ID NO:366)	[[], ['GGG'], []]	0.580645	0.935484	1	89
'GGCAACAAGAUGACACAAAUGCAGCAGAGAC' (SEQ ID NO:367)	[[], [], ['AAAU']]	0.483871	0.935484	1	196

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GCAACAAGAUGACACAA AUGCAGCAGAGACC' (SEQ ID NO:368)	[[], [], ['AAAU']]	0.483871	0.935484	1	197
'GUUAGCAUAAGAUGUGA GAAGUGUUGACAGG' (SEQ ID NO:369)	[[], [], ['AUAA']]	0.419355	0.935484	1	130
'AGCAUAAGAUGUGAGAA GUGUUGACAGGAAG' (SEQ ID NO:370)	[[], [], ['AUAA']]	0.419355	0.935484	1	133
'AUAAGAUGUGAGAAGUG UUGACAGGAAGCUG' (SEQ ID NO:371)	[[], [], ['AUAA']]	0.419355	0.935484	1	136
'UCACCAUCAAACCACUU UAUCUACAGUUAGC' (SEQ ID NO:372)	[[], [], ['UUUA']]	0.387097	0.935484	1	105
'CACCAUCAAACCACUUU AUCUACAGUUAGCA' (SEQ ID NO:373)	[[], [], ['UUUA']]	0.387097	0.935484	1	106
'AGUUAGCAUAAGAUGUG AGAAGUGUUGACAG' (SEQ ID NO:374)	[[], [], ['AUAA']]	0.387097	0.935484	1	129
'UUAGCAUAAGAUGUGAG AAGUGUUGACAGGA' (SEQ ID NO:375)	[[], [], ['AUAA']]	0.387097	0.935484	1	131

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UAGCAUAAGAUGUGAGAAGUGUUGACAGGAA' (SEQ ID NO:376)	[[], [], ['AUAA']]	0.387097	0.935484	1	132
'AAGUCACCAUCAAACCACUUUAUCUACAGUU' (SEQ ID NO:377)	[[], [], ['UUUA']]	0.354839	0.935484	1	102
'AGUCACCAUCAAACCACUUUAUCUACAGUUA' (SEQ ID NO:378)	[[], [], ['UUUA']]	0.354839	0.935484	1	103
'ACCAUCAAACCACUUUAUCUACAGUUAGCAU' (SEQ ID NO:379)	[[], [], ['UUUA']]	0.354839	0.935484	1	107
'CCAUCAAACCACUUUAUCUACAGUUAGCAUA' (SEQ ID NO:380)	[[], [], ['UUUA']]	0.354839	0.935484	1	108
'UACAGUUAGCAUAAGAUGUGAGAAGUGUUGA' (SEQ ID NO:381)	[[], [], ['AUAA']]	0.354839	0.935484	1	126
'CUGAAGUUUAUUCACUUUCAAACCACUUUCA' (SEQ ID NO:382)	[[], [], ['UUUA']]	0.322581	0.935484	1	17
'GUUUAUUCACUUUCAAACCACUUUCAGUAAC' (SEQ ID NO:383)	[[], [], ['UUUA']]	0.322581	0.935484	1	22

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UUAUUCACUUUCAAACC ACUUUCAGUAACAG' (SEQ ID NO:384)	[[], [], ['UUAU']]	0.322581	0.935484	1	24
'AAGUUUAUUCACUUUCA AACCACUUUCAGUA' (SEQ ID NO:385)	[[], [], ['UUUA']]	0.290323	0.935484	1	20
'AGUUUAUUCACUUUCAA ACCACUUUCAGUAA' (SEQ ID NO:386)	[[], [], ['UUUA']]	0.290323	0.935484	1	21
'GGUGGGAGAGGCGAGG AAGUCACCAUCAAAC' (SEQ ID NO:387)	[[], ['GGG'], []]	0.580645	0.903226	1	86
'GUGGGAGAGGCGAGGA AGUCACCAUCAAACC' (SEQ ID NO:388)	[[], ['GGG'], []]	0.580645	0.903226	1	87
'UGGGAGAGGCGAGGAA GUCACCAUCAAACCA' (SEQ ID NO:389)	[[], ['GGG'], []]	0.548387	0.903226	1	88
'CCAUGGCAACAAGAUGA CACAAAUGCAGCAG' (SEQ ID NO:390)	[[], [], ['AAAU']]	0.483871	0.903226	1	192
'GCAUAAGAUGUGAGAAG UGUUGACAGGAAGC' (SEQ ID NO:391)	[[], [], ['AUAA']]	0.451613	0.903226	1	134

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CAUGGCAACAAGAUGACACAAAUGCAGCAGA' (SEQ ID NO:392)	[[], [], ['AAAU']]	0.451613	0.903226	1	193
'AUGGCAACAAGAUGACACAAAUGCAGCAGAG' (SEQ ID NO:393)	[[], [], ['AAAU']]	0.451613	0.903226	1	194
'UGGCAACAAGAUGACACAAAUGCAGCAGAGA' (SEQ ID NO:394)	[[], [], ['AAAU']]	0.451613	0.903226	1	195
'CAUAAGAUGUGAGAAGUGUUGACAGGAAGCU' (SEQ ID NO:395)	[[], [], ['AUAA']]	0.419355	0.903226	1	135
'AGGAAGUCACCAUCAAACCACUUUAUCUACA' (SEQ ID NO:396)	[[], [], ['UUUA']]	0.387097	0.903226	1	99
'GAAGUCACCAUCAAACCACUUUAUCUACAGU' (SEQ ID NO:397)	[[], [], ['UUUA']]	0.387097	0.903226	1	101
'GUCACCAUCAAACCACUUUAUCUACAGUUAG' (SEQ ID NO:398)	[[], [], ['UUUA']]	0.387097	0.903226	1	104
'CUACAGUUAGCAUAAGAUGUGAGAAGUGUUG' (SEQ ID NO:399)	[[], [], ['AUAA']]	0.387097	0.903226	1	125

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'ACAGUUAGCAUAAGAUGUGAGAAGUGUUGAC' (SEQ ID NO:400)	[[], [], ['AUAA']]	0.387097	0.903226	1	127
'CAGUUAGCAUAAGAUGUGAGAAGUGUUGACA' (SEQ ID NO:401)	[[], [], ['AUAA']]	0.387097	0.903226	1	128
'GCUGAAGUUUAUUCACUUUCAAACCACUUUC' (SEQ ID NO:402)	[[], [], ['UUUA']]	0.354839	0.903226	1	16
'UAUUCACUUUCAAACCACUUUCAGUAACAGG' (SEQ ID NO:403)	[[], [], ['UAUU']]	0.354839	0.903226	1	25
'UAUCUACAGUUAGCAUAAGAUGUGAGAAGUG' (SEQ ID NO:404)	[[], [], ['AUAA']]	0.354839	0.903226	1	122
'AUCUACAGUUAGCAUAAGAUGUGAGAAGUGU' (SEQ ID NO:405)	[[], [], ['AUAA']]	0.354839	0.903226	1	123
'UCUACAGUUAGCAUAAGAUGUGAGAAGUGUU' (SEQ ID NO:406)	[[], [], ['AUAA']]	0.354839	0.903226	1	124
'UGCUGAAGUUUAUUCACUUUCAAACCACUUU' (SEQ ID NO:407)	[[], [], ['UUUA']]	0.322581	0.903226	1	15

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UGAAGUUUAUUCACUUUCAAACCACUUUCAG' (SEQ ID NO:408)	[[], [], ['UUUA']]	0.322581	0.903226	1	18
'GAAGUUUAUUCACUUUCAAACCACUUUCAGU' (SEQ ID NO:409)	[[], [], ['UUUA']]	0.322581	0.903226	1	19
'AGUGUUGACAGGAAGCUGCAGCUUAGAUGGG' (SEQ ID NO:410)	[[], ['GGG'], []]	0.516129	0.870968	1	149
'GUGUUGACAGGAAGCUGCAGCUUAGAUGGGA' (SEQ ID NO:411)	[[], ['GGG'], []]	0.516129	0.870968	1	150
'GUUGACAGGAAGCUGCAGCUUAGAUGGGAUG' (SEQ ID NO:412)	[[], ['GGG'], []]	0.516129	0.870968	1	152
'UGUUGACAGGAAGCUGCAGCUUAGAUGGGAU' (SEQ ID NO:413)	[[], ['GGG'], []]	0.483871	0.870968	1	151
'UUGACAGGAAGCUGCAGCUUAGAUGGGAUGA' (SEQ ID NO:414)	[[], ['GGG'], []]	0.483871	0.870968	1	153
'UGACAGGAAGCUGCAGCUUAGAUGGGAUGAU' (SEQ ID NO:415)	[[], ['GGG'], []]	0.483871	0.870968	1	154

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CUCCAUGGCAACAAGAUGACACAAAUGCAGC' (SEQ ID NO:416)	[[], [], ['AAAU']]	0.483871	0.870968	1	190
'CAACUCCAUGGCAACAAGAUGACACAAAUGC' (SEQ ID NO:417)	[[], [], ['AAAU']]	0.451613	0.870968	1	187
'ACUCCAUGGCAACAAGAUGACACAAAUGCAG' (SEQ ID NO:418)	[[], [], ['AAAU']]	0.451613	0.870968	1	189
'UCCAUGGCAACAAGAUGACACAAAUGCAGCA' (SEQ ID NO:419)	[[], [], ['AAAU']]	0.451613	0.870968	1	191
'CGAGGAAGUCACCAUCAAACCACUUUAUCUA' (SEQ ID NO:420)	[[], [], ['UUUA']]	0.419355	0.870968	1	97
'GAGGAAGUCACCAUCAAACCACUUUAUCUAC' (SEQ ID NO:421)	[[], [], ['UUUA']]	0.419355	0.870968	1	98
'GGAAGUCACCAUCAAACCACUUUAUCUACAG' (SEQ ID NO:422)	[[], [], ['UUUA']]	0.419355	0.870968	1	100
'CACAACUCCAUGGCAACAAGAUGACACAAAU' (SEQ ID NO:423)	[[], [], ['AAAU']]	0.419355	0.870968	1	185

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'ACAACUCCAUGGCAACA AGAUGACACAAAUG' (SEQ ID NO:424)	[[], [], ['AAAU']]	0.419355	0.870968	1	186
'AACUCCAUGGCAACAAG AUGACACAAAUGCA' (SEQ ID NO:425)	[[], [], ['AAAU']]	0.419355	0.870968	1	188
'GUGCUGAAGUUUAUUCA CUUUCAAACCACUU' (SEQ ID NO:426)	[[], [], ['UUUA']]	0.354839	0.870968	1	14
'CCAGGGGACAGGAGCCU CUUGCAGUCUGUCC' (SEQ ID NO:427)	[[], ['GGG'], []]	0.645161	0.83871	1	228
'GGACAGGAGCCUCUUGC AGUCUGUCCCUAGG' (SEQ ID NO:428)	[['CCC'], [], []]	0.612903	0.83871	1	233
'GACAGGAGCCUCUUGCA GUCUGUCCCUAGGC' (SEQ ID NO:429)	[['CCC'], [], []]	0.612903	0.83871	1	234
'ACAGGAGCCUCUUGCAG UCUGUCCCUAGGCC' (SEQ ID NO:430)	[['CCC'], [], []]	0.612903	0.83871	1	235
'GACAGGAAGCUGCAGCU UAGAUGGGAUGAUC' (SEQ ID NO:431)	[[], ['GGG'], []]	0.516129	0.83871	1	155

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GAGGCGAGGAAGUCACCAUCAAACCACUUUA' (SEQ ID NO:432)	[[], [], ['UUUA']]	0.483871	0.83871	1	93
'ACAGGAAGCUGCAGCUUAGAUGGGAUGAUCA' (SEQ ID NO:433)	[[], ['GGG'], []]	0.483871	0.83871	1	156
'AGGAAGCUGCAGCUUAGAUGGGAUGAUCACA' (SEQ ID NO:434)	[[], ['GGG'], []]	0.483871	0.83871	1	158
'GGAAGCUGCAGCUUAGAUGGGAUGAUCACAA' (SEQ ID NO:435)	[[], ['GGG'], []]	0.483871	0.83871	1	159
'GAUGGGAUGAUCACAACUCCAUGGCAACAAG' (SEQ ID NO:436)	[[], ['GGG'], []]	0.483871	0.83871	1	174
'GGGAUGAUCACAACUCCAUGGCAACAAGAUG' (SEQ ID NO:437)	[[], ['GGG'], []]	0.483871	0.83871	1	177
'GCGAGGAAGUCACCAUCAAACCACUUUAUCU' (SEQ ID NO:438)	[[], [], ['UUUA']]	0.451613	0.83871	1	96
'AGAUGGGAUGAUCACAACUCCAUGGCAACAA' (SEQ ID NO:439)	[[], ['GGG'], []]	0.451613	0.83871	1	173

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AUGGGAUGAUCACAACUCCAUGGCAACAAGA' (SEQ ID NO:440)	[[], ['GGG'], []]	0.451613	0.83871	1	175
'GUCUUCUGUCCAUGGUGCUGAAGUUUAUUCA' (SEQ ID NO:441)	[[], [], ['UUUA']]	0.419355	0.83871	1	0
'UCUUCUGUCCAUGGUGCUGAAGUUUAUUCAC' (SEQ ID NO:442)	[[], [], ['UUUA']]	0.419355	0.83871	1	1
'CUUCUGUCCAUGGUGCUGAAGUUUAUUCACU' (SEQ ID NO:443)	[[], [], ['UUUA']]	0.419355	0.83871	1	2
'CUGUCCAUGGUGCUGAAGUUUAUUCACUUUC' (SEQ ID NO:444)	[[], [], ['UUUA']]	0.419355	0.83871	1	5
'UUCUGUCCAUGGUGCUGAAGUUUAUUCACUU' (SEQ ID NO:445)	[[], [], ['UUUA']]	0.387097	0.83871	1	3
'UCUGUCCAUGGUGCUGAAGUUUAUUCACUUU' (SEQ ID NO:446)	[[], [], ['UUUA']]	0.387097	0.83871	1	4
'CCAUGGUGCUGAAGUUUAUUCACUUUCAAAC' (SEQ ID NO:447)	[[], [], ['UUUA']]	0.387097	0.83871	1	9

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CAUGGUGCUGAAGUUUA UUCACUUUCAAACC' (SEQ ID NO:448)	[[], [], ['UUUA']]	0.387097	0.83871	1	10
'UGGUGCUGAAGUUUAUU CACUUUCAAACCAC' (SEQ ID NO:449)	[[], [], ['UUUA']]	0.387097	0.83871	1	12
'GGUGCUGAAGUUUAUUC ACUUUCAAACCACU' (SEQ ID NO:450)	[[], [], ['UUUA']]	0.387097	0.83871	1	13
'UCCAUGGUGCUGAAGUU UAUUCACUUUCAAA' (SEQ ID NO:451)	[[], [], ['UUUA']]	0.354839	0.83871	1	8
'AUGGUGCUGAAGUUUAU UCACUUUCAAACCA' (SEQ ID NO:452)	[[], [], ['UUUA']]	0.354839	0.83871	1	11
'UUUCAGUAACAGGUGAG GUUCUACCUUAAAA' (SEQ ID NO:453)	[[], [], ['UUAA']]	0.354839	0.83871	1	43
'UUCAGUAACAGGUGAGG UUCUACCUUAAAAU' (SEQ ID NO:454)	[[], [], ['UUAA']]	0.354839	0.83871	1	44
'CAGGAAGCUGCAGCUUA GAUGGGAUGAUCAC' (SEQ ID NO:455)	[[], ['GGG'], []]	0.516129	0.806452	1	157

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GGCGAGGAAGUCACCAU CAAACCACUUUAUC' (SEQ ID NO:456)	[[], [], ['UUUA']]	0.483871	0.806452	1	95
'GAAGCUGCAGCUUAGAU GGGAUGAUCACAAC' (SEQ ID NO:457)	[[], ['GGG'], []]	0.483871	0.806452	1	160
'AGGCGAGGAAGUCACCA UCAAACCACUUUAU' (SEQ ID NO:458)	[[], [], ['UUUA']]	0.451613	0.806452	1	94
'AAGCUGCAGCUUAGAUG GGAUGAUCACAACU' (SEQ ID NO:459)	[[], ['GGG'], []]	0.451613	0.806452	1	161
'UAGAUGGGAUGAUCACA ACUCCAUGGCAACA' (SEQ ID NO:460)	[[], ['GGG'], []]	0.451613	0.806452	1	172
'UGGGAUGAUCACAACUC CAUGGCAACAAGAU' (SEQ ID NO:461)	[[], ['GGG'], []]	0.451613	0.806452	1	176
'UGUCCAUGGUGCUGAAG UUUAUUCACUUUCA' (SEQ ID NO:462)	[[], [], ['UUUA']]	0.387097	0.806452	1	6
'GUCCAUGGUGCUGAAGU UUAUUCACUUUCAA' (SEQ ID NO:463)	[[], [], ['UUUA']]	0.387097	0.806452	1	7

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'ACUUUCAGUAACAGGUGAGGUUCUACCUUAA' (SEQ ID NO:464)	[[], [], ['UUAA']]	0.387097	0.806452	1	41
'CUUUCAGUAACAGGUGAGGUUCUACCUUAAA' (SEQ ID NO:465)	[[], [], ['UUAA']]	0.387097	0.806452	1	42
'GCUGCAGCUUAGAUGGGAUGAUCACAACUCC' (SEQ ID NO:466)	[[], ['GGG'], []]	0.516129	0.774194	1	163
'AGCUGCAGCUUAGAUGGGAUGAUCACAACUC' (SEQ ID NO:467)	[[], ['GGG'], []]	0.483871	0.774194	1	162
'CUGCAGCUUAGAUGGGAUGAUCACAACUCCA' (SEQ ID NO:468)	[[], ['GGG'], []]	0.483871	0.774194	1	164
'GCAGCUUAGAUGGGAUGAUCACAACUCCAUG' (SEQ ID NO:469)	[[], ['GGG'], []]	0.483871	0.774194	1	166
'CAGCUUAGAUGGGAUGAUCACAACUCCAUGG' (SEQ ID NO:470)	[[], ['GGG'], []]	0.483871	0.774194	1	167
'AGCUUAGAUGGGAUGAUCACAACUCCAUGGC' (SEQ ID NO:471)	[[], ['GGG'], []]	0.483871	0.774194	1	168

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GCUUAGAUGGGAUGAUCACAACUCCAUGGCA' (SEQ ID NO:472)	[[], ['GGG'], []]	0.483871	0.774194	1	169
'UGCAGCUUAGAUGGGAUGAUCACAACUCCAU' (SEQ ID NO:473)	[[], ['GGG'], []]	0.451613	0.774194	1	165
'CUUAGAUGGGAUGAUCACAACUCCAUGGCAA' (SEQ ID NO:474)	[[], ['GGG'], []]	0.451613	0.774194	1	170
'UUAGAUGGGAUGAUCACAACUCCAUGGCAAC' (SEQ ID NO:475)	[[], ['GGG'], []]	0.451613	0.774194	1	171
'AAUGCAGCAGAGACCCCAGGGGACAGGAGCC' (SEQ ID NO:476)	[['CCC'], ['GGG'], []]	0.645161	0.967742	2	213
'UGCAGCAGAGACCCCAGGGGACAGGAGCCUC' (SEQ ID NO:477)	[['CCC'], ['GGG'], []]	0.677419	0.935484	2	215
'GCAGCAGAGACCCCAGGGGACAGGAGCCUCU' (SEQ ID NO:478)	[['CCC'], ['GGG'], []]	0.677419	0.935484	2	216
'AUGCAGCAGAGACCCCAGGGGACAGGAGCCU' (SEQ ID NO:479)	[['CCC'], ['GGG'], []]	0.645161	0.935484	2	214

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CAAGAUGACACAAAUGCAGCAGAGACCCCAG' (SEQ ID NO:480)	[['CCC'], [], ['AAAU']]	0.516129	0.935484	2	201
'AAGAUGACACAAAUGCAGCAGAGACCCCAGG' (SEQ ID NO:481)	[['CCC'], [], ['AAAU']]	0.516129	0.935484	2	202
'CAACAAGAUGACACAAAUGCAGCAGAGACCC' (SEQ ID NO:482)	[['CCC'], [], ['AAAU']]	0.483871	0.935484	2	198
'AACAAGAUGACACAAAUGCAGCAGAGACCCC' (SEQ ID NO:483)	[['CCC'], [], ['AAAU']]	0.483871	0.935484	2	199
'ACAAGAUGACACAAAUGCAGCAGAGACCCCA' (SEQ ID NO:484)	[['CCC'], [], ['AAAU']]	0.483871	0.935484	2	200
'CAUCAAACCACUUUAUCUACAGUUAGCAUAA' (SEQ ID NO:485)	[[], [], ['UUUA', 'AUAA']]	0.322581	0.935484	2	109
'GCAGAGACCCCAGGGGACAGGAGCCUCUUGC' (SEQ ID NO:486)	[['CCC'], ['GGG'], []]	0.677419	0.903226	2	219
'GCAUGGGGUGGGAGAGGCGAGGAAGUCACCA' (SEQ ID NO:487)	[[], ['GGG', 'GGG'], []]	0.645161	0.903226	2	80

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CAGCAGAGACCCCAGGG GACAGGAGCCUCUU' (SEQ ID NO:488)	[['CCC'], ['GGG'], []]	0.645161	0.903226	2	217
'AGCAGAGACCCCAGGGG ACAGGAGCCUCUUG' (SEQ ID NO:489)	[['CCC'], ['GGG'], []]	0.645161	0.903226	2	218
'CAGAGACCCCAGGGGAC AGGAGCCUCUUGCA' (SEQ ID NO:490)	[['CCC'], ['GGG'], []]	0.645161	0.903226	2	220
'AGAGACCCCAGGGGACA GGAGCCUCUUGCAG' (SEQ ID NO:491)	[['CCC'], ['GGG'], []]	0.645161	0.903226	2	221
'GGGGUGGGAGAGGCGA GGAAGUCACCAUCAA' (SEQ ID NO:492)	[[], ['GGG', 'GGG'], []]	0.612903	0.903226	2	84
'AAUGCAUGGGGUGGGA GAGGCGAGGAAGUCA' (SEQ ID NO:493)	[[], ['GGG', 'GGG'], []]	0.580645	0.903226	2	77
'GGGUGGGAGAGGCGAG GAAGUCACCAUCAAA' (SEQ ID NO:494)	[[], ['GGG', 'GGG'], []]	0.580645	0.903226	2	85
'AUCAAACCACUUUAUCU ACAGUUAGCAUAAG' (SEQ ID NO:495)	[[], [], ['UUUA', 'AUAA']]	0.322581	0.903226	2	110

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UCAAACCACUUUAUCUACAGUUAGCAUAAGA' (SEQ ID NO:496)	[[], [], ['UUUA', 'AUAA']]	0.322581	0.903226	2	111
'CAAACCACUUUAUCUACAGUUAGCAUAAGAU' (SEQ ID NO:497)	[[], [], ['UUUA', 'AUAA']]	0.322581	0.903226	2	112
'UUUAUCUACAGUUAGCAUAAGAUGUGAGAAG' (SEQ ID NO:498)	[[], [], ['UUUA', 'AUAA']]	0.322581	0.903226	2	120
'UUAUCUACAGUUAGCAUAAGAUGUGAGAAGU' (SEQ ID NO:499)	[[], [], ['UUAU', 'AUAA']]	0.322581	0.903226	2	121
'UGCAUGGGGUGGGAGAGGCGAGGAAGUCACC' (SEQ ID NO:500)	[[], ['GGG', 'GGG'], []]	0.645161	0.870968	2	79
'GAGACCCCAGGGGACAGGAGCCUCUUGCAGU' (SEQ ID NO:501)	[['CCC'], ['GGG'], []]	0.645161	0.870968	2	222
'AGACCCCAGGGGACAGGAGCCUCUUGCAGUC' (SEQ ID NO:502)	[['CCC'], ['GGG'], []]	0.645161	0.870968	2	223
'CAGGAGCCUCUUGCAGUCUGUCCCUAGGCCC' (SEQ ID NO:503)	[['CCC', 'CCC'], [], []]	0.645161	0.870968	2	236

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GGAGCCUCUUGCAGUCUGUCCCUAGGCCCAG' (SEQ ID NO:504)	[['CCC', 'CCC'], [], []]	0.645161	0.870968	2	238
'GAGCCUCUUGCAGUCUGUCCCUAGGCCCAGC' (SEQ ID NO:505)	[['CCC', 'CCC'], [], []]	0.645161	0.870968	2	239
'AGCCUCUUGCAGUCUGUCCCUAGGCCCAGCC' (SEQ ID NO:506)	[['CCC', 'CCC'], [], []]	0.645161	0.870968	2	240
'AUGCAUGGGGUGGGAGAGGCGAGGAAGUCAC' (SEQ ID NO:507)	[[], ['GGG', 'GGG'], []]	0.612903	0.870968	2	78
'CAUGGGGUGGGAGAGGCGAGGAAGUCACCAU' (SEQ ID NO:508)	[[], ['GGG', 'GGG'], []]	0.612903	0.870968	2	81
'AUGGGGUGGGAGAGGCGAGGAAGUCACCAUC' (SEQ ID NO:509)	[[], ['GGG', 'GGG'], []]	0.612903	0.870968	2	82
'UGGGGUGGGAGAGGCGAGGAAGUCACCAUCA' (SEQ ID NO:510)	[[], ['GGG', 'GGG'], []]	0.612903	0.870968	2	83
'AGUAACAGGUGAGGUUCUACCUUAAAAUUUA' (SEQ ID NO:511)	[[], [], ['UUAA', 'AAUU']]	0.322581	0.870968	2	47

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GUAACAGGUGAGGUUCUACCUUAAAAUUUAA' (SEQ ID NO:512)	[[], [], ['UUAA', 'AAUU']]	0.322581	0.870968	2	48
'AAACCACUUUAUCUACAGUUAGCAUAAGAUG' (SEQ ID NO:513)	[[], [], ['UUUA', 'AUAA']]	0.322581	0.870968	2	113
'AACCACUUUAUCUACAGUUAGCAUAAGAUGU' (SEQ ID NO:514)	[[], [], ['UUUA', 'AUAA']]	0.322581	0.870968	2	114
'ACUUUAUCUACAGUUAGCAUAAGAUGUGAGA' (SEQ ID NO:515)	[[], [], ['UUUA', 'AUAA']]	0.322581	0.870968	2	118
'CUUUAUCUACAGUUAGCAUAAGAUGUGAGAA' (SEQ ID NO:516)	[[], [], ['UUUA', 'AUAA']]	0.322581	0.870968	2	119
'GACCCCAGGGGACAGGAGCCUCUUGCAGUCU' (SEQ ID NO:517)	[['CCC'], ['GGG'], []]	0.645161	0.83871	2	224
'ACCCCAGGGGACAGGAGCCUCUUGCAGUCUG' (SEQ ID NO:518)	[['CCC'], ['GGG'], []]	0.645161	0.83871	2	225
'CCCCAGGGGACAGGAGCCUCUUGCAGUCUGU' (SEQ ID NO:519)	[['CCC'], ['GGG'], []]	0.645161	0.83871	2	226

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CCCAGGGGACAGGAGCCUCUUGCAGUCUGUC' (SEQ ID NO:520)	[['CCC'], ['GGG'], []]	0.645161	0.83871	2	227
'CAGGGGACAGGAGCCUCUUGCAGUCUGUCCC' (SEQ ID NO:521)	[['CCC'], ['GGG'], []]	0.645161	0.83871	2	229
'AGGGGACAGGAGCCUCUUGCAGUCUGUCCCU' (SEQ ID NO:522)	[['CCC'], ['GGG'], []]	0.612903	0.83871	2	230
'GGGGACAGGAGCCUCUUGCAGUCUGUCCCUA' (SEQ ID NO:523)	[['CCC'], ['GGG'], []]	0.612903	0.83871	2	231
'GGGACAGGAGCCUCUUGCAGUCUGUCCCUAG' (SEQ ID NO:524)	[['CCC'], ['GGG'], []]	0.612903	0.83871	2	232
'AGGAGCCUCUUGCAGUCUGUCCCUAGGCCCA' (SEQ ID NO:525)	[['CCC', 'CCC'], [], []]	0.612903	0.83871	2	237
'UCAGUAACAGGUGAGGUUCUACCUUAAAAUU' (SEQ ID NO:526)	[[], [], ['UUAA', 'AAUU']]	0.354839	0.83871	2	45
'CAGUAACAGGUGAGGUUCUACCUUAAAAUUU' (SEQ ID NO:527)	[[], [], ['UUAA', 'AAUU']]	0.354839	0.83871	2	46

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'ACCACUUUAUCUACAGUUAGCAUAAGAUGUG' (SEQ ID NO:528)	[[], [], ['UUUA', 'AUAA']]	0.354839	0.83871	2	115
'CCACUUUAUCUACAGUUAGCAUAAGAUGUGA' (SEQ ID NO:529)	[[], [], ['UUUA', 'AUAA']]	0.354839	0.83871	2	116
'CACUUUAUCUACAGUUAGCAUAAGAUGUGAG' (SEQ ID NO:530)	[[], [], ['UUUA', 'AUAA']]	0.354839	0.83871	2	117
'GGCCCAGCCCUGCUUGUCCUCCCUGGCUGUU' (SEQ ID NO:531)	[['CCC', 'CCC', 'CCC'], [], []]	0.677419	0.967742	3	262
'CACAAAUGCAGCAGAGACCCCAGGGGACAGG' (SEQ ID NO:532)	[['CCC'], ['GGG'], ['AAAU']]	0.612903	0.967742	3	209
'CAAAUGCAGCAGAGACCCCAGGGGACAGGAG' (SEQ ID NO:533)	[['CCC'], ['GGG'], ['AAAU']]	0.612903	0.967742	3	211
'AAAUGCAGCAGAGACCCCAGGGGACAGGAGC' (SEQ ID NO:534)	[['CCC'], ['GGG'], ['AAAU']]	0.612903	0.967742	3	212
'GACACAAAUGCAGCAGAGACCCCAGGGGACA' (SEQ ID NO:535)	[['CCC'], ['GGG'], ['AAAU']]	0.580645	0.967742	3	207

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'ACACAAAUGCAGCAGAG ACCCCAGGGGACAG' (SEQ ID NO:536)	[['CCC'], ['GGG'], ['AAAU']]	0.580645	0.967742	3	208
'ACAAAUGCAGCAGAGAC CCCAGGGGACAGGA' (SEQ ID NO:537)	[['CCC'], ['GGG'], ['AAAU']]	0.580645	0.967742	3	210
'CCUAGGCCCAGCCCUGC UUGUCCUCCCUGGC' (SEQ ID NO:538)	[['CCC', 'CCC', 'CCC'], [], []]	0.709677	0.935484	3	258
'CUGUCCCUAGGCCCAGC CCUGCUUGUCCUCC' (SEQ ID NO:539)	[['CCC', 'CCC', 'CCC'], [], []]	0.677419	0.935484	3	253
'CUAGGCCCAGCCCUGCU UGUCCUCCCUGGCU' (SEQ ID NO:540)	[['CCC', 'CCC', 'CCC'], [], []]	0.677419	0.935484	3	259
'UAGGCCCAGCCCUGCUU GUCCUCCCUGGCUG' (SEQ ID NO:541)	[['CCC', 'CCC', 'CCC'], [], []]	0.677419	0.935484	3	260
'AGGCCCAGCCCUGCUUG UCCUCCCUGGCUGU' (SEQ ID NO:542)	[['CCC', 'CCC', 'CCC'], [], []]	0.677419	0.935484	3	261

FIG. 41 (Cont'd)

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GUCUGUCCCUAGGCCCAGCCCUGCUUGUCCU' (SEQ ID NO:543)	[['CCC', 'CCC', 'CCC'], [], []]	0.645161	0.935484	3	251
'UCUGUCCCUAGGCCCAGCCCUGCUUGUCCUC' (SEQ ID NO:544)	[['CCC', 'CCC', 'CCC'], [], []]	0.645161	0.935484	3	252
'GCCCAGCCCUGCUUGUCCUCCCUGGCUGUUA' (SEQ ID NO:545)	[['CCC', 'CCC', 'CCC'], [], []]	0.645161	0.935484	3	263
'CCAGCCCUGCUUGUCCUCCCUGGCUGUUAUC' (SEQ ID NO:546)	[['CCC', 'CCC'], [], ['UUAU']]	0.612903	0.935484	3	265
'GAUGACACAAAUGCAGCAGAGACCCCAGGGG' (SEQ ID NO:547)	[['CCC'], ['GGG'], ['AAAU']]	0.580645	0.935484	3	204
'UGACACAAAUGCAGCAGAGACCCCAGGGGAC' (SEQ ID NO:548)	[['CCC'], ['GGG'], ['AAAU']]	0.580645	0.935484	3	206
'CAGCCCUGCUUGUCCUCCCUGGCUGUUAUCU' (SEQ ID NO:549)	[['CCC', 'CCC'], [], ['UUAU']]	0.580645	0.935484	3	266
'UUUAAUGCAUGGGGUGGGAGAGGCGAGGAAG' (SEQ ID NO:550)	[[], ['GGG', 'GGG'], ['UUUA']]	0.548387	0.935484	3	74

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UUAAUGCAUGGGGUGG GAGAGGCGAGGAAGU' (SEQ ID NO:551)	[[], ['GGG', 'GGG'], ['UUAA']]	0.548387	0.935484	3	75
'AGAUGACACAAAUGCAG CAGAGACCCCAGGG' (SEQ ID NO:552)	[['CCC'], ['GGG'], ['AAAU']]	0.548387	0.935484	3	203
'AUGACACAAAUGCAGCA GAGACCCCAGGGGA' (SEQ ID NO:553)	[['CCC'], ['GGG'], ['AAAU']]	0.548387	0.935484	3	205
'AUUUAAUGCAUGGGGUG GGAGAGGCGAGGAA' (SEQ ID NO:554)	[[], ['GGG', 'GGG'], ['AUUU']]	0.516129	0.935484	3	73
'GCCUCUUGCAGUCUGUC CCUAGGCCCAGCCC' (SEQ ID NO:555)	[['CCC', 'CCC', 'CCC'], [], []]	0.677419	0.903226	3	241
'CCUCUUGCAGUCUGUCC CUAGGCCCAGCCCU' (SEQ ID NO:556)	[['CCC', 'CCC', 'CCC'], [], []]	0.645161	0.903226	3	242
'CUCUUGCAGUCUGUCCC UAGGCCCAGCCCUG' (SEQ ID NO:557)	[['CCC', 'CCC', 'CCC'], [], []]	0.645161	0.903226	3	243

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UCUUGCAGUCUGUCCCUAGGCCCAGCCCUGC' (SEQ ID NO:558)	[['CCC', 'CCC', 'CCC'], [], []]	0.645161	0.903226	3	244
'CUUGCAGUCUGUCCCUAGGCCCAGCCCUGCU' (SEQ ID NO:559)	[['CCC', 'CCC', 'CCC'], [], []]	0.645161	0.903226	3	245
'UGCAGUCUGUCCCUAGGCCCAGCCCUGCUUG' (SEQ ID NO:560)	[['CCC', 'CCC', 'CCC'], [], []]	0.645161	0.903226	3	247
'GCAGUCUGUCCCUAGGCCCAGCCCUGCUUGU' (SEQ ID NO:561)	[['CCC', 'CCC', 'CCC'], [], []]	0.645161	0.903226	3	248
'CAGUCUGUCCCUAGGCCCAGCCCUGCUUGUC' (SEQ ID NO:562)	[['CCC', 'CCC', 'CCC'], [], []]	0.645161	0.903226	3	249
'AGUCUGUCCCUAGGCCCAGCCCUGCUUGUCC' (SEQ ID NO:563)	[['CCC', 'CCC', 'CCC'], [], []]	0.645161	0.903226	3	250

FIG. 41 (Cont'd)

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UUGCAGUCUGUCCCUAGGCCCAGCCCUGCUU' (SEQ ID NO:564)	[['CCC', 'CCC', 'CCC'], [], []]	0.612903	0.903226	3	246
'UAAUGCAUGGGGUGGGAGAGGCGAGGAAGUC' (SEQ ID NO:565)	[[], ['GGG', 'GGG'], ['UAAU']]	0.580645	0.903226	3	76
'GGUGAGGUUCUACCUUAAAAUUUAAUGCAUG' (SEQ ID NO:566)	[[], [], ['UUAA', 'AAUU', 'UAAU']]	0.354839	0.870968	3	54
'GUGAGGUUCUACCUUAAAAUUUAAUGCAUGG' (SEQ ID NO:567)	[[], [], ['UUAA', 'AAUU', 'UAAU']]	0.354839	0.870968	3	55
'AACAGGUGAGGUUCUACCUUAAAAUUUAAUG' (SEQ ID NO:568)	[[], [], ['UUAA', 'AAUU', 'UAAU']]	0.322581	0.870968	3	50
'AGGUGAGGUUCUACCUUAAAAUUUAAUGCAU' (SEQ ID NO:569)	[[], [], ['UUAA', 'AAUU', 'UAAU']]	0.322581	0.870968	3	53
'UAACAGGUGAGGUUCUACCUUAAAAUUUAAU' (SEQ ID NO:570)	[[], [], ['UUAA', 'AAUU', 'UAAU']]	0.290323	0.870968	3	49

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'ACAGGUGAGGUUCUACCUUAAAAUUUAAUGC' (SEQ ID NO:571)	[[], [], ['UUAA', 'AAUU', 'UAAU']]	0.354839	0.83871	3	51
'CAGGUGAGGUUCUACCUUAAAAUUUAAUGCA' (SEQ ID NO:572)	[[], [], ['UUAA', 'AAUU', 'UAAU']]	0.354839	0.83871	3	52
'CCCUAGGCCCAGCCCUGCUUGUCCUCCCUGG' (SEQ ID NO:573)	[['CCC', 'CCC', 'CCC', 'CCC'], [], []]	0.709677	0.935484	4	257
'UGUCCCUAGGCCCAGCCCUGCUUGUCCUCCC' (SEQ ID NO:574)	[['CCC', 'CCC', 'CCC', 'CCC'], [], []]	0.677419	0.935484	4	254
'GUCCCUAGGCCCAGCCCUGCUUGUCCUCCCU' (SEQ ID NO:575)	[['CCC', 'CCC', 'CCC', 'CCC'], [], []]	0.677419	0.935484	4	255
'UCCCUAGGCCCAGCCCUGCUUGUCCUCCCUG' (SEQ ID NO:576)	[['CCC', 'CCC', 'CCC', 'CCC'], [], []]	0.677419	0.935484	4	256

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CCCAGCCCUGCUUGUCCUCCCUGGCUGUUAU' (SEQ ID NO:577)	[['CCC', 'CCC', 'CCC'], [], ['UUAU']]	0.612903	0.935484	4	264
'AAAUUUAAUGCAUGGGGUGGGAGAGGCGAGG' (SEQ ID NO:578)	[[], ['GGG', 'GGG'], ['AAAU', 'UUAA']]	0.516129	0.935484	4	71
'AAUUUAAUGCAUGGGGUGGGAGAGGCGAGGA' (SEQ ID NO:579)	[[], ['GGG', 'GGG'], ['AAUU', 'UAAU']]	0.516129	0.935484	4	72
'AAAAUUUAAUGCAUGGGGUGGGAGAGGCGAG' (SEQ ID NO:580)	[[], ['GGG', 'GGG'], ['AAAA', 'UUUA']]	0.483871	0.935484	4	70
'UAAAAUUUAAUGCAUGGGGUGGGAGAGGCGA' (SEQ ID NO:581)	[[], ['GGG', 'GGG'], ['UAAA', 'AUUU']]	0.451613	0.935484	4	69
'GAGGUUCUACCUUAAAAUUUAAUGCAUGGGG' (SEQ ID NO:582)	[[], ['GGG'], ['UUAA', 'AAUU', 'UAAU']]	0.387097	0.870968	4	57

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GGUUCUACCUUAAAAUU UAAUGCAUGGGGUG' (SEQ ID NO:583)	[[], ['GGG'], ['UUAA', 'AAUU', 'UAAU']]	0.387097	0.870968	4	59
'GUUCUACCUUAAAAUUU AAUGCAUGGGGUGG' (SEQ ID NO:584)	[[], ['GGG'], ['UUAA', 'AAUU', 'UAAU']]	0.387097	0.870968	4	60
'UGAGGUUCUACCUUAAA AUUUAAUGCAUGGG' (SEQ ID NO:585)	[[], ['GGG'], ['UUAA', 'AAUU', 'UAAU']]	0.354839	0.870968	4	56
'AGGUUCUACCUUAAAAU UUAAUGCAUGGGGU' (SEQ ID NO:586)	[[], ['GGG'], ['UUAA', 'AAUU', 'UAAU']]	0.354839	0.870968	4	58
'UUAAAAUUUAAUGCAUG GGGUGGGAGAGGCG' (SEQ ID NO:587)	[[], ['GGG', 'GGG'], ['UUAA', 'AAUU', 'UAAU']]	0.451613	0.935484	5	68

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CCUUAAAAUUUAAUGCAUGGGGUGGGAGAGG' (SEQ ID NO:588)	[[], ['GGG', 'GGG'], ['UUAA', 'AAUU', 'UAAU']]	0.451613	0.903226	5	66
'CUUAAAAUUUAAUGCAUGGGGUGGGAGAGGC' (SEQ ID NO:589)	[[], ['GGG', 'GGG'], ['UUAA', 'AAUU', 'UAAU']]	0.451613	0.903226	5	67
'ACCUUAAAAUUUAAUGCAUGGGGUGGGAGAG' (SEQ ID NO:590)	[[], ['GGG', 'GGG'], ['UUAA', 'AAUU', 'UAAU']]	0.419355	0.903226	5	65
'UACCUUAAAAUUUAAUGCAUGGGGUGGGAGA' (SEQ ID NO:591)	[[], ['GGG', 'GGG'], ['UUAA', 'AAUU', 'UAAU']]	0.387097	0.903226	5	64
'CUACCUUAAAAUUUAAUGCAUGGGGUGGGAG' (SEQ ID NO:592)	[[], ['GGG', 'GGG'], ['UUAA', 'AAUU', 'UAAU']]	0.419355	0.870968	5	63

FIG. 41 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UUCUACCUUAAAAUUUA AUGCAUGGGGUGGG' (SEQ ID NO:593)	[[], ['GGG', 'GGG'], ['UUAA', 'AAUU', 'UAAU']]	0.387097	0.870968	5	61
'UCUACCUUAAAAUUUAA UGCAUGGGGUGGGA' (SEQ ID NO:594)	[[], ['GGG', 'GGG'], ['UUAA', 'AAUU', 'UAAU']]	0.387097	0.870968	5	62

FIG. 41 (Cont'd)

FIG. 42

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GGCCUCAGCGUCUGUCCGUGGUGCUGAAGUU' (SEQ ID NO:595)	[[], [], []]	0.612903	0.903226	0	2
'GCCUCAGCGUCUGUCCGUGGUGCUGAAGUUU' (SEQ ID NO:596)	[[], [], []]	0.580645	0.903226	0	3
'GAUGAAGACAGGAAGCUGCAGCUCCAGGAGG' (SEQ ID NO:597)	[[], [], []]	0.580645	0.903226	0	154
'AGAUGAAGACAGGAAGCUGCAGCUCCAGGAG' (SEQ ID NO:598)	[[], [], []]	0.548387	0.903226	0	153
'CAGGCCUCAGCGUCUGUCCGUGGUGCUGAAG' (SEQ ID NO:599)	[[], [], []]	0.645161	0.870968	0	0
'AGGCCUCAGCGUCUGUCCGUGGUGCUGAAGU' (SEQ ID NO:600)	[[], [], []]	0.612903	0.870968	0	1
'GGCAAUGCGACCAAGCUGUGUGACACACCGC' (SEQ ID NO:601)	[[], [], []]	0.612903	0.870968	0	204
'GCAAUGCGACCAAGCUGUGUGACACACCGCA' (SEQ ID NO:602)	[[], [], []]	0.580645	0.870968	0	205

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AUGCGACCAAGCUGUG UGACACACCGCAAGG' (SEQ ID NO:603)	[[], [], []]	0.580645	0.870968	0	208
'CAAUGCGACCAAGCUG UGUGACACACCGCAA' (SEQ ID NO:604)	[[], [], []]	0.548387	0.870968	0	206
'AAUGCGACCAAGCUGU GUGACACACCGCAAG' (SEQ ID NO:605)	[[], [], []]	0.548387	0.870968	0	207
'GAUAGAUGAAGACAGG AAGCUGCAGCUCCAG' (SEQ ID NO:606)	[[], [], []]	0.516129	0.870968	0	150
'AUAGAUGAAGACAGGAA GCUGCAGCUCCAGG' (SEQ ID NO:607)	[[], [], []]	0.516129	0.870968	0	151
'UAGAUGAAGACAGGAA GCUGCAGCUCCAGGA' (SEQ ID NO:608)	[[], [], []]	0.516129	0.870968	0	152
'GAUCGUGAUAGAUGAA GACAGGAAGCUGCAG' (SEQ ID NO:609)	[[], [], []]	0.483871	0.870968	0	144
'AUCGAUCGUGAUAGAU GAAGACAGGAAGCUG' (SEQ ID NO:610)	[[], [], []]	0.451613	0.870968	0	141

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AACAUCGAUCGUGAUA GAUGAAGACAGGAAG' (SEQ ID NO:611)	[[], [], []]	0.419355	0.870968	0	138
'UAACAUCGAUCGUGAU AGAUGAAGACAGGAA' (SEQ ID NO:612)	[[], [], []]	0.387097	0.870968	0	137
'UCACCACCUCUCAGUG GCAAUGCGACCAAGC' (SEQ ID NO:613)	[[], [], []]	0.580645	0.83871	0	189
'CACCACCUCUCAGUGG CAAUGCGACCAAGCU' (SEQ ID NO:614)	[[], [], []]	0.580645	0.83871	0	190
'ACCACCUCUCAGUGGC AAUGCGACCAAGCUG' (SEQ ID NO:615)	[[], [], []]	0.580645	0.83871	0	191
'GUGGCAAUGCGACCAA GCUGUGUGACACACC' (SEQ ID NO:616)	[[], [], []]	0.580645	0.83871	0	202
'UGGCAAUGCGACCAAG CUGUGUGACACACCG' (SEQ ID NO:617)	[[], [], []]	0.580645	0.83871	0	203
'CAGUGGCAAUGCGACC AAGCUGUGUGACACA' (SEQ ID NO:618)	[[], [], []]	0.548387	0.83871	0	200

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AGUGGCAAUGCGACCA AGCUGUGUGACACAC' (SEQ ID NO:619)	[[], [], []]	0.548387	0.83871	0	201
'CGUGAUAGAUGAAGAC AGGAAGCUGCAGCUC' (SEQ ID NO:620)	[[], [], []]	0.516129	0.83871	0	147
'GUGAUAGAUGAAGACA GGAAGCUGCAGCUCC' (SEQ ID NO:621)	[[], [], []]	0.516129	0.83871	0	148
'AUUCACCACCUCUCAG UGGCAAUGCGACCAA' (SEQ ID NO:622)	[[], [], []]	0.516129	0.83871	0	187
'UCGAUCGUGAUAGAUG AAGACAGGAAGCUGC' (SEQ ID NO:623)	[[], [], []]	0.483871	0.83871	0	142
'CGAUCGUGAUAGAUGA AGACAGGAAGCUGCA' (SEQ ID NO:624)	[[], [], []]	0.483871	0.83871	0	143
'AUCGUGAUAGAUGAAG ACAGGAAGCUGCAGC' (SEQ ID NO:625)	[[], [], []]	0.483871	0.83871	0	145
'UCGUGAUAGAUGAAGA CAGGAAGCUGCAGCU' (SEQ ID NO:626)	[[], [], []]	0.483871	0.83871	0	146

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UGAUAGAUGAAGACAG GAAGCUGCAGCUCCA' (SEQ ID NO:627)	[[], [], []]	0.483871	0.83871	0	149
'ACAUCGAUCGUGAUAG AUGAAGACAGGAAGC' (SEQ ID NO:628)	[[], [], []]	0.451613	0.83871	0	139
'CAUCGAUCGUGAUAGA UGAAGACAGGAAGCU' (SEQ ID NO:629)	[[], [], []]	0.451613	0.83871	0	140
'CCACCUCUCAGUGGCA AUGCGACCAAGCUGU' (SEQ ID NO:630)	[[], [], []]	0.580645	0.806452	0	192
'CACCUCUCAGUGGCAA UGCGACCAAGCUGUG' (SEQ ID NO:631)	[[], [], []]	0.580645	0.806452	0	193
'CCUCUCAGUGGCAAUG CGACCAAGCUGUGUG' (SEQ ID NO:632)	[[], [], []]	0.580645	0.806452	0	195
'UUCACCACCUCUCAGU GGCAAUGCGACCAAG' (SEQ ID NO:633)	[[], [], []]	0.548387	0.806452	0	188
'CUCAGUGGCAAUGCGA CCAAGCUGUGUGACA' (SEQ ID NO:634)	[[], [], []]	0.548387	0.806452	0	198

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UCAGUGGCAAUGCGACCAAGCUGUGUGACAC' (SEQ ID NO:635)	[[], [], []]	0.548387	0.806452	0	199
'ACCUCUCAGUGGCAAUGCGACCAAGCUGUGU' (SEQ ID NO:636)	[[], [], []]	0.548387	0.774194	0	194
'CUCUCAGUGGCAAUGCGACCAAGCUGUGUGA' (SEQ ID NO:637)	[[], [], []]	0.548387	0.774194	0	196
'UCUCAGUGGCAAUGCGACCAAGCUGUGUGAC' (SEQ ID NO:638)	[[], [], []]	0.548387	0.774194	0	197
'UAAGGCCUCACUAAACCACUCAUCUACACUU' (SEQ ID NO:639)	[[], [], ['UAAA']]	0.419355	0.935484	1	107
'AAGGCCUCACUAAACCACUCAUCUACACUUA' (SEQ ID NO:640)	[[], [], ['UAAA']]	0.419355	0.935484	1	108
'AAACCACUCAUCUACACUUAACAUCGAUCGU' (SEQ ID NO:641)	[[], [], ['UUAA']]	0.387097	0.935484	1	119
'GCGACCAAGCUGUGUGACACACCGCAAGGGC' (SEQ ID NO:642)	[[], ['GGG'], []]	0.645161	0.903226	1	210

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AUGAAGACAGGAAGCUGCAGCUCCAGGAGGG' (SEQ ID NO:643)	[[], ['GGG'], []]	0.580645	0.903226	1	155
'GAAGACAGGAAGCUGCAGCUCCAGGAGGGUA' (SEQ ID NO:644)	[[], ['GGG'], []]	0.580645	0.903226	1	157
'GCGUCUGUCCGUGGUGCUGAAGUUUAUUCGG' (SEQ ID NO:645)	[[], [], ['UUUA']]	0.548387	0.903226	1	9
'GUAAGGCCUCACUAAACCACUCAUCUACACU' (SEQ ID NO:646)	[[], [], ['UAAA']]	0.451613	0.903226	1	106
'AACCACUCAUCUACACUUAACAUCGAUCGUG' (SEQ ID NO:647)	[[], [], ['UUAA']]	0.419355	0.903226	1	120
'ACCACUCAUCUACACUUAACAUCGAUCGUGA' (SEQ ID NO:648)	[[], [], ['UUAA']]	0.419355	0.903226	1	121
'CCACUCAUCUACACUUAACAUCGAUCGUGAU' (SEQ ID NO:649)	[[], [], ['UUAA']]	0.419355	0.903226	1	122
'CACUCAUCUACACUUAACAUCGAUCGUGAUA' (SEQ ID NO:650)	[[], [], ['UUAA']]	0.387097	0.903226	1	123

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UGCGACCAAGCUGUGUGACACACCGCAAGGG' (SEQ ID NO:651)	[[], ['GGG'], []]	0.612903	0.870968	1	209
'CGACCAAGCUGUGUGACACACCGCAAGGGCU' (SEQ ID NO:652)	[[], ['GGG'], []]	0.612903	0.870968	1	211
'UGAAGACAGGAAGCUGCAGCUCCAGGAGGGU' (SEQ ID NO:653)	[[], ['GGG'], []]	0.580645	0.870968	1	156
'CCUCAGCGUCUGUCCGUGGUGCUGAAGUUUA' (SEQ ID NO:654)	[[], [], ['UUUA']]	0.548387	0.870968	1	4
'AAGACAGGAAGCUGCAGCUCCAGGAGGGUAU' (SEQ ID NO:655)	[[], ['GGG'], []]	0.548387	0.870968	1	158
'CUCAGCGUCUGUCCGUGGUGCUGAAGUUUAU' (SEQ ID NO:656)	[[], [], ['UUUA']]	0.516129	0.870968	1	5
'CAGCGUCUGUCCGUGGUGCUGAAGUUUAUUC' (SEQ ID NO:657)	[[], [], ['UUUA']]	0.516129	0.870968	1	7
'AGCGUCUGUCCGUGGUGCUGAAGUUUAUUCG' (SEQ ID NO:658)	[[], [], ['UUUA']]	0.516129	0.870968	1	8

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CGUCUGUCCGUGGUGCUGAAGUUUAUUCGGA' (SEQ ID NO:659)	[[], [], ['UUUA']]	0.516129	0.870968	1	10
'UCAGCGUCUGUCCGUGGUGCUGAAGUUUAUU' (SEQ ID NO:660)	[[], [], ['UUUA']]	0.483871	0.870968	1	6
'GUCUGUCCGUGGUGCUGAAGUUUAUUCGGAU' (SEQ ID NO:661)	[[], [], ['UUUA']]	0.483871	0.870968	1	11
'GGUAAGGCCUCACUAAACCACUCAUCUACAC' (SEQ ID NO:662)	[[], [], ['UAAA']]	0.483871	0.870968	1	105
'UCUGUCCGUGGUGCUGAAGUUUAUUCGGAUU' (SEQ ID NO:663)	[[], [], ['UUUA']]	0.451613	0.870968	1	12
'AGGUAAGGCCUCACUAAACCACUCAUCUACA' (SEQ ID NO:664)	[[], [], ['UAAA']]	0.451613	0.870968	1	104
'ACUCAUCUACACUUAACAUCGAUCGUGAUAG' (SEQ ID NO:665)	[[], [], ['UUAA']]	0.387097	0.870968	1	124
'CUCAUCUACACUUAACAUCGAUCGUGAUAGA' (SEQ ID NO:666)	[[], [], ['UUAA']]	0.387097	0.870968	1	125

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UUAACAUCGAUCGUGA UAGAUGAAGACAGGA' (SEQ ID NO:667)	[[], [], ['UUAA']]	0.387097	0.870968	1	136
'UCAUCUACACUUAACAU CGAUCGUGAUAGAU' (SEQ ID NO:668)	[[], [], ['UUAA']]	0.354839	0.870968	1	126
'CCAAGCUGUGUGACAC ACCGCAAGGGCUUGG' (SEQ ID NO:669)	[[], ['GGG'], []]	0.612903	0.83871	1	214
'GACCAAGCUGUGUGAC ACACCGCAAGGGCUU' (SEQ ID NO:670)	[[], ['GGG'], []]	0.580645	0.83871	1	212
'ACCAAGCUGUGUGACA CACCGCAAGGGCUUG' (SEQ ID NO:671)	[[], ['GGG'], []]	0.580645	0.83871	1	213
'UAUGCAGAGUGGGAGA GGUAAGGCCUCACUA' (SEQ ID NO:672)	[[], ['GGG'], []]	0.516129	0.83871	1	89
'AUGCAGAGUGGGAGAG GUAAGGCCUCACUAA' (SEQ ID NO:673)	[[], ['GGG'], []]	0.516129	0.83871	1	90
'GGAGAGGUAAGGCCUC ACUAAACCACUCAUC' (SEQ ID NO:674)	[[], [], ['UAAA']]	0.516129	0.83871	1	100

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UAUUCACCACCUCUCA GUGGCAAUGCGACCA' (SEQ ID NO:675)	[[], [], ['UAUU']]	0.516129	0.83871	1	186
'GAGGUAAGGCCUCACU AAACCACUCAUCUAC' (SEQ ID NO:676)	[[], [], ['UAAA']]	0.483871	0.83871	1	103
'UUUCCAACUGCUUUCU GAAAGGGGUGAGGAU' (SEQ ID NO:677)	[[], ['GGG'], []]	0.451613	0.83871	1	49
'UGCUUUCUGAAAGGGG UGAGGAUCUACCUUA' (SEQ ID NO:678)	[[], ['GGG'], []]	0.451613	0.83871	1	57
'AGAGGUAAGGCCUCAC UAAACCACUCAUCUA' (SEQ ID NO:679)	[[], [], ['UAAA']]	0.451613	0.83871	1	102
'CUUAACAUCGAUCGUG AUAGAUGAAGACAGG' (SEQ ID NO:680)	[[], [], ['UUAA']]	0.419355	0.83871	1	135
'CAUCUACACUUAACAUC GAUCGUGAUAGAUG' (SEQ ID NO:681)	[[], [], ['UUAA']]	0.387097	0.83871	1	127
'ACUUAACAUCGAUCGU GAUAGAUGAAGACAG' (SEQ ID NO:682)	[[], [], ['UUAA']]	0.387097	0.83871	1	134

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AUCUACACUUAACAUCG AUCGUGAUAGAUGA' (SEQ ID NO:683)	[[], [], ['UUAA']]	0.354839	0.83871	1	128
'UCUACACUUAACAUCGA UCGUGAUAGAUGAA' (SEQ ID NO:684)	[[], [], ['UUAA']]	0.354839	0.83871	1	129
'UACACUUAACAUCGAUC GUGAUAGAUGAAGA' (SEQ ID NO:685)	[[], [], ['UUAA']]	0.354839	0.83871	1	131
'GUAUUCACCACCUCUC AGUGGCAAUGCGACC' (SEQ ID NO:686)	[[], [], ['UAUU']]	0.548387	0.806452	1	185
'UUCCAACUGCUUUCUG AAAGGGGUGAGGAUC' (SEQ ID NO:687)	[[], ['GGG'], []]	0.483871	0.806452	1	50
'UCCAACUGCUUUCUGA AAGGGGUGAGGAUCU' (SEQ ID NO:688)	[[], ['GGG'], []]	0.483871	0.806452	1	51
'CCAACUGCUUUCUGAA AGGGGUGAGGAUCUA' (SEQ ID NO:689)	[[], ['GGG'], []]	0.483871	0.806452	1	52
'CAACUGCUUUCUGAAA GGGGUGAGGAUCUAC' (SEQ ID NO:690)	[[], ['GGG'], []]	0.483871	0.806452	1	53

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AACUGCUUUCUGAAAG GGGUGAGGAUCUACC' (SEQ ID NO:691)	[[], ['GGG'], []]	0.483871	0.806452	1	54
'ACUGCUUUCUGAAAGG GGUGAGGAUCUACCU' (SEQ ID NO:692)	[[], ['GGG'], []]	0.483871	0.806452	1	55
'CUGCUUUCUGAAAGGG GUGAGGAUCUACCUU' (SEQ ID NO:693)	[[], ['GGG'], []]	0.483871	0.806452	1	56
'GAGAGGUAAGGCCUCA CUAAACCACUCAUCU' (SEQ ID NO:694)	[[], [], ['UAAA']]	0.483871	0.806452	1	101
'CUACACUUAACAUCGAU CGUGAUAGAUGAAG' (SEQ ID NO:695)	[[], [], ['UUAA']]	0.387097	0.806452	1	130
'ACACUUAACAUCGAUCG UGAUAGAUGAAGAC' (SEQ ID NO:696)	[[], [], ['UUAA']]	0.387097	0.806452	1	132
'CACUUAACAUCGAUCG UGAUAGAUGAAGACA' (SEQ ID NO:697)	[[], [], ['UUAA']]	0.387097	0.806452	1	133
'GGUAUUCACCACCUCU CAGUGGCAAUGCGAC' (SEQ ID NO:698)	[[], [], ['UAUU']]	0.548387	0.774194	1	184

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CCUCACUAAACCACUCA UCUACACUUAACAU' (SEQ ID NO:699)	[[], [], ['UAAA', 'UUAA']]	0.387097	1	2	112
'CUCACUAAACCACUCAU CUACACUUAACAUC' (SEQ ID NO:700)	[[], [], ['UAAA', 'UUAA']]	0.387097	1	2	113
'GCCUCACUAAACCACUC AUCUACACUUAACA' (SEQ ID NO:701)	[[], [], ['UAAA', 'UUAA']]	0.419355	0.967742	2	111
'UCACUAAACCACUCAUC UACACUUAACAUCG' (SEQ ID NO:702)	[[], [], ['UAAA', 'UUAA']]	0.387097	0.967742	2	114
'CACUAAACCACUCAUCU ACACUUAACAUCGA' (SEQ ID NO:703)	[[], [], ['UAAA', 'UUAA']]	0.387097	0.967742	2	115
'CUAAACCACUCAUCUAC ACUUAACAUCGAUC' (SEQ ID NO:704)	[[], [], ['UAAA', 'UUAA']]	0.387097	0.967742	2	117
'ACUAAACCACUCAUCUA CACUUAACAUCGAU' (SEQ ID NO:705)	[[], [], ['UAAA', 'UUAA']]	0.354839	0.967742	2	116
'GGCCUCACUAAACCAC UCAUCUACACUUAAC' (SEQ ID NO:706)	[[], [], ['UAAA', 'UUAA']]	0.451613	0.935484	2	110

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AGGCCUCACUAAACCAC UCAUCUACACUUAA' (SEQ ID NO:707)	[[], [], ['UAAA', 'UUAA']]	0.419355	0.935484	2	109
'UAAACCACUCAUCUACA CUUAACAUCGAUCG' (SEQ ID NO:708)	[[], [], ['UAAA', 'UUAA']]	0.387097	0.935484	2	118
'UACCUUAAUAUGCAGA GUGGGAGAGGUAAGG' (SEQ ID NO:709)	[[], ['GGG'], ['UUAA']]	0.451613	0.903226	2	81
'GCAGAGUGGGAGAGGU AAGGCCUCACUAAAC' (SEQ ID NO:710)	[[], ['GGG'], ['UAAA']]	0.548387	0.870968	2	92
'CAGAGUGGGAGAGGUA AGGCCUCACUAAACC' (SEQ ID NO:711)	[[], ['GGG'], ['UAAA']]	0.548387	0.870968	2	93
'GAGUGGGAGAGGUAAG GCCUCACUAAACCAC' (SEQ ID NO:712)	[[], ['GGG'], ['UAAA']]	0.548387	0.870968	2	95
'GGCUUGGGAUCUUUUG CGAUCUGCUCGAGCA' (SEQ ID NO:713)	[[], ['GGG'], ['UUUU']]	0.548387	0.870968	2	238
'GCUUGGGAUCUUUUGC GAUCUGCUCGAGCAG' (SEQ ID NO:714)	[[], ['GGG'], ['UUUU']]	0.548387	0.870968	2	239

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AGAGUGGGAGAGGUAAGGCCUCACUAAACCA' (SEQ ID NO:715)	[[], ['GGG'], ['UAAA']]	0.516129	0.870968	2	94
'CUUUUGCGAUCUGCUCGAGCAGAUUUGGCUG' (SEQ ID NO:716)	[[], [], ['UUUU', 'AUUU']]	0.516129	0.870968	2	248
'GGGGUGAGGAUCUACCUUAAUAUGCAGAGUG' (SEQ ID NO:717)	[[], ['GGG'], ['UUAA']]	0.483871	0.870968	2	69
'GGGUGAGGAUCUACCUUAAUAUGCAGAGUGG' (SEQ ID NO:718)	[[], ['GGG'], ['UUAA']]	0.483871	0.870968	2	70
'GGUGAGGAUCUACCUUAAUAUGCAGAGUGGG' (SEQ ID NO:719)	[[], ['GGG'], ['UUAA']]	0.483871	0.870968	2	71
'GGAUCUACCUUAAUAUGCAGAGUGGGAGAGG' (SEQ ID NO:720)	[[], ['GGG'], ['UUAA']]	0.483871	0.870968	2	76
'ACCUUAAUAUGCAGAGUGGGAGAGGUAAGGC' (SEQ ID NO:721)	[[], ['GGG'], ['UUAA']]	0.483871	0.870968	2	82
'CUUAAUAUGCAGAGUGGGAGAGGUAAGGCCU' (SEQ ID NO:722)	[[], ['GGG'], ['UUAA']]	0.483871	0.870968	2	84

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UUAAUAUGCAGAGUGG GAGAGGUAAGGCCUC' (SEQ ID NO:723)	[[], ['GGG'], ['UUAA']]	0.483871	0.870968	2	85
'UAAUAUGCAGAGUGGG AGAGGUAAGGCCUCA' (SEQ ID NO:724)	[[], ['GGG'], ['UAAU']]	0.483871	0.870968	2	86
'UCUUUUGCGAUCUGCU CGAGCAGAUUUGGCU' (SEQ ID NO:725)	[[], [], ['UUUU', 'AUUU']]	0.483871	0.870968	2	247
'CUGUCCGUGGUGCUGA AGUUUAUUCGGAUUU' (SEQ ID NO:726)	[[], [], ['UUUA', 'AUUU']]	0.451613	0.870968	2	13
'GAAAGGGGUGAGGAUC UACCUUAAUAUGCAG' (SEQ ID NO:727)	[[], ['GGG'], ['UUAA']]	0.451613	0.870968	2	65
'AAGGGGUGAGGAUCUA CCUUAAUAUGCAGAG' (SEQ ID NO:728)	[[], ['GGG'], ['UUAA']]	0.451613	0.870968	2	67
'AGGGGUGAGGAUCUAC CUUAAUAUGCAGAGU' (SEQ ID NO:729)	[[], ['GGG'], ['UUAA']]	0.451613	0.870968	2	68
'GUGAGGAUCUACCUUA AUAUGCAGAGUGGGA' (SEQ ID NO:730)	[[], ['GGG'], ['UUAA']]	0.451613	0.870968	2	72

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UGAGGAUCUACCUUAA UAUGCAGAGUGGGAG' (SEQ ID NO:731)	[[], ['GGG'], ['UUAA']]	0.451613	0.870968	2	73
'GAGGAUCUACCUUAAU AUGCAGAGUGGGAGA' (SEQ ID NO:732)	[[], ['GGG'], ['UUAA']]	0.451613	0.870968	2	74
'AGGAUCUACCUUAAUAU GCAGAGUGGGAGAG' (SEQ ID NO:733)	[[], ['GGG'], ['UUAA']]	0.451613	0.870968	2	75
'GAUCUACCUUAAUAUG CAGAGUGGGAGAGGU' (SEQ ID NO:734)	[[], ['GGG'], ['UUAA']]	0.451613	0.870968	2	77
'CUACCUUAAUAUGCAGA GUGGGAGAGGUAAG' (SEQ ID NO:735)	[[], ['GGG'], ['UUAA']]	0.451613	0.870968	2	80
'UGUCCGUGGUGCUGAA GUUUAUUCGGAUUUA' (SEQ ID NO:736)	[[], [], ['UUUA', 'AUUU']]	0.419355	0.870968	2	14
'GUCCGUGGUGCUGAAG UUUAUUCGGAUUUAU' (SEQ ID NO:737)	[[], [], ['UUUA', 'AUUU']]	0.419355	0.870968	2	15
'UCUGAAAGGGGUGAGG AUCUACCUUAAUAUG' (SEQ ID NO:738)	[[], ['GGG'], ['UUAA']]	0.419355	0.870968	2	62

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UGAAAGGGGUGAGGAUCUACCUUAAUAUGCA' (SEQ ID NO:739)	[[], ['GGG'], ['UUAA']]	0.419355	0.870968	2	64
'AAAGGGGUGAGGAUCUACCUUAAUAUGCAGA' (SEQ ID NO:740)	[[], ['GGG'], ['UUAA']]	0.419355	0.870968	2	66
'AUCUACCUUAAUAUGCAGAGUGGGAGAGGUA' (SEQ ID NO:741)	[[], ['GGG'], ['UUAA']]	0.419355	0.870968	2	78
'UCUACCUUAAUAUGCAGAGUGGGAGAGGUAA' (SEQ ID NO:742)	[[], ['GGG'], ['UUAA']]	0.419355	0.870968	2	79
'UCCGUGGUGCUGAAGUUUAUUCGGAUUUAUU' (SEQ ID NO:743)	[[], [], ['UUUA', 'AUUU']]	0.387097	0.870968	2	16
'UUUCUGAAAGGGGUGAGGAUCUACCUUAAUA' (SEQ ID NO:744)	[[], ['GGG'], ['UUAA']]	0.387097	0.870968	2	60
'UUCUGAAAGGGGUGAGGAUCUACCUUAAUAU' (SEQ ID NO:745)	[[], ['GGG'], ['UUAA']]	0.387097	0.870968	2	61
'CAAGCUGUGUGACACACCGCAAGGGCUUGGG' (SEQ ID NO:746)	[[], ['GGG', 'GGG'], []]	0.612903	0.83871	2	215

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GACAGGAAGCUGCAGCUCCAGGAGGGUAUUC' (SEQ ID NO:747)	[[], ['GGG'], ['UAUU']]	0.580645	0.83871	2	160
'CAGGAAGCUGCAGCUCCAGGAGGGUAUUCAC' (SEQ ID NO:748)	[[], ['GGG'], ['UAUU']]	0.580645	0.83871	2	162
'AGGAAGCUGCAGCUCCAGGAGGGUAUUCACC' (SEQ ID NO:749)	[[], ['GGG'], ['UAUU']]	0.580645	0.83871	2	163
'GGAAGCUGCAGCUCCAGGAGGGUAUUCACCA' (SEQ ID NO:750)	[[], ['GGG'], ['UAUU']]	0.580645	0.83871	2	164
'GAAGCUGCAGCUCCAGGAGGGUAUUCACCAC' (SEQ ID NO:751)	[[], ['GGG'], ['UAUU']]	0.580645	0.83871	2	165
'AAGCUGCAGCUCCAGGAGGGUAUUCACCACC' (SEQ ID NO:752)	[[], ['GGG'], ['UAUU']]	0.580645	0.83871	2	166
'AAGCUGUGUGACACACCGCAAGGGCUUGGGA' (SEQ ID NO:753)	[[], ['GGG', 'GGG'], []]	0.580645	0.83871	2	216
'GUGGGAGAGGUAAGGCCUCACUAAACCACUC' (SEQ ID NO:754)	[[], ['GGG'], ['UAAA']]	0.548387	0.83871	2	97

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AGACAGGAAGCUGCAG CUCCAGGAGGGUAUU' (SEQ ID NO:755)	[[], ['GGG'], ['UAUU']]	0.548387	0.83871	2	159
'ACAGGAAGCUGCAGCU CCAGGAGGGUAUUCA' (SEQ ID NO:756)	[[], ['GGG'], ['UAUU']]	0.548387	0.83871	2	161
'CCUUAAUAUGCAGAGU GGGAGAGGUAAGGCC' (SEQ ID NO:757)	[[], ['GGG'], ['UUAA']]	0.516129	0.83871	2	83
'AAUAUGCAGAGUGGGA GAGGUAAGGCCUCAC' (SEQ ID NO:758)	[[], ['GGG'], ['AAUA']]	0.516129	0.83871	2	87
'AUAUGCAGAGUGGGAG AGGUAAGGCCUCACU' (SEQ ID NO:759)	[[], ['GGG'], ['AUAU']]	0.516129	0.83871	2	88
'UGCAGAGUGGGAGAGG UAAGGCCUCACUAAA' (SEQ ID NO:760)	[[], ['GGG'], ['UAAA']]	0.516129	0.83871	2	91
'AGUGGGAGAGGUAAGG CCUCACUAAACCACU' (SEQ ID NO:761)	[[], ['GGG'], ['UAAA']]	0.516129	0.83871	2	96
'UGGGAGAGGUAAGGCC UCACUAAACCACUCA' (SEQ ID NO:762)	[[], ['GGG'], ['UAAA']]	0.516129	0.83871	2	98

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GGGAGAGGUAAGGCCUCACUAAACCACUCAU' (SEQ ID NO:763)	[[], ['GGG'], ['UAAA']]	0.516129	0.83871	2	99
'CUUGGGAUCUUUUGCGAUCUGCUCGAGCAGA' (SEQ ID NO:764)	[[], ['GGG'], ['UUUU']]	0.516129	0.83871	2	240
'UUGGGAUCUUUUGCGAUCUGCUCGAGCAGAU' (SEQ ID NO:765)	[[], ['GGG'], ['UUUU']]	0.483871	0.83871	2	241
'UGGGAUCUUUUGCGAUCUGCUCGAGCAGAUU' (SEQ ID NO:766)	[[], ['GGG'], ['UUUU']]	0.483871	0.83871	2	242
'GGAUCUUUUGCGAUCUGCUCGAGCAGAUUUG' (SEQ ID NO:767)	[[], [], ['UUUU', 'AUUU']]	0.483871	0.83871	2	244
'GAUCUUUUGCGAUCUGCUCGAGCAGAUUUGG' (SEQ ID NO:768)	[[], [], ['UUUU', 'AUUU']]	0.483871	0.83871	2	245
'AUCUUUUGCGAUCUGCUCGAGCAGAUUUGGC' (SEQ ID NO:769)	[[], [], ['UUUU', 'AUUU']]	0.483871	0.83871	2	246
'UUUUUCCAACUGCUUUCUGAAAGGGGUGAGG' (SEQ ID NO:770)	[[], ['GGG'], ['UUUU']]	0.451613	0.83871	2	47

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UUUUCCAACUGCUUUCUGAAAGGGGUGAGGA' (SEQ ID NO:771)	[[], ['GGG'], ['UUUU']]	0.451613	0.83871	2	48
'GCUUUCUGAAAGGGGUGAGGAUCUACCUUAA' (SEQ ID NO:772)	[[], ['GGG'], ['UUAA']]	0.451613	0.83871	2	58
'CUGAAAGGGGUGAGGAUCUACCUUAAUAUGC' (SEQ ID NO:773)	[[], ['GGG'], ['UUAA']]	0.451613	0.83871	2	63
'UUUUUUCCAACUGCUUUCUGAAAGGGGUGAG' (SEQ ID NO:774)	[[], ['GGG'], ['UUUU']]	0.419355	0.83871	2	46
'CUUUCUGAAAGGGGUGAGGAUCUACCUUAAU' (SEQ ID NO:775)	[[], ['GGG'], ['UUAA']]	0.419355	0.83871	2	59
'UUUUUUUCCAACUGCUUUCUGAAAGGGGUGA' (SEQ ID NO:776)	[[], ['GGG'], ['UUUU']]	0.387097	0.83871	2	45
'GCUGCAGCUCCAGGAGGGUAUUCACCACCUC' (SEQ ID NO:777)	[[], ['GGG'], ['UAUU']]	0.612903	0.806452	2	168
'GCUGUGUGACACACCGCAAGGGCUUGGGAUC' (SEQ ID NO:778)	[[], ['GGG', 'GGG'], []]	0.612903	0.806452	2	218

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AGCUGCAGCUCCAGGAGGGUAUUCACCACCU' (SEQ ID NO:779)	[[], ['GGG'], ['UAUU']]	0.580645	0.806452	2	167
'CUGCAGCUCCAGGAGGGUAUUCACCACCUCU' (SEQ ID NO:780)	[[], ['GGG'], ['UAUU']]	0.580645	0.806452	2	169
'UGCAGCUCCAGGAGGGUAUUCACCACCUCUC' (SEQ ID NO:781)	[[], ['GGG'], ['UAUU']]	0.580645	0.806452	2	170
'GCAGCUCCAGGAGGGUAUUCACCACCUCUCA' (SEQ ID NO:782)	[[], ['GGG'], ['UAUU']]	0.580645	0.806452	2	171
'CAGCUCCAGGAGGGUAUUCACCACCUCUCAG' (SEQ ID NO:783)	[[], ['GGG'], ['UAUU']]	0.580645	0.806452	2	172
'GCUCCAGGAGGGUAUUCACCACCUCUCAGUG' (SEQ ID NO:784)	[[], ['GGG'], ['UAUU']]	0.580645	0.806452	2	174
'CUCCAGGAGGGUAUUCACCACCUCUCAGUGG' (SEQ ID NO:785)	[[], ['GGG'], ['UAUU']]	0.580645	0.806452	2	175
'UCCAGGAGGGUAUUCACCACCUCUCAGUGGC' (SEQ ID NO:786)	[[], ['GGG'], ['UAUU']]	0.580645	0.806452	2	176

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CCAGGAGGGUAUUCACCACCUCUCAGUGGCA' (SEQ ID NO:787)	[[], ['GGG'], ['UAUU']]	0.580645	0.806452	2	177
'AGCUGUGUGACACACCGCAAGGGCUUGGGAU' (SEQ ID NO:788)	[[], ['GGG', 'GGG'], []]	0.580645	0.806452	2	217
'CUGUGUGACACACCGCAAGGGCUUGGGAUCU' (SEQ ID NO:789)	[[], ['GGG', 'GGG'], []]	0.580645	0.806452	2	219
'CAGGAGGGUAUUCACCACCUCUCAGUGGCAA' (SEQ ID NO:790)	[[], ['GGG'], ['UAUU']]	0.548387	0.806452	2	178
'UGUGUGACACACCGCAAGGGCUUGGGAUCUU' (SEQ ID NO:791)	[[], ['GGG', 'GGG'], []]	0.548387	0.806452	2	220
'GUGUGACACACCGCAAGGGCUUGGGAUCUUU' (SEQ ID NO:792)	[[], ['GGG', 'GGG'], []]	0.548387	0.806452	2	221
'AGCUCCAGGAGGGUAUUCACCACCUCUCAGU' (SEQ ID NO:793)	[[], ['GGG'], ['UAUU']]	0.548387	0.774194	2	173

FIG. 42 (Cont'd)

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GGAGGGUAUUCACCAC CUCUCAGUGGCAAUG' (SEQ ID NO:794)	[[], ['GGG'], ['UAUU']]	0.548387	0.774194	2	180
'GAGGGUAUUCACCACC UCUCAGUGGCAAUGC' (SEQ ID NO:795)	[[], ['GGG'], ['UAUU']]	0.548387	0.774194	2	181
'AGGGUAUUCACCACCU CUCAGUGGCAAUGCG' (SEQ ID NO:796)	[[], ['GGG'], ['UAUU']]	0.548387	0.774194	2	182
'GGGUAUUCACCACCUC UCAGUGGCAAUGCGA' (SEQ ID NO:797)	[[], ['GGG'], ['UAUU']]	0.548387	0.774194	2	183
'AGGAGGGUAUUCACCA CCUCUCAGUGGCAAU' (SEQ ID NO:798)	[[], ['GGG'], ['UAUU']]	0.516129	0.774194	2	179
'GUGGUGCUGAAGUUUA UUCGGAUUUAUUUUU' (SEQ ID NO:799)	[[], [], ['UUUA', 'AUUU', 'AUUU']]	0.322581	0.935484	3	19
'UGGUGCUGAAGUUUAU UCGGAUUUAUUUUUU' (SEQ ID NO:800)	[[], [], ['UUUA', 'AUUU', 'AUUU']]	0.290323	0.935484	3	20
'GGGCUUGGGAUCUUUU GCGAUCUGCUCGAGC' (SEQ ID NO:801)	[[], ['GGG', 'GGG'], ['UUUU']]	0.580645	0.903226	3	237

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CGUGGUGCUGAAGUUUAUUCGGAUUUAUUUU' (SEQ ID NO:802)	[[], [], ['UUUA', 'AUUU', 'AUUU']]	0.354839	0.903226	3	18
'AUUCGGAUUUAUUUUUUUCCAACUGCUUUCU' (SEQ ID NO:803)	[[], [], ['AUUU', 'AUUU', 'UUUU']]	0.290323	0.903226	3	34
'CCGCAAGGGCUUGGGAUCUUUUGCGAUCUGC' (SEQ ID NO:804)	[[], ['GGG', 'GGG'], ['UUUU']]	0.580645	0.870968	3	231
'CGCAAGGGCUUGGGAUCUUUUGCGAUCUGCU' (SEQ ID NO:805)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387	0.870968	3	232
'GCAAGGGCUUGGGAUCUUUUGCGAUCUGCUC' (SEQ ID NO:806)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387	0.870968	3	233
'CAAGGGCUUGGGAUCUUUUGCGAUCUGCUCG' (SEQ ID NO:807)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387	0.870968	3	234

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AGGGCUUGGGAUCUUUUGCGAUCUGCUCGAG' (SEQ ID NO:808)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387	0.870968	3	236
'CCGUGGUGCUGAAGUUUAUUCGGAUUUAUUU' (SEQ ID NO:809)	[[], [], ['UUUA', 'AUUU', 'AUUU']]	0.387097	0.870968	3	17
'UUCGGAUUUAUUUUUUUCCAACUGCUUUCUG' (SEQ ID NO:810)	[[], [], ['AUUU', 'AUUU', 'UUUU']]	0.322581	0.870968	3	35
'UCGGAUUUAUUUUUUUCCAACUGCUUUCUGA' (SEQ ID NO:811)	[[], [], ['AUUU', 'AUUU', 'UUUU']]	0.322581	0.870968	3	36
'CGGAUUUAUUUUUUUCCAACUGCUUUCUGAA' (SEQ ID NO:812)	[[], [], ['AUUU', 'AUUU', 'UUUU']]	0.322581	0.870968	3	37
'GGAUUUAUUUUUUUCCAACUGCUUUCUGAAA' (SEQ ID NO:813)	[[], [], ['AUUU', 'AUUU', 'UUUU']]	0.290323	0.870968	3	38

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GAUUUAUUUUUUUCCA ACUGCUUUCUGAAAG' (SEQ ID NO:814)	[[], [], ['AUUU', 'AUUU', 'UUUU']]	0.290323	0.870968	3	39
'AUUUAUUUUUUUCCAAC UGCUUUCUGAAAGG' (SEQ ID NO:815)	[[], [], ['AUUU', 'AUUU', 'UUUU']]	0.290323	0.870968	3	40
'CACCGCAAGGGCUUGG GAUCUUUUGCGAUCU' (SEQ ID NO:816)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387	0.83871	3	229
'ACCGCAAGGGCUUGGG AUCUUUUGCGAUCUG' (SEQ ID NO:817)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387	0.83871	3	230
'AAGGGCUUGGGAUCUU UUGCGAUCUGCUCGA' (SEQ ID NO:818)	[[], ['GGG', 'GGG'], ['UUUU']]	0.516129	0.83871	3	235
'GGGAUCUUUUGCGAUC UGCUCGAGCAGAUUU' (SEQ ID NO:819)	[[], ['GGG'], ['UUUU', 'AUUU']]	0.483871	0.83871	3	243

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AUUUUUUUCCAACUGC UUUCUGAAAGGGGUG' (SEQ ID NO:820)	[[], ['GGG'], ['AUUU', 'UUUU']]	0.387097	0.83871	3	44
'UUAUUUUUUUCCAACU GCUUUCUGAAAGGGG' (SEQ ID NO:821)	[[], ['GGG'], ['UUAU', 'UUUU']]	0.354839	0.83871	3	42
'UAUUUUUUUCCAACUG CUUUCUGAAAGGGGU' (SEQ ID NO:822)	[[], ['GGG'], ['UAUU', 'UUUU']]	0.354839	0.83871	3	43
'UUUAUUUUUUUCCAAC UGCUUUCUGAAAGGG' (SEQ ID NO:823)	[[], ['GGG'], ['UUUA', 'UUUU']]	0.322581	0.83871	3	41
'GACACACCGCAAGGGC UUGGGAUCUUUUGCG' (SEQ ID NO:824)	[[], ['GGG', 'GGG'], ['UUUU']]	0.580645	0.806452	3	225
'GUGACACACCGCAAGG GCUUGGGAUCUUUUG' (SEQ ID NO:825)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387	0.806452	3	223

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UGACACACCGCAAGGG CUUGGGAUCUUUUGC' (SEQ ID NO:826)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387	0.806452	3	224
'CACACCGCAAGGGCUU GGGAUCUUUUGCGAU' (SEQ ID NO:827)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387	0.806452	3	227
'ACACCGCAAGGGCUUG GGAUCUUUUGCGAUC' (SEQ ID NO:828)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387	0.806452	3	228
'UGUGACACACCGCAAG GGCUUGGGAUCUUUU' (SEQ ID NO:829)	[[], ['GGG', 'GGG'], ['UUUU']]	0.516129	0.806452	3	222
'ACACACCGCAAGGGCU UGGGAUCUUUUGCGA' (SEQ ID NO:830)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387	0.774194	3	226
'GGUGCUGAAGUUUAUU CGGAUUUAUUUUUUU' (SEQ ID NO:831)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.290323	0.935484	4	21

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GUGCUGAAGUUUAUUCGGAUUUAUUUUUUUC' (SEQ ID NO:832)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.290323	0.903226	4	22
'UAUUCGGAUUUAUUUUUUUCCAACUGCUUUC' (SEQ ID NO:833)	[[], [], ['UAUU', 'AUUU', 'AUUU', 'UUUU']]	0.290323	0.903226	4	33
'UUUAUUCGGAUUUAUUUUUUUCCAACUGCUU' (SEQ ID NO:834)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.258065	0.903226	4	31
'UUAUUCGGAUUUAUUUUUUUCCAACUGCUUU' (SEQ ID NO:835)	[[], [], ['UUAU', 'AUUU', 'AUUU', 'UUUU']]	0.258065	0.903226	4	32
'UGCUGAAGUUUAUUCGGAUUUAUUUUUUUCC' (SEQ ID NO:836)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.290323	0.870968	4	23

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GCUGAAGUUUAUUCGGAUUUAUUUUUUUCCA' (SEQ ID NO:837)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.290323	0.870968	4	24
'AGUUUAUUCGGAUUUAUUUUUUUCCAACUGC' (SEQ ID NO:838)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.290323	0.870968	4	29
'GUUUAUUCGGAUUUAUUUUUUUCCAACUGCU' (SEQ ID NO:839)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.290323	0.870968	4	30
'CUGAAGUUUAUUCGGAUUUAUUUUUUUCCAA' (SEQ ID NO:840)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.258065	0.870968	4	25
'UGAAGUUUAUUCGGAUUUAUUUUUUUCCAAC' (SEQ ID NO:841)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.258065	0.870968	4	26

FIG. 42 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GAAGUUUAUUCGGAUU UAUUUUUUUCCAACU' (SEQ ID NO:842)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.258065	0.870968	4	27
'AAGUUUAUUCGGAUUU AUUUUUUUCCAACUG' (SEQ ID NO:843)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.258065	0.870968	4	28

FIG. 42 (Cont'd)

FIG. 43

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GGAAUCAGAAGCAGGUGUCUGCAGCCAGGAC' (SEQ ID NO:844)	[[], [], []]	0.580645	0.870968	0	153
'GUGGAAUCAGAAGCAGGUGUCUGCAGCCAGG' (SEQ ID NO:845)	[[], [], []]	0.580645	0.83871	0	151
'UGGAAUCAGAAGCAGGUGUCUGCAGCCAGGA' (SEQ ID NO:846)	[[], [], []]	0.548387	0.83871	0	152
'GAAUCAGAAGCAGGUGUCUGCAGCCAGGACU' (SEQ ID NO:847)	[[], [], []]	0.548387	0.83871	0	154
'UCAGAAGCAGGUGUCUGCAGCCAGGACUUCC' (SEQ ID NO:848)	[[], [], []]	0.580645	0.806452	0	157
'CAGAAGCAGGUGUCUGCAGCCAGGACUUCCU' (SEQ ID NO:849)	[[], [], []]	0.580645	0.806452	0	158
'AGAAGCAGGUGUCUGCAGCCAGGACUUCCUC' (SEQ ID NO:850)	[[], [], []]	0.580645	0.806452	0	159
'UGUGGAAUCAGAAGCAGGUGUCUGCAGCCAG' (SEQ ID NO:851)	[[], [], []]	0.548387	0.806452	0	150

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AUCAGAAGCAGGUGUCUGCAGCCAGGACUUC' (SEQ ID NO:852)	[[], [], []]	0.548387	0.806452	0	156
'UUGUGGAAUCAGAAGCAGGUGUCUGCAGCCA' (SEQ ID NO:853)	[[], [], []]	0.516129	0.806452	0	149
'AAUCAGAAGCAGGUGUCUGCAGCCAGGACUU' (SEQ ID NO:854)	[[], [], []]	0.516129	0.806452	0	155
'CCUUGUGGAAUCAGAAGCAGGUGUCUGCAGC' (SEQ ID NO:855)	[[], [], []]	0.548387	0.774194	0	147
'CUUGUGGAAUCAGAAGCAGGUGUCUGCAGCC' (SEQ ID NO:856)	[[], [], []]	0.548387	0.774194	0	148
'CACUUCAAAGGCGGCCACAGGGUUGAGGAAA' (SEQ ID NO:857)	[[], ['GGG'], []]	0.548387	0.870968	1	111
'AAAAAUGAGUCACUUCAAAGGCGGCCACAGG' (SEQ ID NO:858)	[[], [], ['AAAA']]	0.483871	0.870968	1	101
'AAAAAAUGAGUCACUUCAAAGGCGGCCACAG' (SEQ ID NO:859)	[[], [], ['AAAA']]	0.451613	0.870968	1	100

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'ACCGUGGAAAUUUUGUGCUCAAAGGUAAGAA' (SEQ ID NO:860)	[[], [], ['AAAU']]	0.387097	0.870968	1	26
'CCGUGGAAAUUUUGUGCUCAAAGGUAAGAAA' (SEQ ID NO:861)	[[], [], ['AAAU']]	0.387097	0.870968	1	27
'CGUGGAAAUUUUGUGCUCAAAGGUAAGAAAC' (SEQ ID NO:862)	[[], [], ['AAAU']]	0.387097	0.870968	1	28
'GUGGAAAUUUUGUGCUCAAAGGUAAGAAACC' (SEQ ID NO:863)	[[], [], ['AAAU']]	0.387097	0.870968	1	29
'UGGAAAUUUUGUGCUCAAAGGUAAGAAACCA' (SEQ ID NO:864)	[[], [], ['AAAU']]	0.354839	0.870968	1	30
'GGAAAUUUUGUGCUCAAAGGUAAGAAACCAU' (SEQ ID NO:865)	[[], [], ['AAAU']]	0.354839	0.870968	1	31
'GAGUCACUUCAAAGGCGGCCACAGGGUUGAG' (SEQ ID NO:866)	[[], ['GGG'], []]	0.580645	0.83871	1	107
'AGUCACUUCAAAGGCGGCCACAGGGUUGAGG' (SEQ ID NO:867)	[[], ['GGG'], []]	0.580645	0.83871	1	108

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GUCACUUCAAAGGCGGCCACAGGGUUGAGGA' (SEQ ID NO:868)	[[], ['GGG'], []]	0.580645	0.83871	1	109
'UCACUUCAAAGGCGGCCACAGGGUUGAGGAA' (SEQ ID NO:869)	[[], ['GGG'], []]	0.548387	0.83871	1	110
'UCACCGUGGAAAUUUUGUGCUCAAAGGUAAG' (SEQ ID NO:870)	[[], [], ['AAAU']]	0.419355	0.83871	1	24
'CACCGUGGAAAUUUUGUGCUCAAAGGUAAGA' (SEQ ID NO:871)	[[], [], ['AAAU']]	0.419355	0.83871	1	25
'UUUCACCGUGGAAAUUUUGUGCUCAAAGGUA' (SEQ ID NO:872)	[[], [], ['AAAU']]	0.387097	0.83871	1	22
'UUCACCGUGGAAAUUUUGUGCUCAAAGGUAA' (SEQ ID NO:873)	[[], [], ['AAAU']]	0.387097	0.83871	1	23
'GAAAUUUUGUGCUCAAAGGUAAGAAACCAUC' (SEQ ID NO:874)	[[], [], ['AAAU']]	0.354839	0.83871	1	32
'AAAUUUUGUGCUCAAAGGUAAGAAACCAUCU' (SEQ ID NO:875)	[[], [], ['AAAU']]	0.322581	0.83871	1	33

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AAUUUUGUGCUCAAAG GUAAGAAACCAUCUU' (SEQ ID NO:876)	[[], [], ['AAUU']]	0.322581	0.83871	1	34
'AUUUUGUGCUCAAAGG UAAGAAACCAUCUUA' (SEQ ID NO:877)	[[], [], ['AUUU']]	0.322581	0.83871	1	35
'UUUGUGCUCAAAGGUA AGAAACCAUCUUAUA' (SEQ ID NO:878)	[[], [], ['UUAU']]	0.322581	0.83871	1	37
'UUGUGCUCAAAGGUAA GAAACCAUCUUAUAU' (SEQ ID NO:879)	[[], [], ['UUAU']]	0.322581	0.83871	1	38
'UGUGCUCAAAGGUAAG AAACCAUCUUAUAUA' (SEQ ID NO:880)	[[], [], ['UUAU']]	0.322581	0.83871	1	39
'GCCCCUUGUGGAAUCA GAAGCAGGUGUCUGC' (SEQ ID NO:881)	[['CCC'], [], []]	0.580645	0.806452	1	144
'AUGAGUCACUUCAAAG GCGGCCACAGGGUUG' (SEQ ID NO:882)	[[], ['GGG'], []]	0.548387	0.806452	1	105
'UGAGUCACUUCAAAGG CGGCCACAGGGUUGA' (SEQ ID NO:883)	[[], ['GGG'], []]	0.548387	0.806452	1	106

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AAUGAGUCACUUCAAAGGCGGCCACAGGGUU' (SEQ ID NO:884)	[[], ['GGG'], []]	0.516129	0.806452	1	104
'AAAGCCCCUUGUGGAAUCAGAAGCAGGUGUC' (SEQ ID NO:885)	[['CCC'], [], []]	0.516129	0.806452	1	141
'AGCCCCUUGUGGAAUCAGAAGCAGGUGUCUG' (SEQ ID NO:886)	[['CCC'], [], []]	0.548387	0.774194	1	143
'CCCCUUGUGGAAUCAGAAGCAGGUGUCUGCA' (SEQ ID NO:887)	[['CCC'], [], []]	0.548387	0.774194	1	145
'CCCUUGUGGAAUCAGAAGCAGGUGUCUGCAG' (SEQ ID NO:888)	[['CCC'], [], []]	0.548387	0.774194	1	146
'AAGCCCCUUGUGGAAUCAGAAGCAGGUGUCU' (SEQ ID NO:889)	[['CCC'], [], []]	0.516129	0.774194	1	142
'CAAAGGCGGCCACAGGGUUGAGGAAAAAGCC' (SEQ ID NO:890)	[[], ['GGG'], ['AAAA']]	0.580645	0.935484	2	116
'GUAAGAAACCAUCUUAUAUAAAACAAUCAAA' (SEQ ID NO:891)	[[], [], ['UUAU', 'AUAA']]	0.225806	0.935484	2	50

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UCAAAGGCGGCCACAGGGUUGAGGAAAAAGC' (SEQ ID NO:892)	[[], ['GGG'], ['AAAA']]	0.548387	0.903226	2	115
'CUCAAAGGUAAGAAACCAUCUUAUAUAAAAC' (SEQ ID NO:893)	[[], [], ['UUAU', 'AUAA']]	0.290323	0.903226	2	43
'UCAAAGGUAAGAAACCAUCUUAUAUAAAACA' (SEQ ID NO:894)	[[], [], ['UUAU', 'AUAA']]	0.258065	0.903226	2	44
'CAAAGGUAAGAAACCAUCUUAUAUAAAACAA' (SEQ ID NO:895)	[[], [], ['UUAU', 'AUAA']]	0.258065	0.903226	2	45
'AAGGUAAGAAACCAUCUUAUAUAAAACAAUC' (SEQ ID NO:896)	[[], [], ['UUAU', 'AUAA']]	0.258065	0.903226	2	47
'AGGUAAGAAACCAUCUUAUAUAAAACAAUCA' (SEQ ID NO:897)	[[], [], ['UUAU', 'AUAA']]	0.258065	0.903226	2	48
'GGUAAGAAACCAUCUUAUAUAAAACAAUCAA' (SEQ ID NO:898)	[[], [], ['UUAU', 'AUAA']]	0.258065	0.903226	2	49
'AAAGGUAAGAAACCAUCUUAUAUAAAACAAU' (SEQ ID NO:899)	[[], [], ['UUAU', 'AUAA']]	0.225806	0.903226	2	46

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AAAAUGAGUCACUUCAAAGGCGGCCACAGGG' (SEQ ID NO:900)	[[], ['GGG'], ['AAAA']]	0.516129	0.870968	2	102
'ACUUCAAAGGCGGCCACAGGGUUGAGGAAAA' (SEQ ID NO:901)	[[], ['GGG'], ['AAAA']]	0.516129	0.870968	2	112
'CUUCAAAGGCGGCCACAGGGUUGAGGAAAAA' (SEQ ID NO:902)	[[], ['GGG'], ['AAAA']]	0.516129	0.870968	2	113
'UUCAAAGGCGGCCACAGGGUUGAGGAAAAAG' (SEQ ID NO:903)	[[], ['GGG'], ['AAAA']]	0.516129	0.870968	2	114
'GGAAAAAGCCCCUUGUGGAAUCAGAAGCAGG' (SEQ ID NO:904)	[['CCC'], [], ['AAAA']]	0.516129	0.870968	2	137
'GAGGAAAAAGCCCCUUGUGGAAUCAGAAGCA' (SEQ ID NO:905)	[['CCC'], [], ['AAAA']]	0.483871	0.870968	2	135
'AGGAAAAAGCCCCUUGUGGAAUCAGAAGCAG' (SEQ ID NO:906)	[['CCC'], [], ['AAAA']]	0.483871	0.870968	2	136
'AAAAAAAUGAGUCACUUCAAAGGCGGCCACA' (SEQ ID NO:907)	[[], [], ['AAAA', 'AAAU']]	0.419355	0.870968	2	99

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GUUGACUUUAUUUCACCGUGGAAAUUUUGUG' (SEQ ID NO:908)	[[], [], ['UUUA', 'AAAU']]	0.354839	0.870968	2	12
'AUGUUGACUUUAUUUCACCGUGGAAAUUUUG' (SEQ ID NO:909)	[[], [], ['UUUA', 'AAAU']]	0.322581	0.870968	2	10
'UGUUGACUUUAUUUCACCGUGGAAAUUUUGU' (SEQ ID NO:910)	[[], [], ['UUUA', 'AAAU']]	0.322581	0.870968	2	11
'AAAGCUUAUAAUGUUGACUUUAUUUCACCGU' (SEQ ID NO:911)	[[], [], ['UUAU', 'UUUA']]	0.290323	0.870968	2	0
'UUAUAAUGUUGACUUUAUUUCACCGUGGAAA' (SEQ ID NO:912)	[[], [], ['UUAU', 'UUUA']]	0.290323	0.870968	2	5
'AAUGUUGACUUUAUUUCACCGUGGAAAUUUU' (SEQ ID NO:913)	[[], [], ['UUUA', 'AAAU']]	0.290323	0.870968	2	9
'UGCUCAAAGGUAAGAAACCAUCUUAUAUAAA' (SEQ ID NO:914)	[[], [], ['UUAU', 'AUAA']]	0.290323	0.870968	2	41
'GCUCAAAGGUAAGAAACCAUCUUAUAUAAAA' (SEQ ID NO:915)	[[], [], ['UUAU', 'AUAA']]	0.290323	0.870968	2	42

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AUACAUUAAAAAAAUGAGUCACUUCAAAGGC' (SEQ ID NO:916)	[[], [], ['AUUA', 'AAAA']]	0.290323	0.870968	2	92
'AAAUGAGUCACUUCAAAGGCGGCCACAGGGU' (SEQ ID NO:917)	[[], ['GGG'], ['AAAU']]	0.516129	0.83871	2	103
'GGUUGAGGAAAAAGCCCCUUGUGGAAUCAGA' (SEQ ID NO:918)	[['CCC'], [], ['AAAA']]	0.483871	0.83871	2	131
'UGAGGAAAAAGCCCCUUGUGGAAUCAGAAGC' (SEQ ID NO:919)	[['CCC'], [], ['AAAA']]	0.483871	0.83871	2	134
'GAAAAAGCCCCUUGUGGAAUCAGAAGCAGGU' (SEQ ID NO:920)	[['CCC'], [], ['AAAA']]	0.483871	0.83871	2	138
'AAAAAGCCCCUUGUGGAAUCAGAAGCAGGUG' (SEQ ID NO:921)	[['CCC'], [], ['AAAA']]	0.483871	0.83871	2	139
'GUUGAGGAAAAAGCCCCUUGUGGAAUCAGAA' (SEQ ID NO:922)	[['CCC'], [], ['AAAA']]	0.451613	0.83871	2	132
'UUGAGGAAAAAGCCCCUUGUGGAAUCAGAAG' (SEQ ID NO:923)	[['CCC'], [], ['AAAA']]	0.451613	0.83871	2	133

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UAAAAAAAUGAGUCAC UUCAAAGGCGGCCAC' (SEQ ID NO:924)	[[], [], ['UAAA', 'AAAA']]	0.419355	0.83871	2	98
'UAUUUCACCGUGGAAA UUUUGUGCUCAAAGG' (SEQ ID NO:925)	[[], [], ['UAUU', 'AAAU']]	0.387097	0.83871	2	20
'AUUUCACCGUGGAAAU UUUGUGCUCAAAGGU' (SEQ ID NO:926)	[[], [], ['AUUU', 'AAAU']]	0.387097	0.83871	2	21
'AGCUUAUAAUGUUGAC UUUAUUUCACCGUGG' (SEQ ID NO:927)	[[], [], ['UUAU', 'UUUA']]	0.354839	0.83871	2	2
'GCUUAUAAUGUUGACU UUAUUUCACCGUGGA' (SEQ ID NO:928)	[[], [], ['UUAU', 'UUUA']]	0.354839	0.83871	2	3
'UUGACUUUAUUUCACC GUGGAAAUUUUGUGC' (SEQ ID NO:929)	[[], [], ['UUUA', 'AAAU']]	0.354839	0.83871	2	13
'UGACUUUAUUUCACCG UGGAAAUUUUGUGCU' (SEQ ID NO:930)	[[], [], ['UUUA', 'AAAU']]	0.354839	0.83871	2	14
'ACUUUAUUUCACCGUG GAAAUUUUGUGCUCA' (SEQ ID NO:931)	[[], [], ['UUUA', 'AAAU']]	0.354839	0.83871	2	16

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CUUUAUUUCACCGUGGAAAUUUUGUGCUCAA' (SEQ ID NO:932)	[[], [], ['UUUA', 'AAAU']]	0.354839	0.83871	2	17
'UUAUUUCACCGUGGAAAUUUUGUGCUCAAAG' (SEQ ID NO:933)	[[], [], ['UUAU', 'AAAU']]	0.354839	0.83871	2	19
'ACAUUAAAAAAAUGAGUCACUUCAAAGGCGG' (SEQ ID NO:934)	[[], [], ['AUUA', 'AAAA']]	0.354839	0.83871	2	94
'AAGCUUAUAAUGUUGACUUUAUUUCACCGUG' (SEQ ID NO:935)	[[], [], ['UUAU', 'UUUA']]	0.322581	0.83871	2	1
'CUUAUAAUGUUGACUUUAUUUCACCGUGGAA' (SEQ ID NO:936)	[[], [], ['UUAU', 'UUUA']]	0.322581	0.83871	2	4
'UUUAUUUCACCGUGGAAAUUUUGUGCUCAAA' (SEQ ID NO:937)	[[], [], ['UUUA', 'AAAU']]	0.322581	0.83871	2	18
'UUUUGUGCUCAAAGGUAAGAAACCAUCUUAU' (SEQ ID NO:938)	[[], [], ['UUUU', 'UUAU']]	0.322581	0.83871	2	36
'GUGCUCAAAGGUAAGAAACCAUCUUAUAUAA' (SEQ ID NO:939)	[[], [], ['UUAU', 'AUAA']]	0.322581	0.83871	2	40

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UACAUUAAAAAAAUGA GUCACUUCAAAGGCG' (SEQ ID NO:940)	[[], [], ['AUUA', 'AAAA']]	0.322581	0.83871	2	93
'AAAAGCCCCUUGUGGA AUCAGAAGCAGGUGU' (SEQ ID NO:941)	[['CCC'], [], ['AAAA']]	0.483871	0.806452	2	140
'GACUUUAUUUCACCGU GGAAAUUUUGUGCUC' (SEQ ID NO:942)	[[], [], ['UUUA', 'AAAU']]	0.387097	0.806452	2	15
'CAUUAAAAAAAUGAGU CACUUCAAAGGCGGC' (SEQ ID NO:943)	[[], [], ['AUUA', 'AAAA']]	0.387097	0.806452	2	95
'AUUAAAAAAAUGAGUC ACUUCAAAGGCGGCC' (SEQ ID NO:944)	[[], [], ['AUUA', 'AAAA']]	0.387097	0.806452	2	96
'UUAAAAAAAUGAGUCA CUUCAAAGGCGGCCA' (SEQ ID NO:945)	[[], [], ['UUAA', 'AAAA']]	0.387097	0.806452	2	97
'UAAGAAACCAUCUUAU AUAAAACAAUCAAAU' (SEQ ID NO:946)	[[], [], ['UUAU', 'AUAA', 'AAAU']]	0.193548	0.967742	3	51
'AAGAAACCAUCUUAUA UAAAACAAUCAAAUA' (SEQ ID NO:947)	[[], [], ['UUAU', 'AUAA', 'AAAU']]	0.193548	0.967742	3	52

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AGAAACCAUCUUAUAU AAAACAAUCAAAUAA' (SEQ ID NO:948)	[[], [], ['UUAU', 'AUAA', 'AAAU']]	0.193548	0.96774 2	3	53
'GAAACCAUCUUAUAUA AAACAAUCAAAUAAA' (SEQ ID NO:949)	[[], [], ['UUAU', 'AUAA', 'AAAU']]	0.193548	0.96774 2	3	54
'AAGGCGGCCACAGGGU UGAGGAAAAAGCCCC' (SEQ ID NO:950)	[['CCC'], ['GGG'], ['AAAA']]	0.612903	0.93548 4	3	118
'AAAGGCGGCCACAGGG UUGAGGAAAAAGCCC' (SEQ ID NO:951)	[['CCC'], ['GGG'], ['AAAA']]	0.580645	0.93548 4	3	117
'ACAUAAAUACAUUAAAA AAAUGAGUCACUUC' (SEQ ID NO:952)	[[], [], ['AUAA', 'AUUA', 'AAAA']]	0.225806	0.93548 4	3	86
'CAUAAAUACAUUAAAAA AAUGAGUCACUUCA' (SEQ ID NO:953)	[[], [], ['AUAA', 'AUUA', 'AAAA']]	0.225806	0.93548 4	3	87
'AUACAUAAAUACAUUAA AAAAAUGAGUCACU' (SEQ ID NO:954)	[[], [], ['AUAA', 'AUUA', 'AAAA']]	0.193548	0.93548 4	3	84
'UACAUAAAUACAUUAAA AAAAUGAGUCACUU' (SEQ ID NO:955)	[[], [], ['AUAA', 'AUUA', 'AAAA']]	0.193548	0.93548 4	3	85

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AUAAAUACAUUAAAAAA AUGAGUCACUUCAA' (SEQ ID NO:956)	[[], [], ['AUAA', 'AUUA', 'AAAA']]	0.193548	0.93548 4	3	88
'UAAAUACAUUAAAAAAA UGAGUCACUUCAAA' (SEQ ID NO:957)	[[], [], ['UAAA', 'AUUA', 'AAAA']]	0.193548	0.93548 4	3	89
'AGGCGGCCACAGGGU UGAGGAAAAAGCCCCU' (SEQ ID NO:958)	[['CCC'], ['GGG'], ['AAAA']]	0.612903	0.90322 6	3	119
'AAAUACAUUAAAAAAAU GAGUCACUUCAAAG' (SEQ ID NO:959)	[[], [], ['AAAU', 'AUUA', 'AAAA']]	0.225806	0.90322 6	3	90
'GGCGGCCACAGGGUU GAGGAAAAAGCCCCUU' (SEQ ID NO:960)	[['CCC'], ['GGG'], ['AAAA']]	0.612903	0.87096 8	3	120
'GCGGCCACAGGGUUG AGGAAAAAGCCCCUUG' (SEQ ID NO:961)	[['CCC'], ['GGG'], ['AAAA']]	0.612903	0.87096 8	3	121
'UAUAAUGUUGACUUUA UUUCACCGUGGAAAU' (SEQ ID NO:962)	[[], [], ['UAUA', 'UUUA', 'AAAU']]	0.290323	0.87096 8	3	6
'AUAAUGUUGACUUUAU UUCACCGUGGAAAUU' (SEQ ID NO:963)	[[], [], ['AUAA', 'UUUA', 'AAAU']]	0.290323	0.87096 8	3	7

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UAAUGUUGACUUUAUUUCACCGUGGAAAUUU' (SEQ ID NO:964)	[[], [], ['UAAU', 'UUUA', 'AAAU']]	0.290323	0.870968	3	8
'AAUACAUUAAAAAAAUGAGUCACUUCAAAGG' (SEQ ID NO:965)	[[], [], ['AAUA', 'AUUA', 'AAAA']]	0.258065	0.870968	3	91
'CGGCCACAGGGUUGAGGAAAAAGCCCCUUGU' (SEQ ID NO:966)	[['CCC'], ['GGG'], ['AAAA']]	0.580645	0.83871	3	122
'GGCCACAGGGUUGAGGAAAAAGCCCCUUGUG' (SEQ ID NO:967)	[['CCC'], ['GGG'], ['AAAA']]	0.580645	0.83871	3	123
'GCCACAGGGUUGAGGAAAAAGCCCCUUGUGG' (SEQ ID NO:968)	[['CCC'], ['GGG'], ['AAAA']]	0.580645	0.83871	3	124
'CCACAGGGUUGAGGAAAAAGCCCCUUGUGGA' (SEQ ID NO:969)	[['CCC'], ['GGG'], ['AAAA']]	0.548387	0.83871	3	125
'CACAGGGUUGAGGAAAAAGCCCCUUGUGGAA' (SEQ ID NO:970)	[['CCC'], ['GGG'], ['AAAA']]	0.516129	0.83871	3	126
'GGGUUGAGGAAAAAGCCCCUUGUGGAAUCAG' (SEQ ID NO:971)	[['CCC'], ['GGG'], ['AAAA']]	0.516129	0.83871	3	130

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'ACAGGGUUGAGGAAAA AGCCCCUUGUGGAAU' (SEQ ID NO:972)	[['CCC'], ['GGG'], ['AAAA']]	0.483871	0.83 871	3	127
'AGGGUUGAGGAAAAAG CCCCUUGUGGAAUCA' (SEQ ID NO:973)	[['CCC'], ['GGG'], ['AAAA']]	0.483871	0.83 871	3	129
'CAGGGUUGAGGAAAAA GCCCCUUGUGGAAUC' (SEQ ID NO:974)	[['CCC'], ['GGG'], ['AAAA']]	0.516129	0.80 645 2	3	128
'ACCAUCUUAUAUAAAA CAAUCAAAUAAAUAC' (SEQ ID NO:975)	[[], [], ['UUAU', 'AUAA', 'AAAU', 'AAAU']]	0.193548	1	4	57
'CCAUCUUAUAUAAAAC AAUCAAAUAAAUACA' (SEQ ID NO:976)	[[], [], ['UUAU', 'AUAA', 'AAAU', 'AAAU']]	0.193548	1	4	58
'AAACCAUCUUAUAUAA AACAAUCAAAUAAAU' (SEQ ID NO:977)	[[], [], ['UUAU', 'AUAA', 'AAAU', 'AAAU']]	0.16129	1	4	55
'AACCAUCUUAUAUAAA ACAAUCAAAUAAAUA' (SEQ ID NO:978)	[[], [], ['UUAU', 'AUAA', 'AAAU', 'AAAU']]	0.16129	1	4	56
'CAUCUUAUAUAAAACA AUCAAAUAAAUACAU' (SEQ ID NO:979)	[[], [], ['UUAU', 'AUAA', 'AAAU', 'AAAU']]	0.16129	1	4	59

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AUCUUAUAUAAAACAA UCAAAUAAAUACAUA' (SEQ ID NO:980)	[[], [], ['UUAU', 'AUAA', 'AAAU', 'AAAU']]	0.129032	1	4	60
'UAUAAAACAAUCAAAUA AAUACAUAAAUACA' (SEQ ID NO:981)	[[], [], ['UAUA', 'AAAU', 'AAAU', 'AUAA']]	0.129032	1	4	66
'AUAAAACAAUCAAAUAA AUACAUAAAUACAU' (SEQ ID NO:982)	[[], [], ['AUAA', 'AAAU', 'AAAU', 'AUAA']]	0.129032	1	4	67
'UAAAACAAUCAAAUAAA UACAUAAAUACAUU' (SEQ ID NO:983)	[[], [], ['UAAA', 'AAAU', 'AAAU', 'AUAA']]	0.129032	1	4	68
'AAACAAUCAAAUAAAUA CAUAAAUACAUUAA' (SEQ ID NO:984)	[[], [], ['AAAU', 'AAAU', 'AUAA', 'AUUA']]	0.129032	1	4	70
'AACAAUCAAAUAAAUAC AUAAAUACAUUAAA' (SEQ ID NO:985)	[[], [], ['AAAU', 'AAAU', 'AUAA', 'AUUA']]	0.129032	1	4	71
'ACAAUCAAAUAAAUACA UAAAUACAUUAAAA' (SEQ ID NO:986)	[[], [], ['AAAU', 'AAAU', 'AUAA', 'AUUA']]	0.129032	1	4	72
'AAUACAUAAAUACAUUA AAAAAAUGAGUCAC' (SEQ ID NO:987)	[[], [], ['AAUA', 'AUAA', 'AUUA', 'AAAA']]	0.193548	0.93548 4	4	83

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UAAAUACAUAAAUACAUUAAAAAAAUGAGUC' (SEQ ID NO:988)	[[], [], ['UAAA', 'AUAA', 'AUUA', 'AAAA']]	0.16129	0.93548 4	4	81
'AAAUACAUAAAUACAUUAAAAAAAUGAGUCA' (SEQ ID NO:989)	[[], [], ['AAAU', 'AUAA', 'AUUA', 'AAAA']]	0.16129	0.93548 4	4	82
'AUAAAUACAUAAAUACAUUAAAAAAAUGAGU' (SEQ ID NO:990)	[[], [], ['AUAA', 'AUAA', 'AUUA', 'AAAA']]	0.129032	0.93548 4	4	80
'UCUUAUAUAAAACAAUCAAAUAAAUACAUAA' (SEQ ID NO:991)	[[], [], ['UUAU', 'AUAA', 'AAAU', 'AAAU', 'AUAA']]	0.129032	1	5	61
'CUUAUAUAAAACAAUCAAAUAAAUACAUAAA' (SEQ ID NO:992)	[[], [], ['UUAU', 'AUAA', 'AAAU', 'AAAU', 'AUAA']]	0.129032	1	5	62
'AUAUAAAACAAUCAAAUAAAUACAUAAAUAC' (SEQ ID NO:993)	[[], [], ['AUAU', 'AAAA', 'AAAU', 'AAAU', 'AUAA']]	0.129032	1	5	65
'AAAACAAUCAAAUAAAUACAUAAAUACAUUA' (SEQ ID NO:994)	[[], [], ['AAAA', 'AAAU', 'AAAU', 'AUAA', 'AUUA']]	0.129032	1	5	69
'CAAUCAAAUAAAUACAUAAAUACAUUAAAAA' (SEQ ID NO:995)	[[], [], ['AAAU', 'AAAU', 'AUAA', 'AUUA', 'AAAA']]	0.129032	1	5	73

FIG. 43 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UUAUAUAAAACAAUCAAAUAAAUACAUAAAU' (SEQ ID NO:996)	[[], [], ['UUAU', 'AUAA', 'AAAU', 'AAAU', 'AUAA']]	0.096774	1	5	63
'UAUAUAAAACAAUCAAAUAAAUACAUAAAUA' (SEQ ID NO:997)	[[], [], ['UAUA', 'UAAA', 'AAAU', 'AAAU', 'AUAA']]	0.096774	1	5	64
'AAUCAAAUAAAUACAUAAAUACAUUAAAAAA' (SEQ ID NO:998)	[[], [], ['AAAU', 'AAAU', 'AUAA', 'AUUA', 'AAAA']]	0.096774	1	5	74
'AUCAAAUAAAUACAUAAAUACAUUAAAAAAA' (SEQ ID NO:999)	[[], [], ['AAAU', 'AAAU', 'AUAA', 'AUUA', 'AAAA']]	0.096774	1	5	75
'UCAAAUAAAUACAUAAAUACAUUAAAAAAAU' (SEQ ID NO:1000)	[[], [], ['AAAU', 'AAAU', 'AUAA', 'AUUA', 'AAAA']]	0.096774	1	5	76
'CAAAUAAAUACAUAAAUACAUUAAAAAAAUG' (SEQ ID NO:1001)	[[], [], ['AAAU', 'AAAU', 'AUAA', 'AUUA', 'AAAA']]	0.129032	0.96774 2	5	77
'AAAUAAAUACAUAAAUACAUUAAAAAAAUGA' (SEQ ID NO:1002)	[[], [], ['AAAU', 'AAAU', 'AUAA', 'AUUA', 'AAAA']]	0.096774	0.96774 2	5	78
'AAUAAAUACAUAAAUACAUUAAAAAAAUGAG' (SEQ ID NO:1003)	[[], [], ['AAUA', 'AAUA', 'AUAA', 'AUUA', 'AAAA']]	0.129032	0.93548 4	5	79

FIG. 43 (Cont'd)

FIG. 44

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GGCCUCAGCGUCUGUCCGUGGUGCUGAAGUU' (SEQ ID NO:1004)	[[], [], []]	0.612903226	0.903225806	0	2
'GCCUCAGCGUCUGUCCGUGGUGCUGAAGUUU' (SEQ ID NO:1005)	[[], [], []]	0.580645161	0.903225806	0	3
'GAUGAAGACAGGAAGCUGCAGCUCCAGGAGG' (SEQ ID NO:1006)	[[], [], []]	0.580645161	0.903225806	0	154
'AGAUGAAGACAGGAAGCUGCAGCUCCAGGAG' (SEQ ID NO:1007)	[[], [], []]	0.548387097	0.903225806	0	153
'CAGGCCUCAGCGUCUGUCCGUGGUGCUGAAG' (SEQ ID NO:1008)	[[], [], []]	0.64516129	0.870967742	0	0
'AGGCCUCAGCGUCUGUCCGUGGUGCUGAAGU' (SEQ ID NO:1009)	[[], [], []]	0.612903226	0.870967742	0	1

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GGCAAUGCGACCAAGCUGUGUGACACACCGC' (SEQ ID NO:1010)	[[], [], []]	0.612903226	0.870967742	0	204
'GCAAUGCGACCAAGCUGUGUGACACACCGCA' (SEQ ID NO:1011)	[[], [], []]	0.580645161	0.870967742	0	205
'AUGCGACCAAGCUGUGUGACACACCGCAAGG' (SEQ ID NO:1012)	[[], [], []]	0.580645161	0.870967742	0	208
'CAAUGCGACCAAGCUGUGUGACACACCGCAA' (SEQ ID NO:1013)	[[], [], []]	0.548387097	0.870967742	0	206
'AAUGCGACCAAGCUGUGUGACACACCGCAAG' (SEQ ID NO:1014)	[[], [], []]	0.548387097	0.870967742	0	207
'GAUAGAUGAAGACAGGAAGCUGCAGCUCCAG' (SEQ ID NO:1015)	[[], [], []]	0.516129032	0.870967742	0	150
'AUAGAUGAAGACAGGAAGCUGCAGCUCCAGG' (SEQ ID NO:1016)	[[], [], []]	0.516129032	0.870967742	0	151

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UAGAUGAAGACAGGAAGCUGCAGCUCCAGGA' (SEQ ID NO:1017)	[[], [], []]	0.516129032	0.870967742	0	152
'GAUCGUGAUAGAUGAAGACAGGAAGCUGCAG' (SEQ ID NO:1018)	[[], [], []]	0.483870968	0.870967742	0	144
'AUCGAUCGUGAUAGAUGAAGACAGGAAGCUG' (SEQ ID NO:1019)	[[], [], []]	0.451612903	0.870967742	0	141
'AACAUCGAUCGUGAUAGAUGAAGACAGGAAG' (SEQ ID NO:1020)	[[], [], []]	0.419354839	0.870967742	0	138
'UAACAUCGAUCGUGAUAGAUGAAGACAGGAA' (SEQ ID NO:1021)	[[], [], []]	0.387096774	0.870967742	0	137
'UCACCACCUCUCAGUGGCAAUGCGACCAAGC' (SEQ ID NO:1022)	[[], [], []]	0.580645161	0.838709677	0	189
'CACCACCUCUCAGUGGCAAUGCGACCAAGCU' (SEQ ID NO:1023)	[[], [], []]	0.580645161	0.838709677	0	190
'ACCACCUCUCAGUGGCAAUGCGACCAAGCUG' (SEQ ID NO:1024)	[[], [], []]	0.580645161	0.838709677	0	191

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GUGGCAAUGCGACCAAGCUGUGUGACACACC' (SEQ ID NO:1025)	[[], [], []]	0.580645161	0.838709677	0	202
'UGGCAAUGCGACCAAGCUGUGUGACACACCG' (SEQ ID NO:1026)	[[], [], []]	0.580645161	0.838709677	0	203
'CAGUGGCAAUGCGACCAAGCUGUGUGACACA' (SEQ ID NO:1027)	[[], [], []]	0.548387097	0.838709677	0	200
'AGUGGCAAUGCGACCAAGCUGUGUGACACAC' (SEQ ID NO:1028)	[[], [], []]	0.548387097	0.838709677	0	201
'CGUGAUAGAUGAAGACAGGAAGCUGCAGCUC' (SEQ ID NO:1029)	[[], [], []]	0.516129032	0.838709677	0	147
'GUGAUAGAUGAAGACAGGAAGCUGCAGCUCC' (SEQ ID NO:1030)	[[], [], []]	0.516129032	0.838709677	0	148
'AUUCACCACCUCUCAGUGGCAAUGCGACCAA' (SEQ ID NO:1031)	[[], [], []]	0.516129032	0.838709677	0	187

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UCGAUCGUGAUAGAUGAAGACAGGAAGCUGC' (SEQ ID NO:1032)	[[], [], []]	0.483870968	0.838709677	0	142
'CGAUCGUGAUAGAUGAAGACAGGAAGCUGCA' (SEQ ID NO:1033)	[[], [], []]	0.483870968	0.838709677	0	143
'AUCGUGAUAGAUGAAGACAGGAAGCUGCAGC' (SEQ ID NO:1034)	[[], [], []]	0.483870968	0.838709677	0	145
'UCGUGAUAGAUGAAGACAGGAAGCUGCAGCU' (SEQ ID NO:1035)	[[], [], []]	0.483870968	0.838709677	0	146
'UGAUAGAUGAAGACAGGAAGCUGCAGCUCCA' (SEQ ID NO:1036)	[[], [], []]	0.483870968	0.838709677	0	149
'ACAUCGAUCGUGAUAGAUGAAGACAGGAAGC' (SEQ ID NO:1037)	[[], [], []]	0.451612903	0.838709677	0	139
'CAUCGAUCGUGAUAGAUGAAGACAGGAAGCU' (SEQ ID NO:1038)	[[], [], []]	0.451612903	0.838709677	0	140
'CCACCUCUCAGUGGCAAUGCGACCAAGCUGU' (SEQ ID NO:1039)	[[], [], []]	0.580645161	0.806451613	0	192

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CACCUCUCAGUGGCAAUGCGACCAAGCUGUG' (SEQ ID NO:1040)	[[], [], []]	0.580645161	0.806451613	0	193
'CCUCUCAGUGGCAAUGCGACCAAGCUGUGUG' (SEQ ID NO:1041)	[[], [], []]	0.580645161	0.806451613	0	195
'UUCACCACCUCUCAGUGGCAAUGCGACCAAG' (SEQ ID NO:1042)	[[], [], []]	0.548387097	0.806451613	0	188
'CUCAGUGGCAAUGCGACCAAGCUGUGUGACA' (SEQ ID NO:1043)	[[], [], []]	0.548387097	0.806451613	0	198
'UCAGUGGCAAUGCGACCAAGCUGUGUGACAC' (SEQ ID NO:1044)	[[], [], []]	0.548387097	0.806451613	0	199
'ACCUCUCAGUGGCAAUGCGACCAAGCUGUGU' (SEQ ID NO:1045)	[[], [], []]	0.548387097	0.774193548	0	194
'CUCUCAGUGGCAAUGCGACCAAGCUGUGUGA' (SEQ ID NO:1046)	[[], [], []]	0.548387097	0.774193548	0	196

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UCUCAGUGGCAAUGCGACCAAGCUGUGUGAC' (SEQ ID NO:1047)	[[], [], []]	0.548387097	0.774193548	0	197
'UAAGGCCUCACUAAACCACUCAUCUACACUU' (SEQ ID NO:1048)	[[], [], ['UAAA']]	0.419354839	0.935483871	1	107
'AAGGCCUCACUAAACCACUCAUCUACACUUA' (SEQ ID NO:1049)	[[], [], ['UAAA']]	0.419354839	0.935483871	1	108
'AAACCACUCAUCUACACUUAACAUCGAUCGU' (SEQ ID NO:1050)	[[], [], ['UUAA']]	0.387096774	0.935483871	1	119
'GCGACCAAGCUGUGUGACACACCGCAAGGGC' (SEQ ID NO:1051)	[[], ['GGG'], []]	0.64516129	0.903225806	1	210
'AUGAAGACAGGAAGCUGCAGCUCCAGGAGGG' (SEQ ID NO:1052)	[[], ['GGG'], []]	0.580645161	0.903225806	1	155
'GAAGACAGGAAGCUGCAGCUCCAGGAGGGUA' (SEQ ID NO:1053)	[[], ['GGG'], []]	0.580645161	0.903225806	1	157

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GCGUCUGUCCGUGGUGCUGAAGUUUAUUCGG' (SEQ ID NO:1054)	[[], [], ['UUUA']]	0.548387097	0.903225806	1	9
'GUAAGGCCUCACUAAACCACUCAUCUACACU' (SEQ ID NO:1055)	[[], [], ['UAAA']]	0.451612903	0.903225806	1	106
'AACCACUCAUCUACACUUAACAUCGAUCGUG' (SEQ ID NO:1056)	[[], [], ['UUAA']]	0.419354839	0.903225806	1	120
'ACCACUCAUCUACACUUAACAUCGAUCGUGA' (SEQ ID NO:1057)	[[], [], ['UUAA']]	0.419354839	0.903225806	1	121
'CCACUCAUCUACACUUAACAUCGAUCGUGAU' (SEQ ID NO:1058)	[[], [], ['UUAA']]	0.419354839	0.903225806	1	122
'CACUCAUCUACACUUAACAUCGAUCGUGAUA' (SEQ ID NO:1059)	[[], [], ['UUAA']]	0.387096774	0.903225806	1	123
'UGCGACCAAGCUGUGUGACACACCGCAAGGG' (SEQ ID NO:1060)	[[], ['GGG'], []]	0.612903226	0.870967742	1	209
'CGACCAAGCUGUGUGACACACCGCAAGGGCU' (SEQ ID NO:1061)	[[], ['GGG'], []]	0.612903226	0.870967742	1	211

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UGAAGACAGGAAGCUGCAGCUCCAGGAGGGU' (SEQ ID NO:1062)	[[], ['GGG'], []]	0.580645161	0.870967742	1	156
'CCUCAGCGUCUGUCCGUGGUGCUGAAGUUUA' (SEQ ID NO:1063)	[[], [], ['UUUA']]	0.548387097	0.870967742	1	4
'AAGACAGGAAGCUGCAGCUCCAGGAGGGUAU' (SEQ ID NO:1064)	[[], ['GGG'], []]	0.548387097	0.870967742	1	158
'CUCAGCGUCUGUCCGUGGUGCUGAAGUUUAU' (SEQ ID NO:1065)	[[], [], ['UUUA']]	0.516129032	0.870967742	1	5
'CAGCGUCUGUCCGUGGUGCUGAAGUUUAUUC' (SEQ ID NO:1066)	[[], [], ['UUUA']]	0.516129032	0.870967742	1	7
'AGCGUCUGUCCGUGGUGCUGAAGUUUAUUCG' (SEQ ID NO:1067)	[[], [], ['UUUA']]	0.516129032	0.870967742	1	8

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CGUCUGUCCGUGGUGCUGAAGUUUAUUCGGA' (SEQ ID NO:1068)	[[], [], ['UUUA']]	0.516129032	0.870967742	1	10
'UCAGCGUCUGUCCGUGGUGCUGAAGUUUAUU' (SEQ ID NO:1069)	[[], [], ['UUUA']]	0.483870968	0.870967742	1	6
'GUCUGUCCGUGGUGCUGAAGUUUAUUCGGAU' (SEQ ID NO:1070)	[[], [], ['UUUA']]	0.483870968	0.870967742	1	11
'GGUAAGGCCUCACUAAACCACUCAUCUACAC' (SEQ ID NO:1071)	[[], [], ['UAAA']]	0.483870968	0.870967742	1	105
'UCUGUCCGUGGUGCUGAAGUUUAUUCGGAUU' (SEQ ID NO:1072)	[[], [], ['UUUA']]	0.451612903	0.870967742	1	12
'AGGUAAGGCCUCACUAAACCACUCAUCUACA' (SEQ ID NO:1073)	[[], [], ['UAAA']]	0.451612903	0.870967742	1	104
'ACUCAUCUACACUUAACAUCGAUCGUGAUAG' (SEQ ID NO:1074)	[[], [], ['UUAA']]	0.387096774	0.870967742	1	124

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CUCAUCUACACUUAACAUCGAUCGUGAUAGA' (SEQ ID NO:1075)	[[], [], ['UUAA']]	0.387096774	0.870967742	1	125
'UUAACAUCGAUCGUGAUAGAUGAAGACAGGA' (SEQ ID NO:1076)	[[], [], ['UUAA']]	0.387096774	0.870967742	1	136
'UCAUCUACACUUAACAUCGAUCGUGAUAGAU' (SEQ ID NO:1077)	[[], [], ['UUAA']]	0.35483871	0.870967742	1	126
'CCAAGCUGUGUGACACACCGCAAGGGCUUGG' (SEQ ID NO:1078)	[[], ['GGG'], []]	0.612903226	0.838709677	1	214
'GACCAAGCUGUGUGACACACCGCAAGGGCUU' (SEQ ID NO:1079)	[[], ['GGG'], []]	0.580645161	0.838709677	1	212
'ACCAAGCUGUGUGACACACCGCAAGGGCUUG' (SEQ ID NO:1080)	[[], ['GGG'], []]	0.580645161	0.838709677	1	213
'UAUGCAGAGUGGGAGAGGUAAGGCCUCACUA' (SEQ ID NO:1081)	[[], ['GGG'], []]	0.516129032	0.838709677	1	89

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AUGCAGAGUGGGAGAGGUAAGGCCUCACUAA' (SEQ ID NO:1082)	[[], ['GGG'], []]	0.516129032	0.838709677	1	90
'GGAGAGGUAAGGCCUCACUAAACCACUCAUC' (SEQ ID NO:1083)	[[], [], ['UAAA']]	0.516129032	0.838709677	1	100
'UAUUCACCACCUCUCAGUGGCAAUGCGACCA' (SEQ ID NO:1084)	[[], [], ['UAUU']]	0.516129032	0.838709677	1	186
'GAGGUAAGGCCUCACUAAACCACUCAUCUAC' (SEQ ID NO:1085)	[[], [], ['UAAA']]	0.483870968	0.838709677	1	103
'UUUCCAACUGCUUUCUGAAAGGGGUGAGGAU' (SEQ ID NO:1086)	[[], ['GGG'], []]	0.451612903	0.838709677	1	49
'UGCUUUCUGAAAGGGGUGAGGAUCUACCUUA' (SEQ ID NO:1087)	[[], ['GGG'], []]	0.451612903	0.838709677	1	57
'AGAGGUAAGGCCUCACUAAACCACUCAUCUA' (SEQ ID NO:1088)	[[], [], ['UAAA']]	0.451612903	0.838709677	1	102

FIG. 44 (Cont'd)

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CUUAACAUCGAUCG UGAUAGAUGAAGACA GG' (SEQ ID NO:1089)	[[], [], ['UUAA']]	0.419354839	0.838709677	1	135
'CAUCUACACUUAACA UCGAUCGUGAUAGA UG' (SEQ ID NO:1090)	[[], [], ['UUAA']]	0.387096774	0.838709677	1	127
'ACUUAACAUCGAUC GUGAUAGAUGAAGAC AG' (SEQ ID NO:1091)	[[], [], ['UUAA']]	0.387096774	0.838709677	1	134
'AUCUACACUUAACAU CGAUCGUGAUAGAU GA' (SEQ ID NO:1092)	[[], [], ['UUAA']]	0.35483871	0.838709677	1	128
'UCUACACUUAACAUC GAUCGUGAUAGAUG AA' (SEQ ID NO:1093)	[[], [], ['UUAA']]	0.35483871	0.838709677	1	129
'UACACUUAACAUCGA UCGUGAUAGAUGAA GA' (SEQ ID NO:1094)	[[], [], ['UUAA']]	0.35483871	0.838709677	1	131
'GUAUUCACCACCUC UCAGUGGCAAUGCG ACC' (SEQ ID NO:1095)	[[], [], ['UAUU']]	0.548387097	0.806451613	1	185
'UUCCAACUGCUUUC UGAAAGGGGUGAGG AUC' (SEQ ID NO:1096)	[[], ['GGG'], []]	0.483870968	0.806451613	1	50

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UCCAACUGCUUUCUGAAAGGGGUGAGGAUCU' (SEQ ID NO:1097)	[[], ['GGG'], []]	0.483870968	0.806451613	1	51
'CCAACUGCUUUCUGAAAGGGGUGAGGAUCUA' (SEQ ID NO:1098)	[[], ['GGG'], []]	0.483870968	0.806451613	1	52
'CAACUGCUUUCUGAAAGGGGUGAGGAUCUAC' (SEQ ID NO:1099)	[[], ['GGG'], []]	0.483870968	0.806451613	1	53
'AACUGCUUUCUGAAAGGGGUGAGGAUCUACC' (SEQ ID NO:1100)	[[], ['GGG'], []]	0.483870968	0.806451613	1	54
'ACUGCUUUCUGAAAGGGGUGAGGAUCUACCU' (SEQ ID NO:1101)	[[], ['GGG'], []]	0.483870968	0.806451613	1	55
'CUGCUUUCUGAAAGGGGUGAGGAUCUACCUU' (SEQ ID NO:1102)	[[], ['GGG'], []]	0.483870968	0.806451613	1	56
'GAGAGGUAAGGCCUCACUAAACCACUCAUCU' (SEQ ID NO:1103)	[[], [], ['UAAA']]	0.483870968	0.806451613	1	101

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CUACACUUAACAUCGAUCGUGAUAGAUGAAG' (SEQ ID NO:1104)	[[], [], ['UUAA']]	0.387096774	0.806451613	1	130
'ACACUUAACAUCGAUCGUGAUAGAUGAAGAC' (SEQ ID NO:1105)	[[], [], ['UUAA']]	0.387096774	0.806451613	1	132
'CACUUAACAUCGAUCGUGAUAGAUGAAGACA' (SEQ ID NO:1106)	[[], [], ['UUAA']]	0.387096774	0.806451613	1	133
'GGUAUUCACCACCUCUCAGUGGCAAUGCGAC' (SEQ ID NO:1107)	[[], [], ['UAUU']]	0.548387097	0.774193548	1	184
'CCUCACUAAACCACUCAUCUACACUUAACAU' (SEQ ID NO:1108)	[[], [], ['UAAA', 'UUAA']]	0.387096774	1	2	112
'CUCACUAAACCACUCAUCUACACUUAACAUC' (SEQ ID NO:1109)	[[], [], ['UAAA', 'UUAA']]	0.387096774	1	2	113
'GCCUCACUAAACCACUCAUCUACACUUAACA' (SEQ ID NO:1110)	[[], [], ['UAAA', 'UUAA']]	0.419354839	0.967741935	2	111
'UCACUAAACCACUCAUCUACACUUAACAUCG' (SEQ ID NO:1111)	[[], [], ['UAAA', 'UUAA']]	0.387096774	0.967741935	2	114

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CACUAAACCACUCAUCUACACUUAACAUCGA' (SEQ ID NO:1112)	[[], [], ['UAAA', 'UUAA']]	0.387096774	0.967741935	2	115
'CUAAACCACUCAUCUACACUUAACAUCGAUC' (SEQ ID NO:1113)	[[], [], ['UAAA', 'UUAA']]	0.387096774	0.967741935	2	117
'ACUAAACCACUCAUCUACACUUAACAUCGAU' (SEQ ID NO:1114)	[[], [], ['UAAA', 'UUAA']]	0.35483871	0.967741935	2	116
'GGCCUCACUAAACCACUCAUCUACACUUAAC' (SEQ ID NO:1115)	[[], [], ['UAAA', 'UUAA']]	0.451612903	0.935483871	2	110
'AGGCCUCACUAAACCACUCAUCUACACUUAA' (SEQ ID NO:1116)	[[], [], ['UAAA', 'UUAA']]	0.419354839	0.935483871	2	109
'UAAACCACUCAUCUACACUUAACAUCGAUCG' (SEQ ID NO:1117)	[[], [], ['UAAA', 'UUAA']]	0.387096774	0.935483871	2	118
'UACCUUAAUAUGCAGAGUGGGAGAGGUAAGG' (SEQ ID NO:1118)	[[], ['GGG'], ['UUAA']]	0.451612903	0.903225806	2	81
'GCAGAGUGGGAGAGGUAAGGCCUCACUAAAC' (SEQ ID NO:1119)	[[], ['GGG'], ['UAAA']]	0.548387097	0.870967742	2	92

FIG. 44 (Cont'd)

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CAGAGUGGGAGAGGUAAGGCCUCACUAAACC' (SEQ ID NO:1120)	[[], ['GGG'], ['UAAA']]	0.548387097	0.870967742	2	93
'GAGUGGGAGAGGUAAGGCCUCACUAAACCAC' (SEQ ID NO:1121)	[[], ['GGG'], ['UAAA']]	0.548387097	0.870967742	2	95
'GGCUUGGGAUCUUUUGCGAUCUGCUCGAGCA' (SEQ ID NO:1122)	[[], ['GGG'], ['UUUU']]	0.548387097	0.870967742	2	238
'GCUUGGGAUCUUUUGCGAUCUGCUCGAGCAG' (SEQ ID NO:1123)	[[], ['GGG'], ['UUUU']]	0.548387097	0.870967742	2	239
'AGAGUGGGAGAGGUAAGGCCUCACUAAACCA' (SEQ ID NO:1124)	[[], ['GGG'], ['UAAA']]	0.516129032	0.870967742	2	94
'CUUUUGCGAUCUGCUCGAGCAGAUUUGGCUG' (SEQ ID NO:1125)	[[], [], ['UUUU', 'AUUU']]	0.516129032	0.870967742	2	248
'GGGGUGAGGAUCUACCUUAAUAUGCAGAGUG' (SEQ ID NO:1126)	[[], ['GGG'], ['UUAA']]	0.483870968	0.870967742	2	69
'GGGUGAGGAUCUACCUUAAUAUGCAGAGUGG' (SEQ ID NO:1127)	[[], ['GGG'], ['UUAA']]	0.483870968	0.870967742	2	70

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GGUGAGGAUCUACCUUAAUAUGCAGAGUGGG' (SEQ ID NO:1128)	[[], ['GGG'], ['UUAA']]	0.483870968	0.870967742	2	71
'GGAUCUACCUUAAUAUGCAGAGUGGGAGAGG' (SEQ ID NO:1129)	[[], ['GGG'], ['UUAA']]	0.483870968	0.870967742	2	76
'ACCUUAAUAUGCAGAGUGGGAGAGGUAAGGC' (SEQ ID NO:1130)	[[], ['GGG'], ['UUAA']]	0.483870968	0.870967742	2	82
'CUUAAUAUGCAGAGUGGGAGAGGUAAGGCCU' (SEQ ID NO:1131)	[[], ['GGG'], ['UUAA']]	0.483870968	0.870967742	2	84
'UUAAUAUGCAGAGUGGGAGAGGUAAGGCCUC' (SEQ ID NO:1132)	[[], ['GGG'], ['UUAA']]	0.483870968	0.870967742	2	85
'UAAUAUGCAGAGUGGGAGAGGUAAGGCCUCA' (SEQ ID NO:1133)	[[], ['GGG'], ['UAAU']]	0.483870968	0.870967742	2	86
'UCUUUUGCGAUCUGCUCGAGCAGAUUUGGCU' (SEQ ID NO:1134)	[[], [], ['UUUU', 'AUUU']]	0.483870968	0.870967742	2	247

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CUGUCCGUGGUGCUGAAGUUUAUUCGGAUUU' (SEQ ID NO:1135)	[[], [], ['UUUA', 'AUUU']]	0.451612903	0.870967742	2	13
'GAAAGGGGUGAGGAUCUACCUUAAUAUGCAG' (SEQ ID NO:1136)	[[], ['GGG'], ['UUAA']]	0.451612903	0.870967742	2	65
'AAGGGGUGAGGAUCUACCUUAAUAUGCAGAG' (SEQ ID NO:1137)	[[], ['GGG'], ['UUAA']]	0.451612903	0.870967742	2	67
'AGGGGUGAGGAUCUACCUUAAUAUGCAGAGU' (SEQ ID NO:1138)	[[], ['GGG'], ['UUAA']]	0.451612903	0.870967742	2	68
'GUGAGGAUCUACCUUAAUAUGCAGAGUGGGA' (SEQ ID NO:1139)	[[], ['GGG'], ['UUAA']]	0.451612903	0.870967742	2	72
'UGAGGAUCUACCUUAAUAUGCAGAGUGGGAG' (SEQ ID NO:1140)	[[], ['GGG'], ['UUAA']]	0.451612903	0.870967742	2	73
'GAGGAUCUACCUUAAUAUGCAGAGUGGGAGA' (SEQ ID NO:1141)	[[], ['GGG'], ['UUAA']]	0.451612903	0.870967742	2	74

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AGGAUCUACCUUAA UAUGCAGAGUGGGA GAG' (SEQ ID NO:1142)	[[], ['GGG'], ['UUAA']]	0.451612903	0.870967742	2	75
'GAUCUACCUUAAUA UGCAGAGUGGGAGA GGU' (SEQ ID NO:1143)	[[], ['GGG'], ['UUAA']]	0.451612903	0.870967742	2	77
'CUACCUUAAUAUGC AGAGUGGGAGAGGU AAG' (SEQ ID NO:1144)	[[], ['GGG'], ['UUAA']]	0.451612903	0.870967742	2	80
'UGUCCGUGGUGCUG AAGUUUAUUCGGAUU UA' (SEQ ID NO:1145)	[[], [], ['UUUA', 'AUUU']]	0.419354839	0.870967742	2	14
'GUCCGUGGUGCUGA AGUUUAUUCGGAUU UAU' (SEQ ID NO:1146)	[[], [], ['UUUA', 'AUUU']]	0.419354839	0.870967742	2	15
'UCUGAAAGGGGUGA GGAUCUACCUUAAUA UG' (SEQ ID NO:1147)	[[], ['GGG'], ['UUAA']]	0.419354839	0.870967742	2	62
'UGAAAGGGGUGAGG AUCUACCUUAAUAUG CA' (SEQ ID NO:1148)	[[], ['GGG'], ['UUAA']]	0.419354839	0.870967742	2	64

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AAAGGGGUGAGGAUCUACCUUAAUAUGCAGA' (SEQ ID NO:1149)	[[], ['GGG'], ['UUAA']]	0.419354839	0.870967742	2	66
'AUCUACCUUAAUAUGCAGAGUGGGAGAGGUA' (SEQ ID NO:1150)	[[], ['GGG'], ['UUAA']]	0.419354839	0.870967742	2	78
'UCUACCUUAAUAUGCAGAGUGGGAGAGGUAA' (SEQ ID NO:1151)	[[], ['GGG'], ['UUAA']]	0.419354839	0.870967742	2	79
'UCCGUGGUGCUGAAGUUUAUUCGGAUUUAUU' (SEQ ID NO:1152)	[[], [], ['UUUA', 'AUUU']]	0.387096774	0.870967742	2	16
'UUUCUGAAAGGGGUGAGGAUCUACCUUAAUA' (SEQ ID NO:1153)	[[], ['GGG'], ['UUAA']]	0.387096774	0.870967742	2	60
'UUCUGAAAGGGGUGAGGAUCUACCUUAAUAU' (SEQ ID NO:1154)	[[], ['GGG'], ['UUAA']]	0.387096774	0.870967742	2	61
'CAAGCUGUGUGACACACCGCAAGGGCUUGGG' (SEQ ID NO:1155)	[[], ['GGG', 'GGG'], []]	0.612903226	0.838709677	2	215

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GACAGGAAGCUGCAGCUCCAGGAGGGUAUUC' (SEQ ID NO:1156)	[[], ['GGG'], ['UAUU']]	0.580645161	0.838709677	2	160
'CAGGAAGCUGCAGCUCCAGGAGGGUAUUCAC' (SEQ ID NO:1157)	[[], ['GGG'], ['UAUU']]	0.580645161	0.838709677	2	162
'AGGAAGCUGCAGCUCCAGGAGGGUAUUCACC' (SEQ ID NO:1158)	[[], ['GGG'], ['UAUU']]	0.580645161	0.838709677	2	163
'GGAAGCUGCAGCUCCAGGAGGGUAUUCACCA' (SEQ ID NO:1159)	[[], ['GGG'], ['UAUU']]	0.580645161	0.838709677	2	164
'GAAGCUGCAGCUCCAGGAGGGUAUUCACCAC' (SEQ ID NO:1160)	[[], ['GGG'], ['UAUU']]	0.580645161	0.838709677	2	165
'AAGCUGCAGCUCCAGGAGGGUAUUCACCACC' (SEQ ID NO:1161)	[[], ['GGG'], ['UAUU']]	0.580645161	0.838709677	2	166

FIG. 44 (Cont'd)

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AAGCUGUGUGACACACCGCAAGGGCUUGGGA' (SEQ ID NO:1162)	[[], ['GGG', 'GGG'], []]	0.580645161	0.838709677	2	216
'GUGGGAGAGGUAAGGCCUCACUAAACCACUC' (SEQ ID NO:1163)	[[], ['GGG'], ['UAAA']]	0.548387097	0.838709677	2	97
'AGACAGGAAGCUGCAGCUCCAGGAGGGUAUU' (SEQ ID NO:1164)	[[], ['GGG'], ['UAUU']]	0.548387097	0.838709677	2	159
'ACAGGAAGCUGCAGCUCCAGGAGGGUAUUCA' (SEQ ID NO:1165)	[[], ['GGG'], ['UAUU']]	0.548387097	0.838709677	2	161
'CCUUAAUAUGCAGAGUGGGAGAGGUAAGGCC' (SEQ ID NO:1166)	[[], ['GGG'], ['UUAA']]	0.516129032	0.838709677	2	83
'AAUAUGCAGAGUGGGAGAGGUAAGGCCUCAC' (SEQ ID NO:1167)	[[], ['GGG'], ['AAUA']]	0.516129032	0.838709677	2	87
'AUAUGCAGAGUGGGAGAGGUAAGGCCUCACU' (SEQ ID NO:1168)	[[], ['GGG'], ['AUAU']]	0.516129032	0.838709677	2	88

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UGCAGAGUGGGAGAGGUAAGGCCUCACUAAA' (SEQ ID NO:1169)	[[], ['GGG'], ['UAAA']]	0.516129032	0.838709677	2	91
'AGUGGGAGAGGUAAGGCCUCACUAAACCACU' (SEQ ID NO:1170)	[[], ['GGG'], ['UAAA']]	0.516129032	0.838709677	2	96
'UGGGAGAGGUAAGGCCUCACUAAACCACUCA' (SEQ ID NO:1171)	[[], ['GGG'], ['UAAA']]	0.516129032	0.838709677	2	98
'GGGAGAGGUAAGGCCUCACUAAACCACUCAU' (SEQ ID NO:1172)	[[], ['GGG'], ['UAAA']]	0.516129032	0.838709677	2	99
'CUUGGGAUCUUUUGCGAUCUGCUCGAGCAGA' (SEQ ID NO:1173)	[[], ['GGG'], ['UUUU']]	0.516129032	0.838709677	2	240
'UUGGGAUCUUUUGCGAUCUGCUCGAGCAGAU' (SEQ ID NO:1174)	[[], ['GGG'], ['UUUU']]	0.483870968	0.838709677	2	241
'UGGGAUCUUUUGCGAUCUGCUCGAGCAGAUU' (SEQ ID NO:1175)	[[], ['GGG'], ['UUUU']]	0.483870968	0.838709677	2	242

FIG. 44 (Cont'd)

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GGAUCUUUUGCGAUCUGCUCGAGCAGAUUUG' (SEQ ID NO:1176)	[[], [], ['UUUU', 'AUUU']]	0.483870968	0.838709677	2	244
'GAUCUUUUGCGAUCUGCUCGAGCAGAUUUGG' (SEQ ID NO:1177)	[[], [], ['UUUU', 'AUUU']]	0.483870968	0.838709677	2	245
'AUCUUUUGCGAUCUGCUCGAGCAGAUUUGGC' (SEQ ID NO:1178)	[[], [], ['UUUU', 'AUUU']]	0.483870968	0.838709677	2	246
'UUUUUCCAACUGCUUUCUGAAAGGGGUGAGG' (SEQ ID NO:1179)	[[], ['GGG'], ['UUUU']]	0.451612903	0.838709677	2	47
'UUUUCCAACUGCUUUCUGAAAGGGGUGAGGA' (SEQ ID NO:1180)	[[], ['GGG'], ['UUUU']]	0.451612903	0.838709677	2	48
'GCUUUCUGAAAGGGGUGAGGAUCUACCUUAA' (SEQ ID NO:1181)	[[], ['GGG'], ['UUAA']]	0.451612903	0.838709677	2	58
'CUGAAAGGGGUGAGGAUCUACCUUAAUAUGC' (SEQ ID NO:1182)	[[], ['GGG'], ['UUAA']]	0.451612903	0.838709677	2	63

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UUUUUUCCAACUGCUUUCUGAAAGGGGUGAG' (SEQ ID NO:1183)	[[], ['GGG'], ['UUUU']]	0.419354839	0.838709677	2	46
'CUUUCUGAAAGGGGUGAGGAUCUACCUUAAU' (SEQ ID NO:1184)	[[], ['GGG'], ['UUAA']]	0.419354839	0.838709677	2	59
'UUUUUUUCCAACUGCUUUCUGAAAGGGGUGA' (SEQ ID NO:1185)	[[], ['GGG'], ['UUUU']]	0.387096774	0.838709677	2	45
'GCUGCAGCUCCAGGAGGGUAUUCACCACCUC' (SEQ ID NO:1186)	[[], ['GGG'], ['UAUU']]	0.612903226	0.806451613	2	168
'GCUGUGUGACACACCGCAAGGGCUUGGGAUC' (SEQ ID NO:1187)	[[], ['GGG', 'GGG'], []]	0.612903226	0.806451613	2	218
'AGCUGCAGCUCCAGGAGGGUAUUCACCACCU' (SEQ ID NO:1188)	[[], ['GGG'], ['UAUU']]	0.580645161	0.806451613	2	167
'CUGCAGCUCCAGGAGGGUAUUCACCACCUCU' (SEQ ID NO:1189)	[[], ['GGG'], ['UAUU']]	0.580645161	0.806451613	2	169

FIG. 44 (Cont'd)

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UGCAGCUCCAGGAGGGUAUUCACCACCUCUC' (SEQ ID NO:1190)	[[], ['GGG'], ['UAUU']]	0.580645161	0.806451613	2	170
'GCAGCUCCAGGAGGGUAUUCACCACCUCUCA' (SEQ ID NO:1191)	[[], ['GGG'], ['UAUU']]	0.580645161	0.806451613	2	171
'CAGCUCCAGGAGGGUAUUCACCACCUCUCAG' (SEQ ID NO:1192)	[[], ['GGG'], ['UAUU']]	0.580645161	0.806451613	2	172
'GCUCCAGGAGGGUAUUCACCACCUCUCAGUG' (SEQ ID NO:1193)	[[], ['GGG'], ['UAUU']]	0.580645161	0.806451613	2	174
'CUCCAGGAGGGUAUUCACCACCUCUCAGUGG' (SEQ ID NO:1194)	[[], ['GGG'], ['UAUU']]	0.580645161	0.806451613	2	175
'UCCAGGAGGGUAUUCACCACCUCUCAGUGGC' (SEQ ID NO:1195)	[[], ['GGG'], ['UAUU']]	0.580645161	0.806451613	2	176
'CCAGGAGGGUAUUCACCACCUCUCAGUGGCA' (SEQ ID NO:1196)	[[], ['GGG'], ['UAUU']]	0.580645161	0.806451613	2	177
'AGCUGUGUGACACACCGCAAGGGCUUGGGAU' (SEQ ID NO:1197)	[[], ['GGG', 'GGG'], []]	0.580645161	0.806451613	2	217

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CUGUGUGACACACCGCAAGGGCUUGGGAUCU' (SEQ ID NO:1198)	[[], ['GGG', 'GGG'], []]	0.580645161	0.806451613	2	219
'CAGGAGGGUAUUCACCACCUCUCAGUGGCAA' (SEQ ID NO:1199)	[[], ['GGG'], ['UAUU']]	0.548387097	0.806451613	2	178
'UGUGUGACACACCGCAAGGGCUUGGGAUCUU' (SEQ ID NO:1200)	[[], ['GGG', 'GGG'], []]	0.548387097	0.806451613	2	220
'GUGUGACACACCGCAAGGGCUUGGGAUCUUU' (SEQ ID NO:1201)	[[], ['GGG', 'GGG'], []]	0.548387097	0.806451613	2	221
'AGCUCCAGGAGGGUAUUCACCACCUCUCAGU' (SEQ ID NO:1202)	[[], ['GGG'], ['UAUU']]	0.548387097	0.774193548	2	173
'GGAGGGUAUUCACCACCUCUCAGUGGCAAUG' (SEQ ID NO:1203)	[[], ['GGG'], ['UAUU']]	0.548387097	0.774193548	2	180
'GAGGGUAUUCACCACCUCUCAGUGGCAAUGC' (SEQ ID NO:1204)	[[], ['GGG'], ['UAUU']]	0.548387097	0.774193548	2	181

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AGGGUAUUCACCACCUCUCAGUGGCAAUGCG' (SEQ ID NO:1205)	[[], ['GGG'], ['UAUU']]	0.548387097	0.774193548	2	182
'GGGUAUUCACCACCUCUCAGUGGCAAUGCGA' (SEQ ID NO:1206)	[[], ['GGG'], ['UAUU']]	0.548387097	0.774193548	2	183
'AGGAGGGUAUUCACCACCUCUCAGUGGCAAU' (SEQ ID NO:1207)	[[], ['GGG'], ['UAUU']]	0.516129032	0.774193548	2	179
'GUGGUGCUGAAGUUUAUUCGGAUUUAUUUUU' (SEQ ID NO:1208)	[[], [], ['UUUA', 'AUUU', 'AUUU']]	0.322580645	0.935483871	3	19
'UGGUGCUGAAGUUUAUUCGGAUUUAUUUUU' (SEQ ID NO:1209)	[[], [], ['UUUA', 'AUUU', 'AUUU']]	0.290322581	0.935483871	3	20
'GGGCUUGGGAUCUUUUGCGAUCUGCUCGAGC' (SEQ ID NO:1210)	[[], ['GGG', 'GGG'], ['UUUU']]	0.580645161	0.903225806	3	237

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'CGUGGUGCUGAAGUUUAUUCGGAUUUAUUUU' (SEQ ID NO:1211)	[[], [], ['UUUA', 'AUUU', 'AUUU']]	0.35483871	0.903225806	3	18
'AUUCGGAUUUAUUUUUUUCCAACUGCUUUCU' (SEQ ID NO:1212)	[[], [], ['AUUU', 'AUUU', 'UUUU']]	0.290322581	0.903225806	3	34
'CCGCAAGGGCUUGGGAUCUUUUGCGAUCUGC' (SEQ ID NO:1213)	[[], ['GGG', 'GGG'], ['UUUU']]	0.580645161	0.870967742	3	231
'CGCAAGGGCUUGGGAUCUUUUGCGAUCUGCU' (SEQ ID NO:1214)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387097	0.870967742	3	232
'GCAAGGGCUUGGGAUCUUUUGCGAUCUGCUC' (SEQ ID NO:1215)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387097	0.870967742	3	233
'CAAGGGCUUGGGAUCUUUUGCGAUCUGCUCG' (SEQ ID NO:1216)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387097	0.870967742	3	234

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AGGGCUUGGGAUCUUUUGCGAUCUGCUCGAG' (SEQ ID NO:1217)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387097	0.870967742	3	236
'CCGUGGUGCUGAAGUUUAUUCGGAUUUAUUU' (SEQ ID NO:1218)	[[], [], ['UUUA', 'AUUU', 'AUUU']]	0.387096774	0.870967742	3	17
'UUCGGAUUUAUUUUUUUCCAACUGCUUUCUG' (SEQ ID NO:1219)	[[], [], ['AUUU', 'AUUU', 'UUUU']]	0.322580645	0.870967742	3	35
'UCGGAUUUAUUUUUUUCCAACUGCUUUCUGA' (SEQ ID NO:1220)	[[], [], ['AUUU', 'AUUU', 'UUUU']]	0.322580645	0.870967742	3	36
'CGGAUUUAUUUUUUUCCAACUGCUUUCUGAA' (SEQ ID NO:1221)	[[], [], ['AUUU', 'AUUU', 'UUUU']]	0.322580645	0.870967742	3	37
'GGAUUUAUUUUUUUCCAACUGCUUUCUGAAA' (SEQ ID NO:1222)	[[], [], ['AUUU', 'AUUU', 'UUUU']]	0.290322581	0.870967742	3	38

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GAUUUAUUUUUUUCCAACUGCUUUCUGAAAG' (SEQ ID NO:1223)	[[], [], ['AUUU', 'AUUU', 'UUUU']]	0.290322581	0.870967742	3	39
'AUUUAUUUUUUUCCAACUGCUUUCUGAAAGG' (SEQ ID NO:1224)	[[], [], ['AUUU', 'AUUU', 'UUUU']]	0.290322581	0.870967742	3	40
'CACCGCAAGGGCUUGGGAUCUUUUGCGAUCU' (SEQ ID NO:1225)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387097	0.838709677	3	229
'ACCGCAAGGGCUUGGGAUCUUUUGCGAUCUG' (SEQ ID NO:1226)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387097	0.838709677	3	230
'AAGGGCUUGGGAUCUUUUGCGAUCUGCUCGA' (SEQ ID NO:1227)	[[], ['GGG', 'GGG'], ['UUUU']]	0.516129032	0.838709677	3	235
'GGGAUCUUUUGCGAUCUGCUCGAGCAGAUUU' (SEQ ID NO:1228)	[[], ['GGG'], ['UUUU', 'AUUU']]	0.483870968	0.838709677	3	243

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'AUUUUUUUCCAACUGCUUUCUGAAAGGGGUG' (SEQ ID NO:1229)	[[], ['GGG'], ['AUUU', 'UUUU']]	0.387096774	0.838709677	3	44
'UUAUUUUUUUCCAACUGCUUUCUGAAAGGGG' (SEQ ID NO:1230)	[[], ['GGG'], ['UUAU', 'UUUU']]	0.35483871	0.838709677	3	42
'UAUUUUUUUCCAACUGCUUUCUGAAAGGGGU' (SEQ ID NO:1231)	[[], ['GGG'], ['UAUU', 'UUUU']]	0.35483871	0.838709677	3	43
'UUUAUUUUUUUCCAACUGCUUUCUGAAAGGG' (SEQ ID NO:1232)	[[], ['GGG'], ['UUUA', 'UUUU']]	0.322580645	0.838709677	3	41
'GACACACCGCAAGGGCUUGGGAUCUUUUGCG' (SEQ ID NO:1233)	[[], ['GGG', 'GGG'], ['UUUU']]	0.580645161	0.806451613	3	225
'GUGACACACCGCAAGGGCUUGGGAUCUUUUUG' (SEQ ID NO:1234)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387097	0.806451613	3	223

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'UGACACACCGCAAGGGCUUGGGAUCUUUUGC' (SEQ ID NO:1235)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387097	0.806451613	3	224
'CACACCGCAAGGGCUUGGGAUCUUUUGCGAU' (SEQ ID NO:1236)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387097	0.806451613	3	227
'ACACCGCAAGGGCUUGGGAUCUUUUGCGAUC' (SEQ ID NO:1237)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387097	0.806451613	3	228
'UGUGACACACCGCAAGGGCUUGGGAUCUUUU' (SEQ ID NO:1238)	[[], ['GGG', 'GGG'], ['UUUU']]	0.516129032	0.806451613	3	222
'ACACACCGCAAGGGCUUGGGAUCUUUUGCGA' (SEQ ID NO:1239)	[[], ['GGG', 'GGG'], ['UUUU']]	0.548387097	0.774193548	3	226
'GGUGCUGAAGUUUAUUCGGAUUUAUUUUUUU' (SEQ ID NO:1240)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.290322581	0.935483871	4	21

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GUGCUGAAGUUUAUUCGGAUUUAUUUUUUUC' (SEQ ID NO:1241)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.290322581	0.903225806	4	22
'UAUUCGGAUUUAUUUUUUCCAACUGCUUUC' (SEQ ID NO:1242)	[[], [], ['UAUU', 'AUUU', 'AUUU', 'UUUU']]	0.290322581	0.903225806	4	33
'UUUAUUCGGAUUUAUUUUUUUCCAACUGCUU' (SEQ ID NO:1243)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.258064516	0.903225806	4	31
'UUAUUCGGAUUUAUUUUUUCCAACUGCUUU' (SEQ ID NO:1244)	[[], [], ['UUAU', 'AUUU', 'AUUU', 'UUUU']]	0.258064516	0.903225806	4	32
'UGCUGAAGUUUAUUCGGAUUUAUUUUUUUCC' (SEQ ID NO:1245)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.290322581	0.870967742	4	23

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GCUGAAGUUUAUUCGGAUUUAUUUUUUUCCA' (SEQ ID NO:1246)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.290322581	0.870967742	4	24
'AGUUUAUUCGGAUUUAUUUUUUUCCAACUGC' (SEQ ID NO:1247)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.290322581	0.870967742	4	29
'GUUUAUUCGGAUUUAUUUUUUUCCAACUGCU' (SEQ ID NO:1248)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.290322581	0.870967742	4	30
'CUGAAGUUUAUUCGGAUUUAUUUUUUUCCAA' (SEQ ID NO:1249)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.258064516	0.870967742	4	25
'UGAAGUUUAUUCGGAUUUAUUUUUUUCCAAC' (SEQ ID NO:1250)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.258064516	0.870967742	4	26

FIG. 44 (Cont'd)

SEQUENCE	BS	GCNESS	3LN	NBP	P
'GAAGUUUAUUCGGAUUUAUUUUUUUCCAACU' (SEQ ID NO:1251)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.258064516	0.870967742	4	27
'AAGUUUAUUCGGAUUUAUUUUUUUCCAACUG' (SEQ ID NO:1252)	[[], [], ['UUUA', 'AUUU', 'AUUU', 'UUUU']]	0.258064516	0.870967742	4	28

FIG. 44 (Cont'd)

FIG. 45

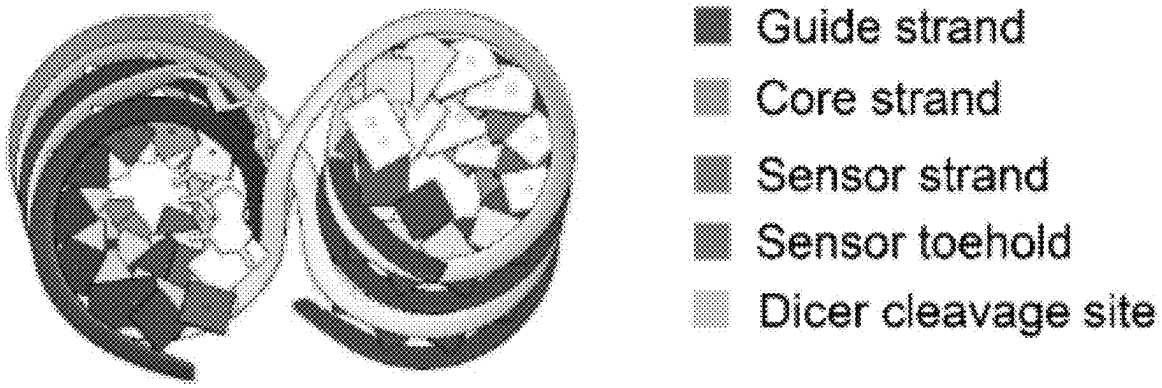

Guide strand
Core strand
Sensor strand
Sensor toehold
Dicer cleavage site

FIG. 46

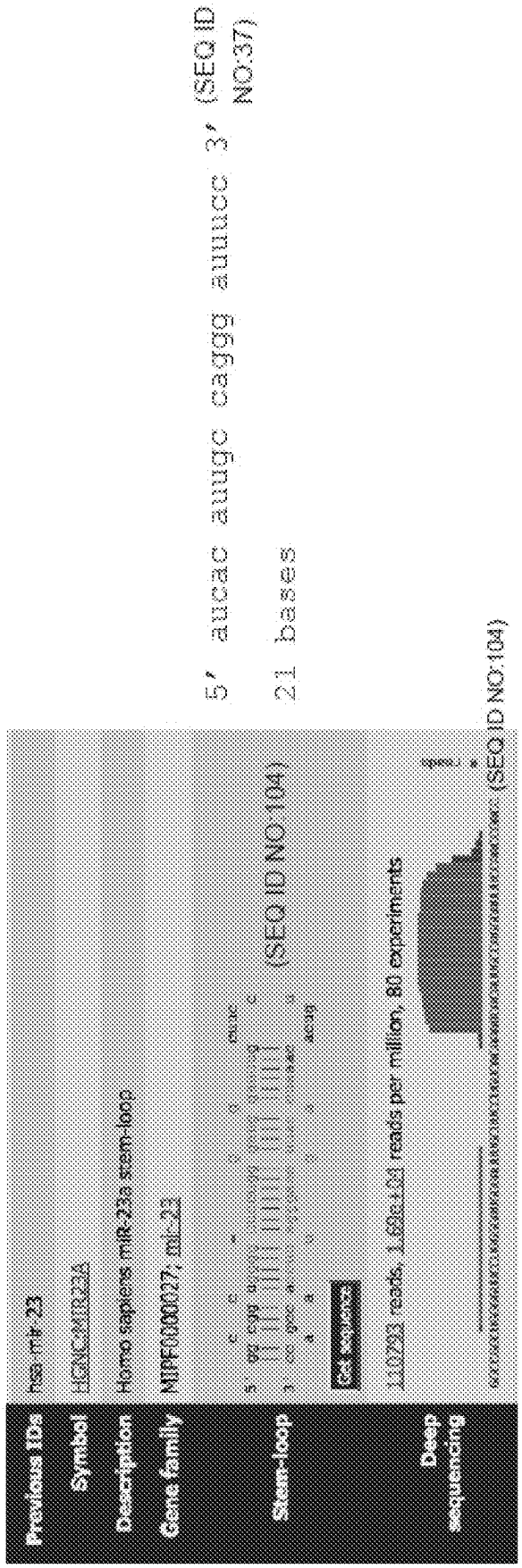
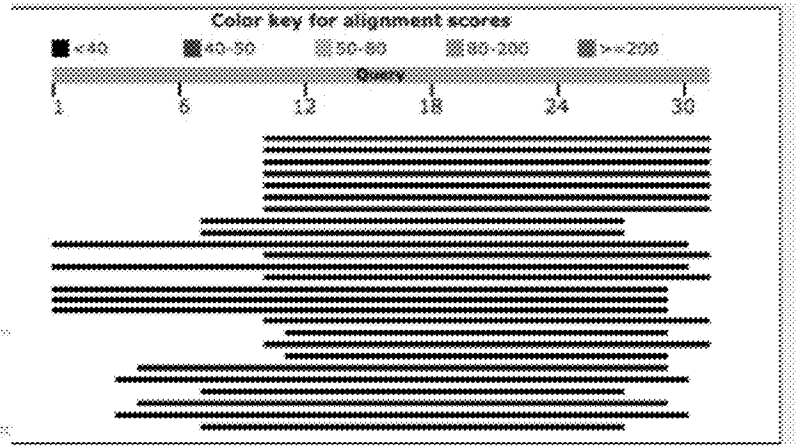

Previous IDs
hsa-mir-23
Symbol
HGNC:MIR23A
Description
Homo sapiens miR-23a stem-loop
Gene family
MIPF0000027, mi-23
Stem-loop
(SEQ ID NO:104)
Cel browser
Deep sequencing
110293 reads, 1.69e+03 reads per million, 80 experiments
(SEQ ID NO:104)
5' aucac auugc caggg auuucc 3' (SEQ ID NO:37)
21 bases

FIG. 47

NCBI Check for sensor strand

- miR-23a-3p match and match of primary concern:
  - https://blast.ncbi.nlm.nih.gov/Blast.cgi



Homo sapiens microRNA 23a (MIR23A), microRNA
Sequence ID: NR_029486.1 Length: 73 Number of Matches: 1

Range 1: 45 to 65 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
39.2 bits(42)	0.045	21/21(100%)	0/21(0%)	Plus/Minus

Query 11 GGAAATCCCTGGCAATGTGAT 31
Sbjct 65 GGAAATCCCTGGCAATGTGAT 45

SEQ ID NO:105

Download GenBank Graphics

PREDICTED: Homo sapiens chromosome 9 open reading frame 3 (C9orf3), transcript variant X30, mRNA
Sequence ID: XM_017015237.1 Length: 6723 Number of Matches: 1

Range 1: 4829 to 4849 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
33.7 bits(36)	1.9	20/21(95%)	0/21(0%)	Plus/Minus

Query 11 GGAAATCCCTGGCAATGTGAT 31 SEQ ID NO:105
Sbjct 4849 GGTAATCCCTGGCAATGTGAT 4829 SEQ ID NO:106

FIG. 48

- Calcineurin (PPP3CA) guide check: 5′ CGAG **UGUUG UUUGG CUUUU CCUG UU** 3′ (SEQ ID NO:11)

https://blast.ncbi.nlm.nih.gov/Blast.cgi

Homo sapiens protein phosphatase 3 catalytic subunit alpha (PPP3CA), transcript variant 3, mRNA

Sequence ID: NM_001130692.1 Length: 4520 Number of Matches: 1

Range 1: 1547 to 1566 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
40.1 bits(20)	0.040	20/20(100%)	0/20(0%)	Plus/Minus

```
Query  5     TGTTGTTTGGCTTTTCCTGT  24
             ||||||||||||||||||||
Sbjct  1566  TGTTGTTTGGCTTTTCCTGT  1547
```

(SEQ ID NO:107)

- HDAC2 check guide: 5′ GC ACUUA GAUUG AAACA ACCCA GUU 3′ (25 bp) (SEQ ID NO: 13)

https://blast.ncbi.nlm.nih.gov/Blast.cgi

PREDICTED: Homo sapiens histone deacetylase 2 (HDAC2), transcript variant X2, mRNA

Sequence ID: XM_017010799.1 Length: 2072 Number of Matches: 1

Range 1: 1074 to 1093 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
40.1 bits(20)	0.040	20/20(100%)	0/20(0%)	Plus/Minus

```
Query  5     TTAGATTGAAACAACCCAGT  24
             ||||||||||||||||||||
Sbjct  1093  TTAGATTGAAACAACCCAGT  1074
```

(SEQ ID NO: 108)

FIG. 49

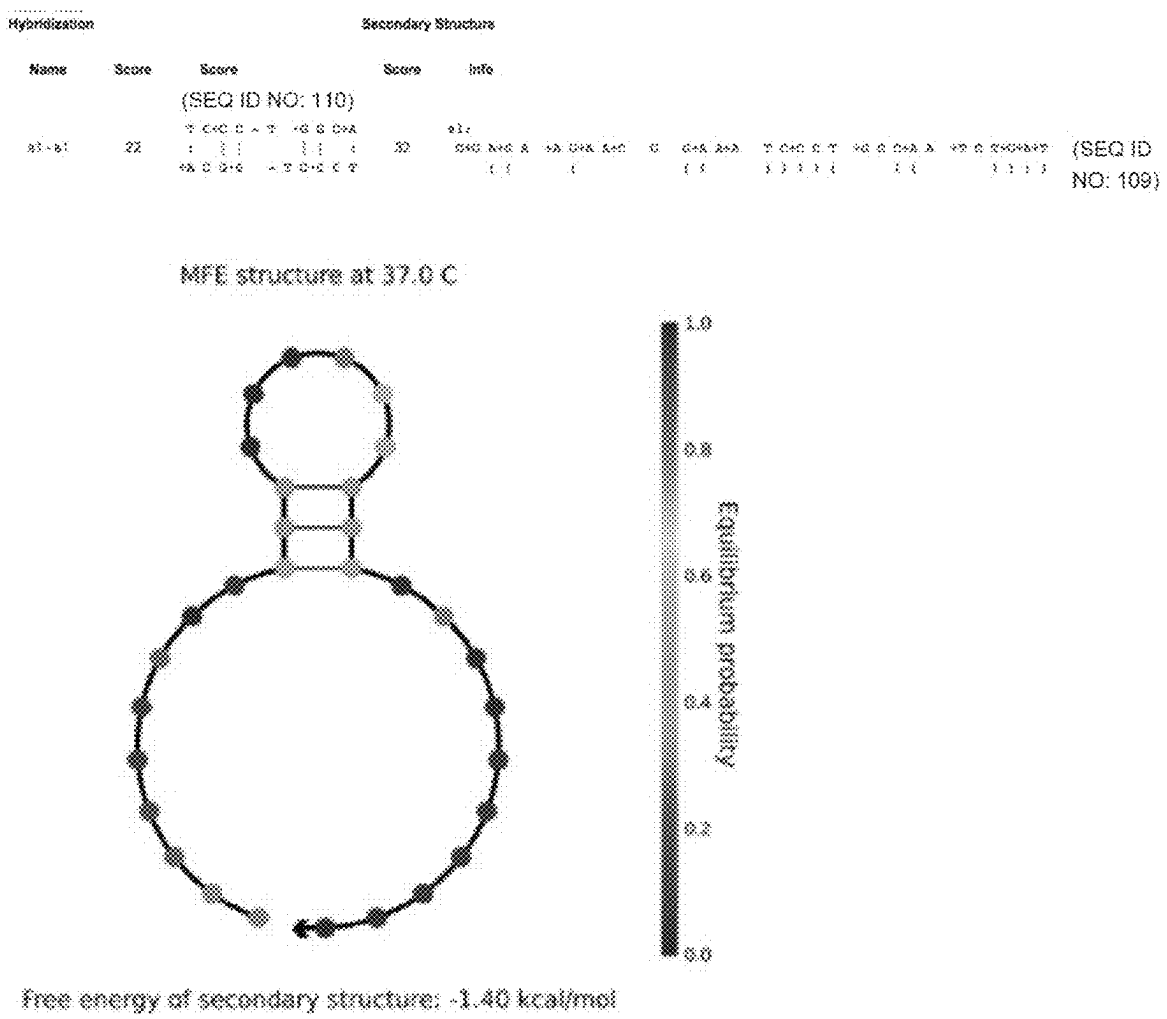
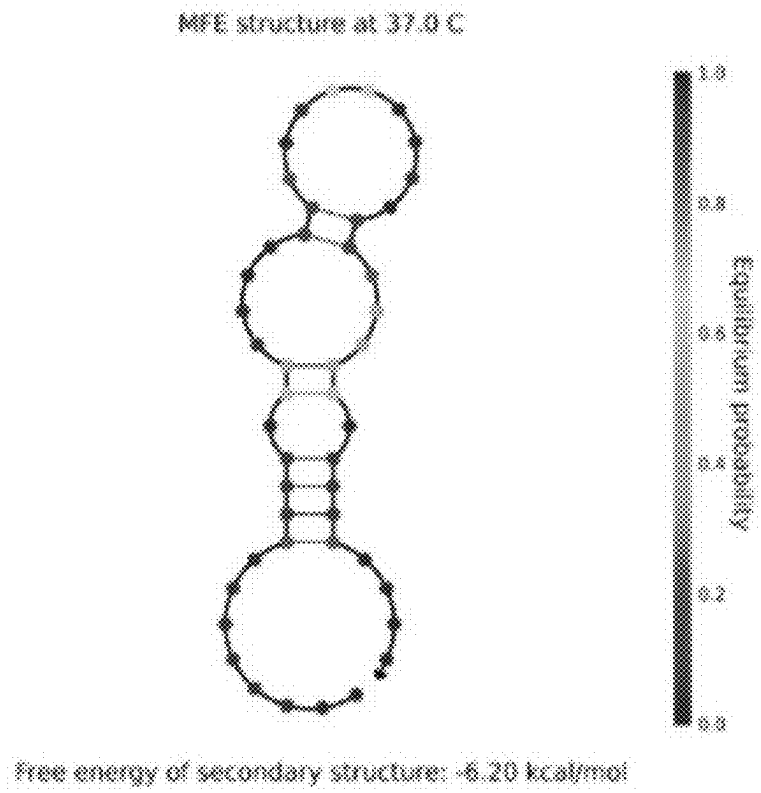
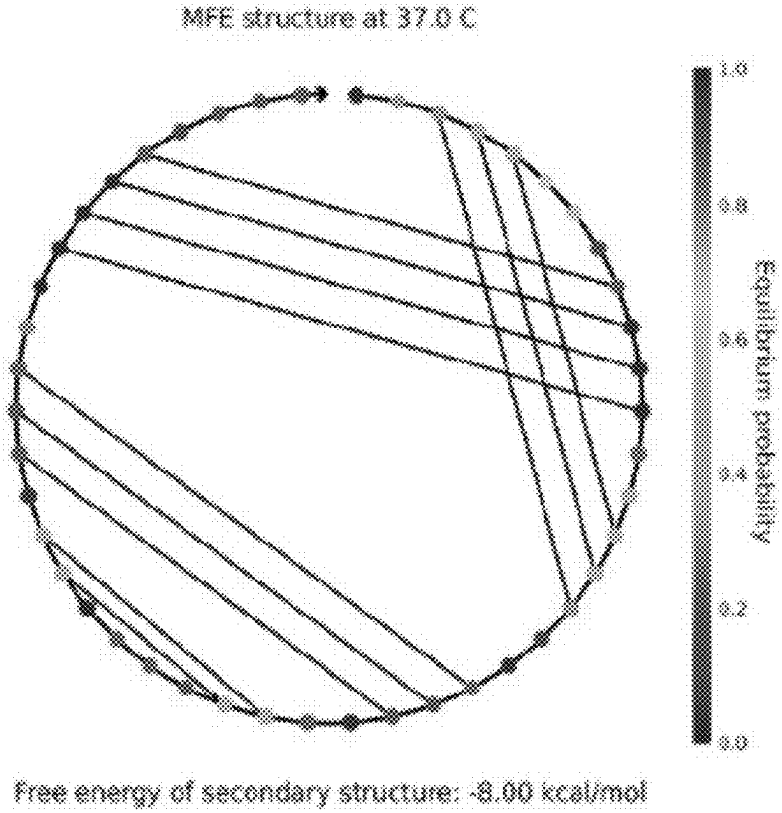

Hybridization
Secondary Structure
Name
Score
Score
Score
Info
(SEQ ID NO: 110)
22
32
(SEQ ID NO: 109)
MFE structure at 37.0 C
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: -1.40 kcal/mol

FIG. 50A


MFE structure at 37.0 C
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: -6.20 kcal/mol


MFE structure at 37.0 C
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: -8.00 kcal/mol

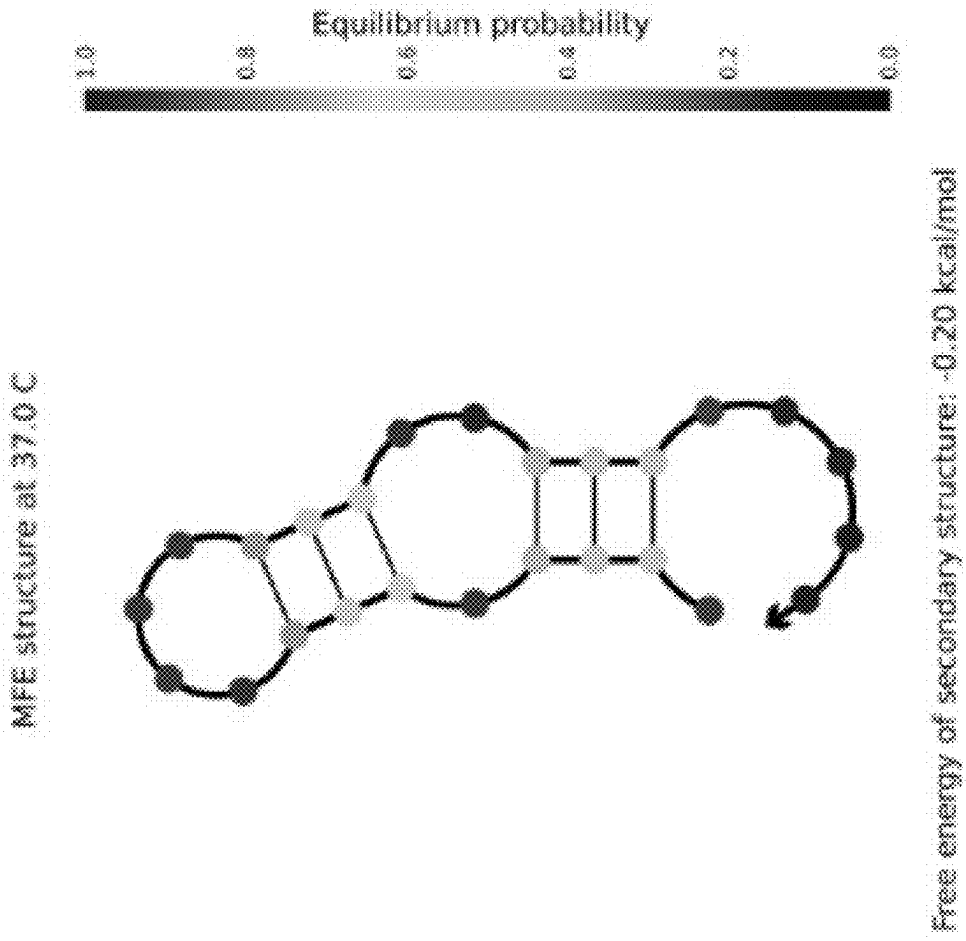

MFE structure at 37.0 C
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: -0.20 kcal/mol

FIG. 50B

FIG. 50C

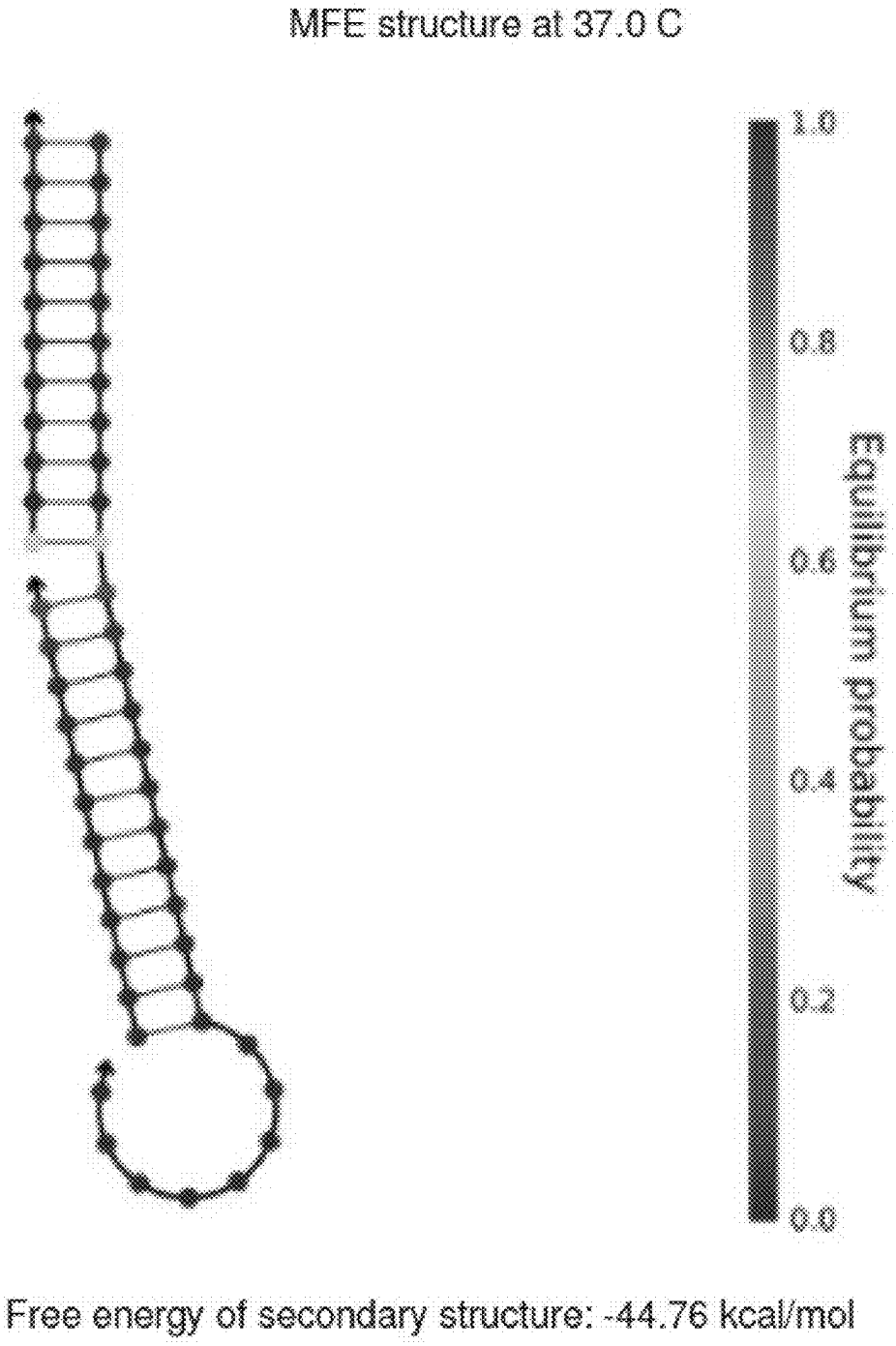

MFE structure at 37.0 C
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: -44.76 kcal/mol

FIG. 50D

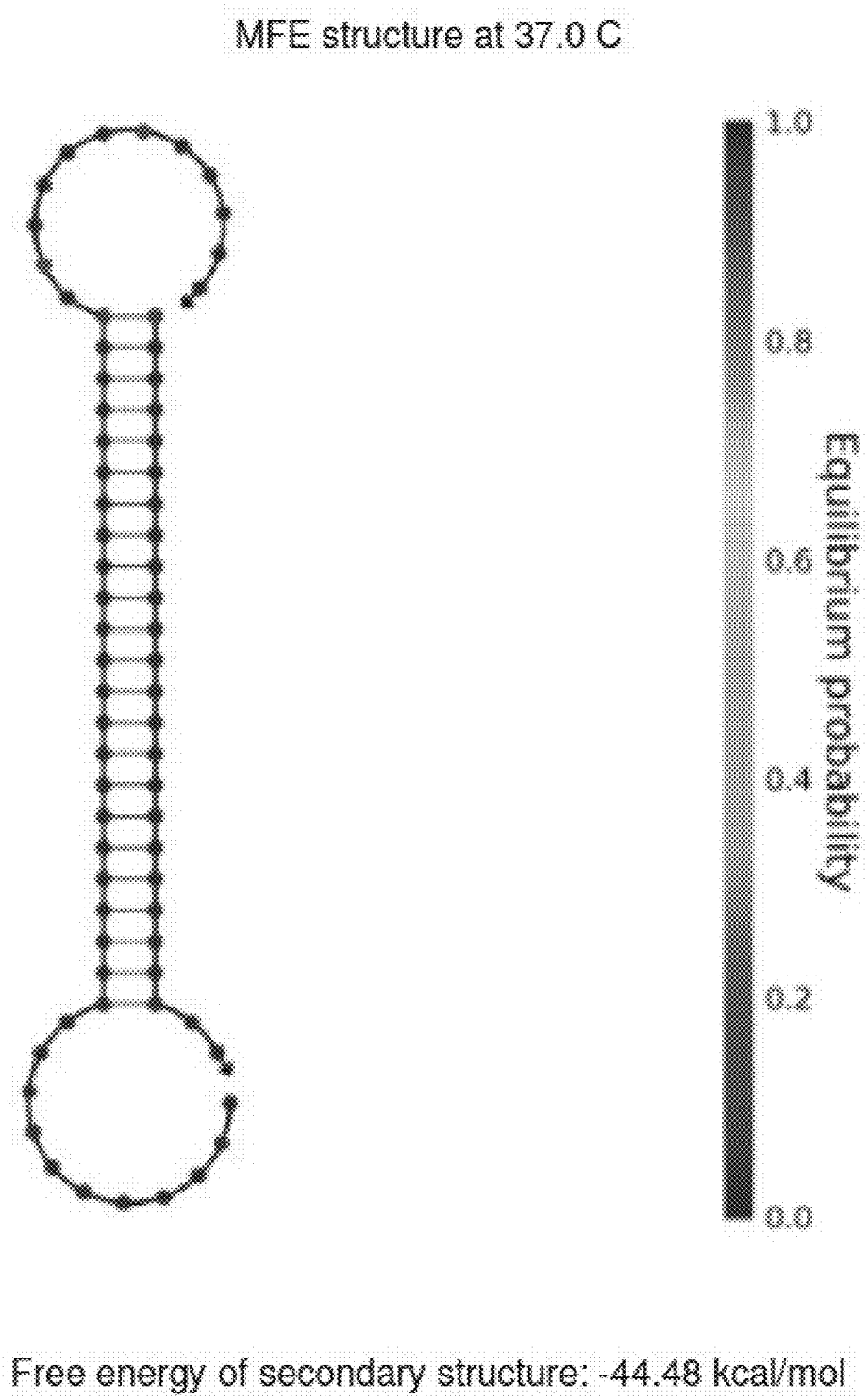

MFE structure at 37.0 C
1.0
0.8
0.6
0.4
0.2
0.0
Equilibrium probability
Free energy of secondary structure: -44.48 kcal/mol

FIG. 51

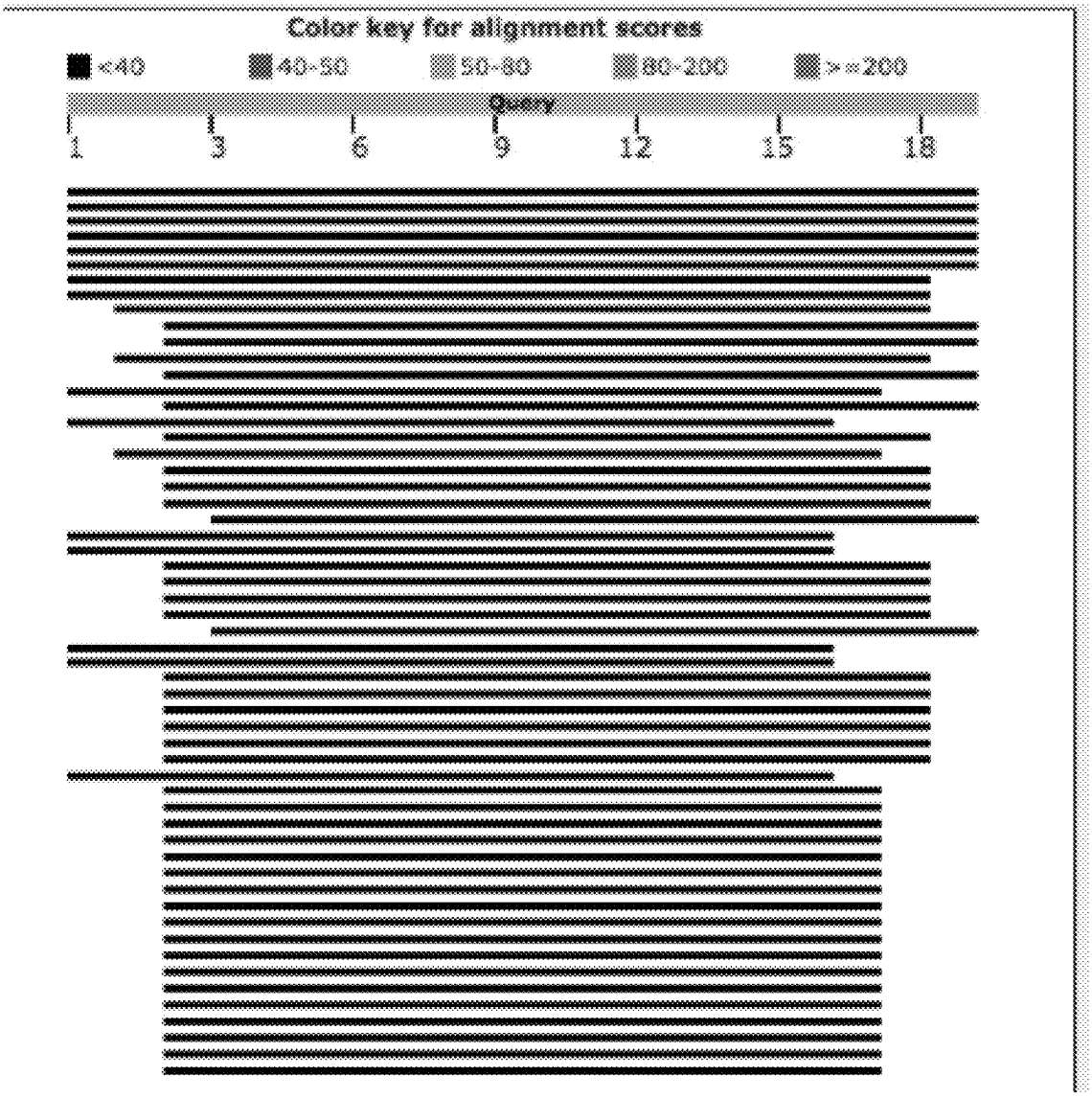

Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
3
6
9
12
15
18

FIG. 52A

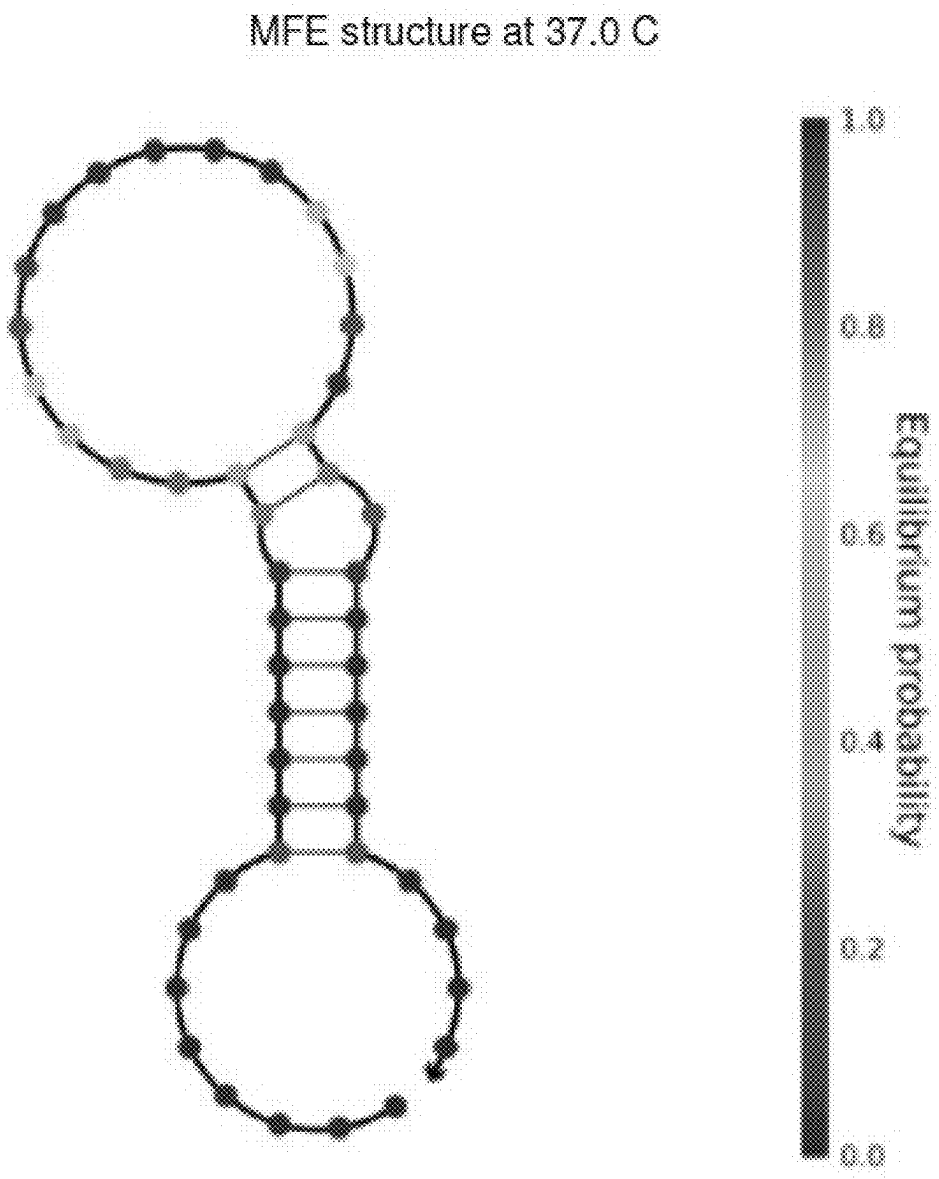

MFE structure at 37.0 C
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: -12.60 kcal/mol

FIG. 52B

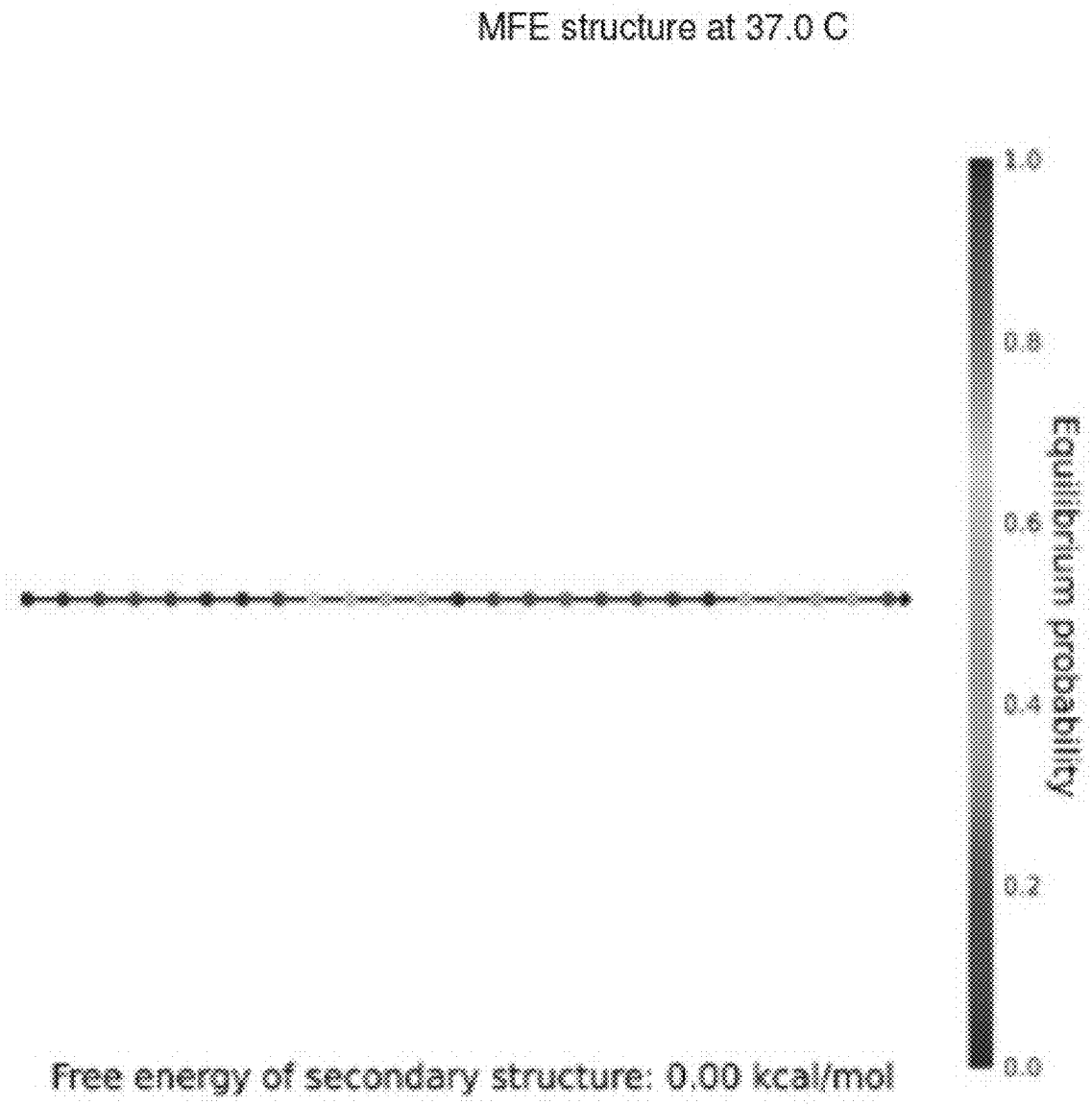

MFE structure at 37.0 C
Free energy of secondary structure: 0.00 kcal/mol
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0

FIG. 52C

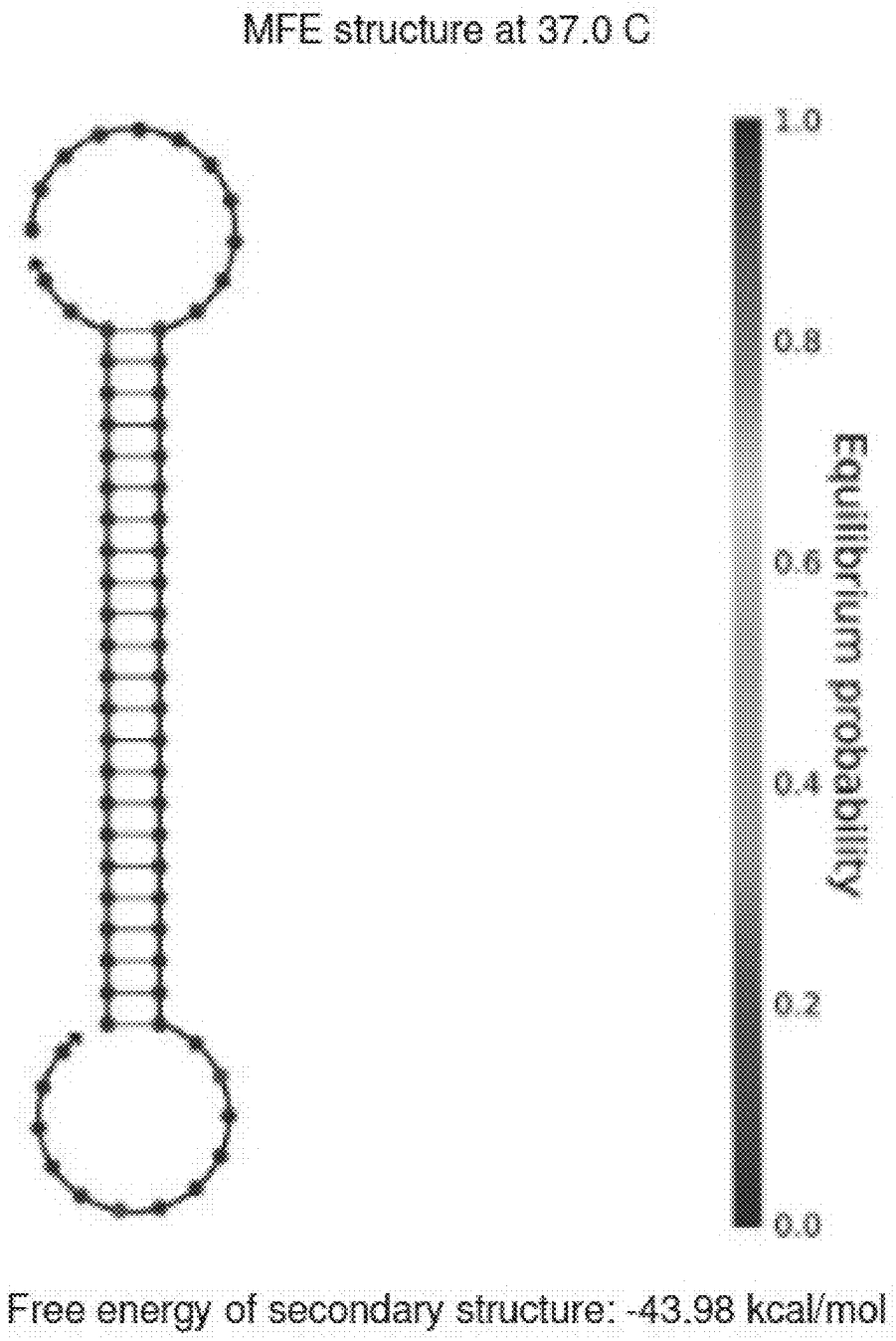

MFE structure at 37.0 C
1.0
0.8
0.6
0.4
0.2
0.0
Equilibrium probability
Free energy of secondary structure: -43.98 kcal/mol

FIG. 52D

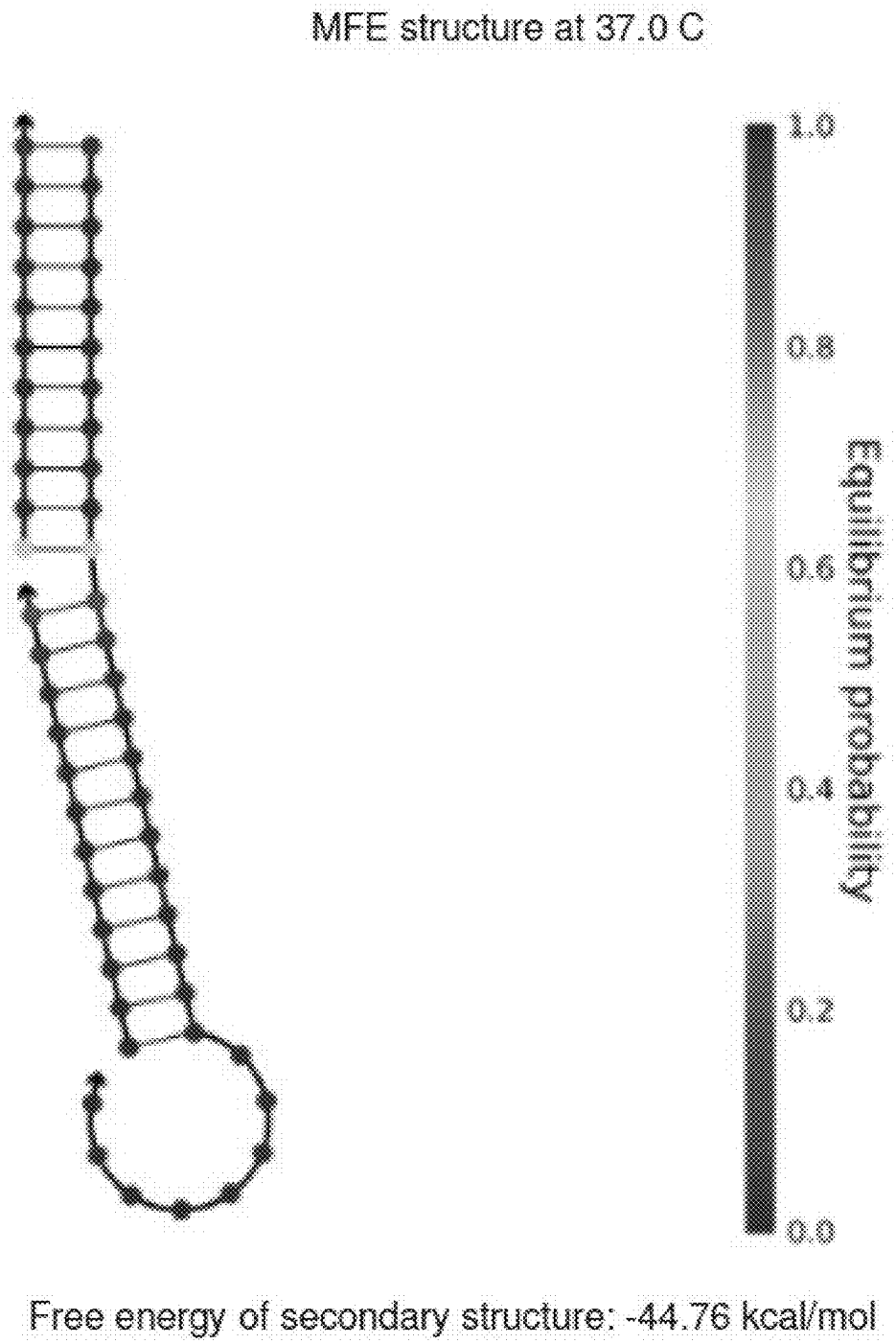

MFE structure at 37.0 C
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: -44.76 kcal/mol

FIG. 53

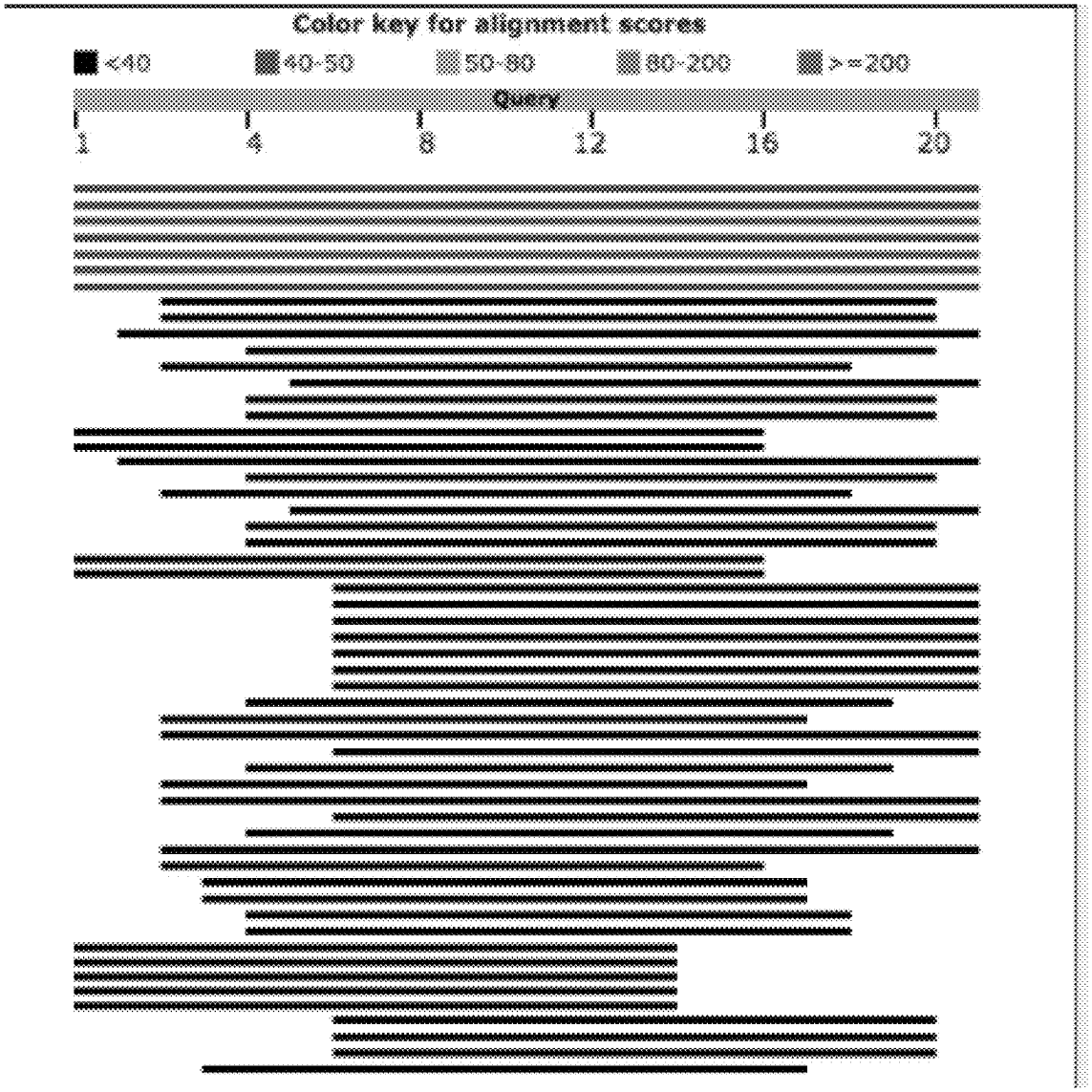

Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
4
8
12
16
20

FIG. 54A

PREDICTED: Homo sapiens lysine acetyltransferase 2A (KAT2A), transcript variant X1, mRNA
Sequence ID: XM_0267219113.3 Length: 3143 Number of Matches: 1

Range 1: 956 to 972 Graphics Graphics

Score	Expect	Identities	Gaps	Strand
26.3 bits(13)	596	16/17(94%)	0/17(0%)	Plus/Minus

Query 5 ATCTCCTCTTATTCCTC 21 SEQ ID NO:113
Sbjct 972 ATCTCCTCTTATTCCAC 956 SEQ ID NO:114

Download Gene Back Graphics

PREDICTED: Homo sapiens lysophosphatidylcholine acyltransferase 2 (LPCAT2), transcript variant X1, mRNA
Sequence ID: XM_017022375.1 Length: 5358 Number of Matches: 1

Range 1: 271 to 283 Graphics Graphics

Score	Expect	Identities	Gaps	Strand
26.3 bits(13)	596	13/13(100%)	0/13(0%)	Plus/Minus

Query 5 ATCTCCTCTTATT 17 SEQ ID NO:115
Sbjct 283 ATCTCCTCTTATT 271

PREDICTED: Homo sapiens synaptonemal complex protein 2 (SYCP2), transcript variant X1, mRNA
Sequence ID: XM_017027566.1 Length: 6093 Number of Matches: 1

Range 1: 450 to 466 Graphics Graphics

Score	Expect	Identities	Gaps	Strand
26.3 bits(13)	596	16/17(94%)	0/17(0%)	Plus/Minus

Query 2 GAGATCTCCTCTTATTC 18 SEQ ID NO:116
Sbjct 466 GAGATCTCCACCTTATTC 450 SEQ ID NO:117

Homo sapiens ADAM metallopeptidase with thrombospondin type 1 motif 12 (ADAMTS12), mRNA
Sequence ID: NM_030955.2 Length: 4955 Number of Matches: 1

Range 1: 3762 to 3775 Graphics Graphics

Score	Expect	Identities	Gaps	Strand
28.2 bits(14)	151	14/14(100%)	0/14(0%)	Plus/Minus

Query 2 GAGATCTCCTCTTA 15
Sbjct 3775 GAGATCTCCTCTTA 3762 SEQ ID NO:118

PREDICTED: Homo sapiens acetyl-CoA carboxylase beta (ACACB), transcript variant X3, mRNA
Sequence ID: XM_011538203.2 Length: 8808 Number of Matches: 1

Range 1: 5307 to 5319 Graphics Graphics

Score	Expect	Identities	Gaps	Strand
26.3 bits(13)	596	13/13(100%)	0/13(0%)	Plus/Minus

Query 7 CTCCTCTTATTCC 19
Sbjct 5319 CTCCTCTTATTCC 5307 SEQ ID NO:119

Download Gene Back Graphics

PREDICTED: Homo sapiens uncharacterized LOC105370511 (LOC105370511), ncRNA
Sequence ID: XR_312832.2 Length: 623 Number of Matches: 1

Range 1: 211 to 224 Graphics Graphics

Score	Expect	Identities	Gaps	Strand
28.2 bits(14)	151	14/14(100%)	0/14(0%)	Plus/Minus

Query 8 CCTCTCCTCTTATT 17
Sbjct 224 CCTCTCCTCTTATT 211 SEQ ID NO:120

FIG. 54B

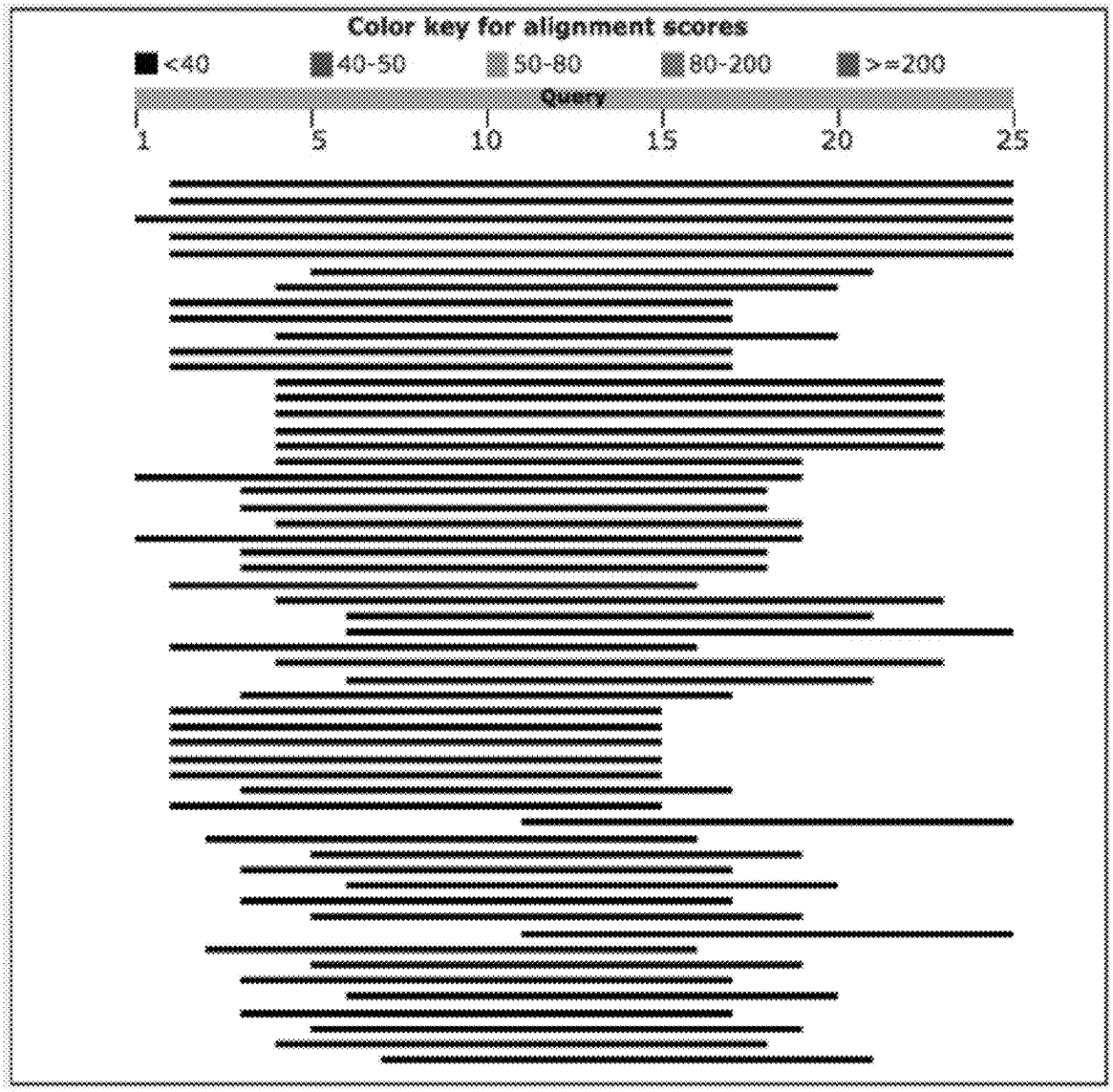

Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
5
10
15
20
25

FIG. 55

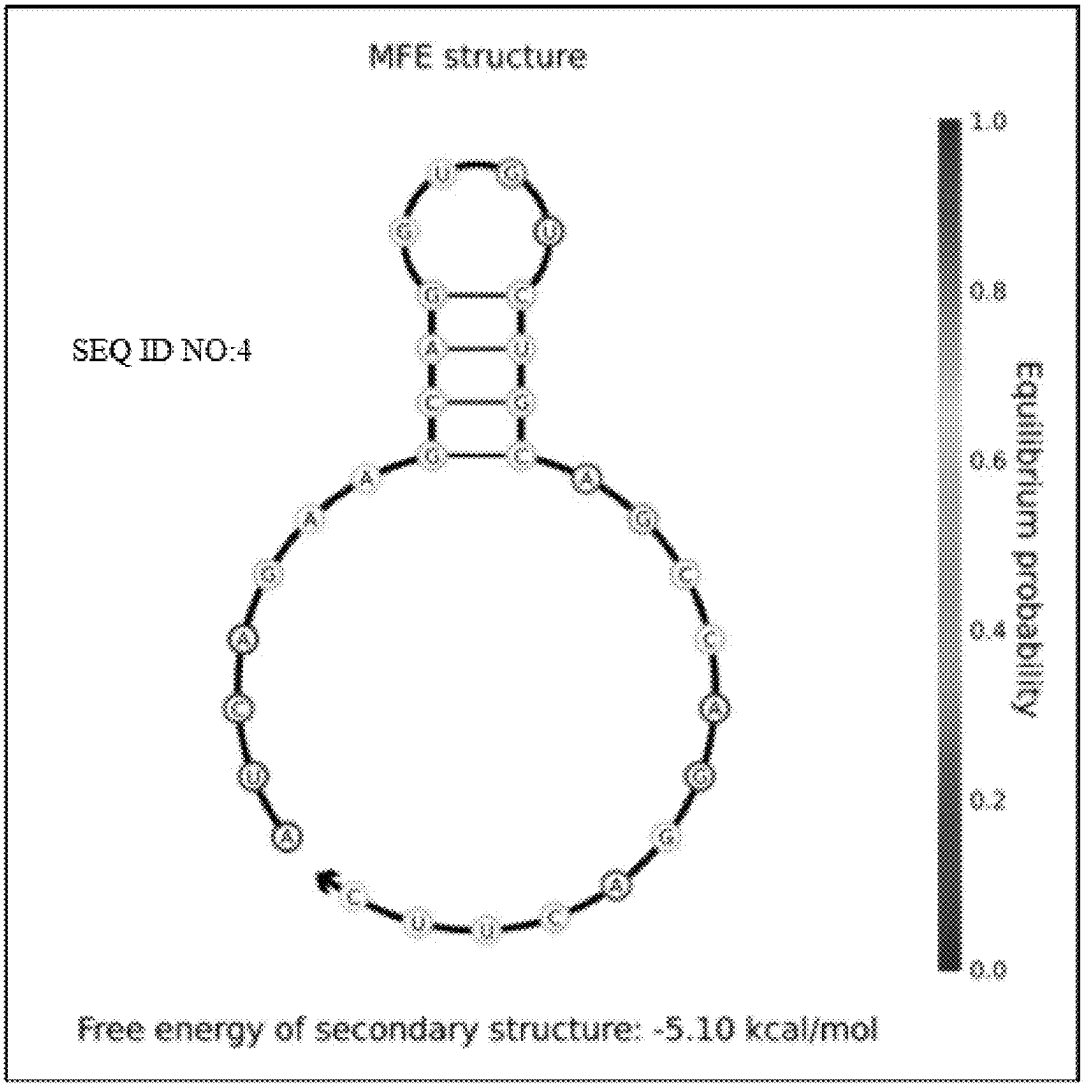

MFE structure
SEQ ID NO:4
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: -5.10 kcal/mol

FIG. 56

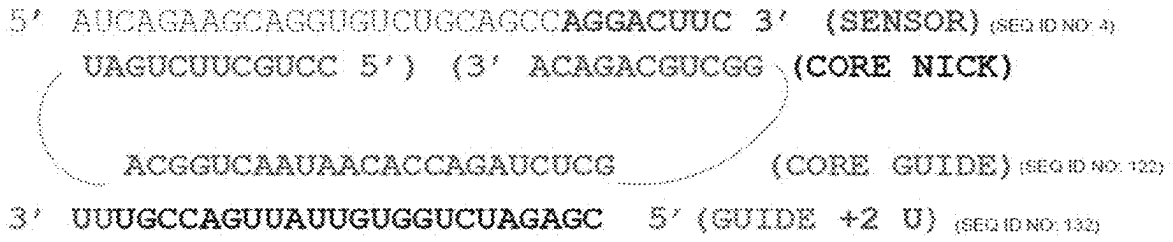
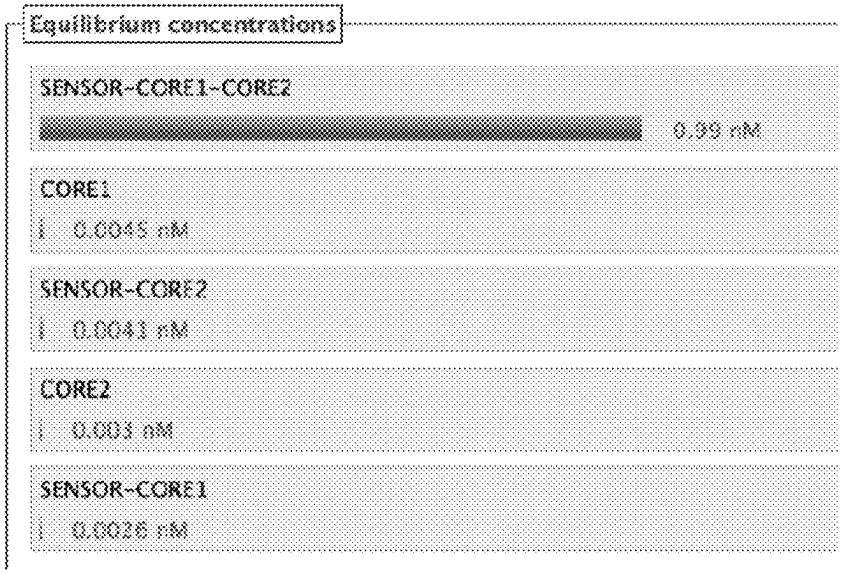
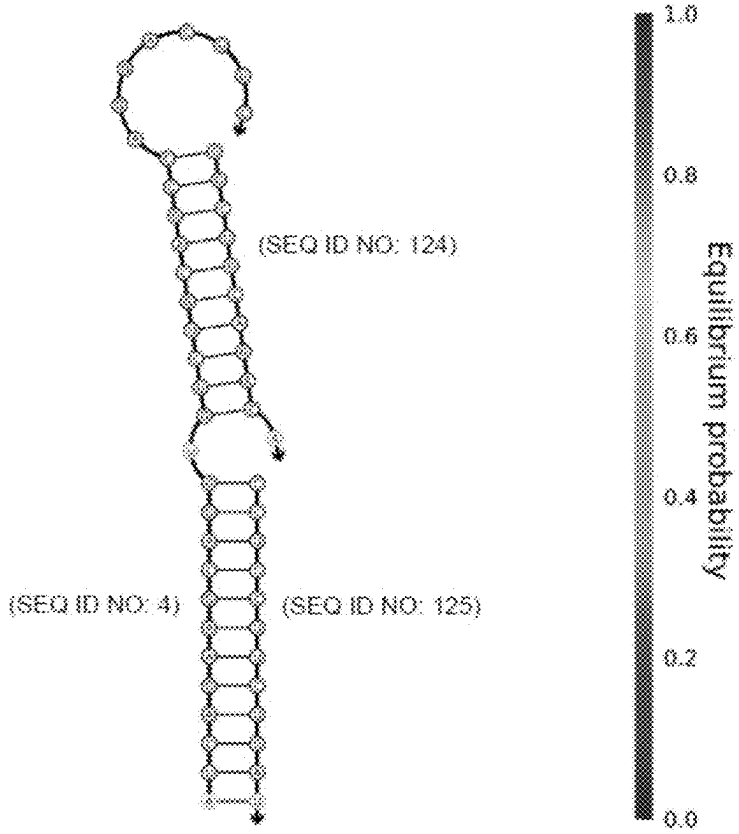

5′ AUCAGAAGCAGGUGUCUGCAGCCAGGACUUC 3′ (SENSOR) (SEQ ID NO: 4)
UAGUCUUCGUCC 5′) (3′ ACAGACGUCGG (CORE NICK)
ACGGUCAAUAACACCAGAUCUCG (CORE GUIDE) (SEQ ID NO: 122)
3′ UUUGCCAGUUAUUGUGGUCUAGAGC 5′ (GUIDE +2 U) (SEQ ID NO: 133)

FIG. 57A

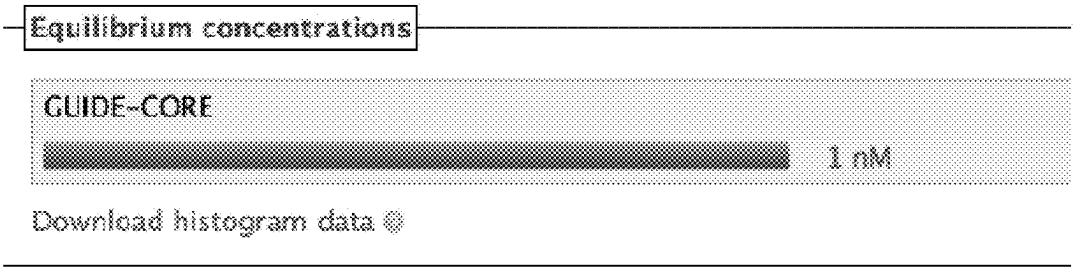


SENSOR WITH CORE OVERHANGS



Free energy of secondary structure: -47.36 kcal/mol

FIG. 57B


Equilibrium concentrations
GUIDE-CORE
1 nM
Download histogram data

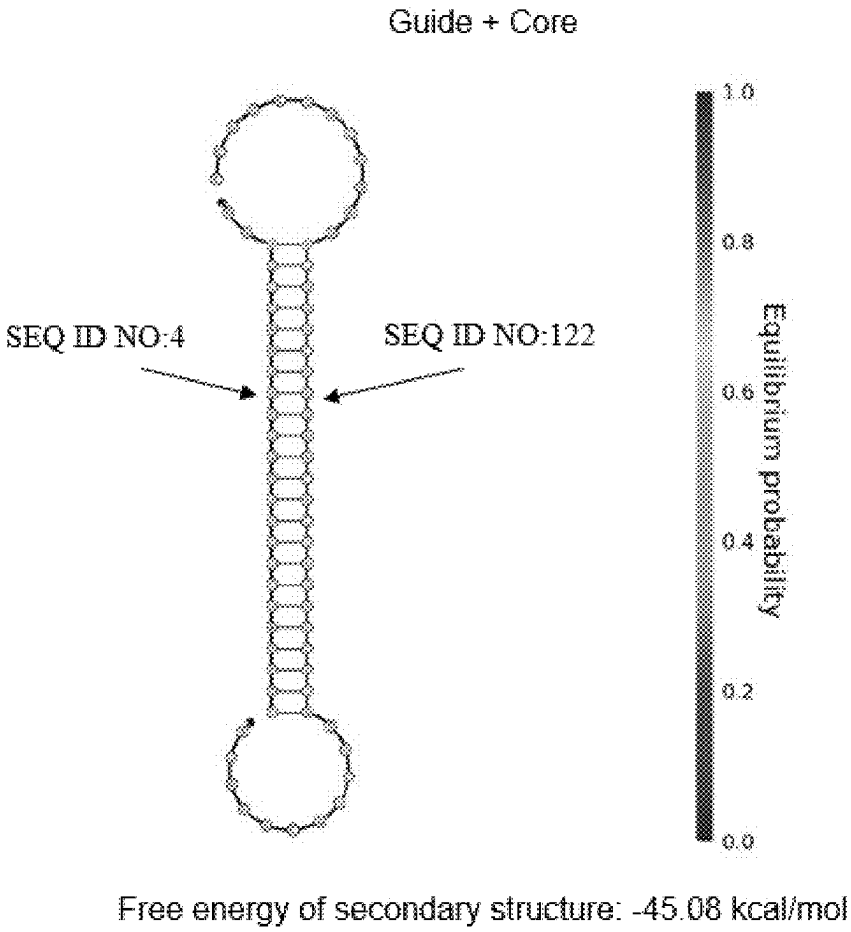

Guide + Core
SEQ ID NO:4
SEQ ID NO:122
1.0
0.8
0.6
0.4
0.2
0.0
Equilibrium probability
Free energy of secondary structure: -45.08 kcal/mol

FIG. 58

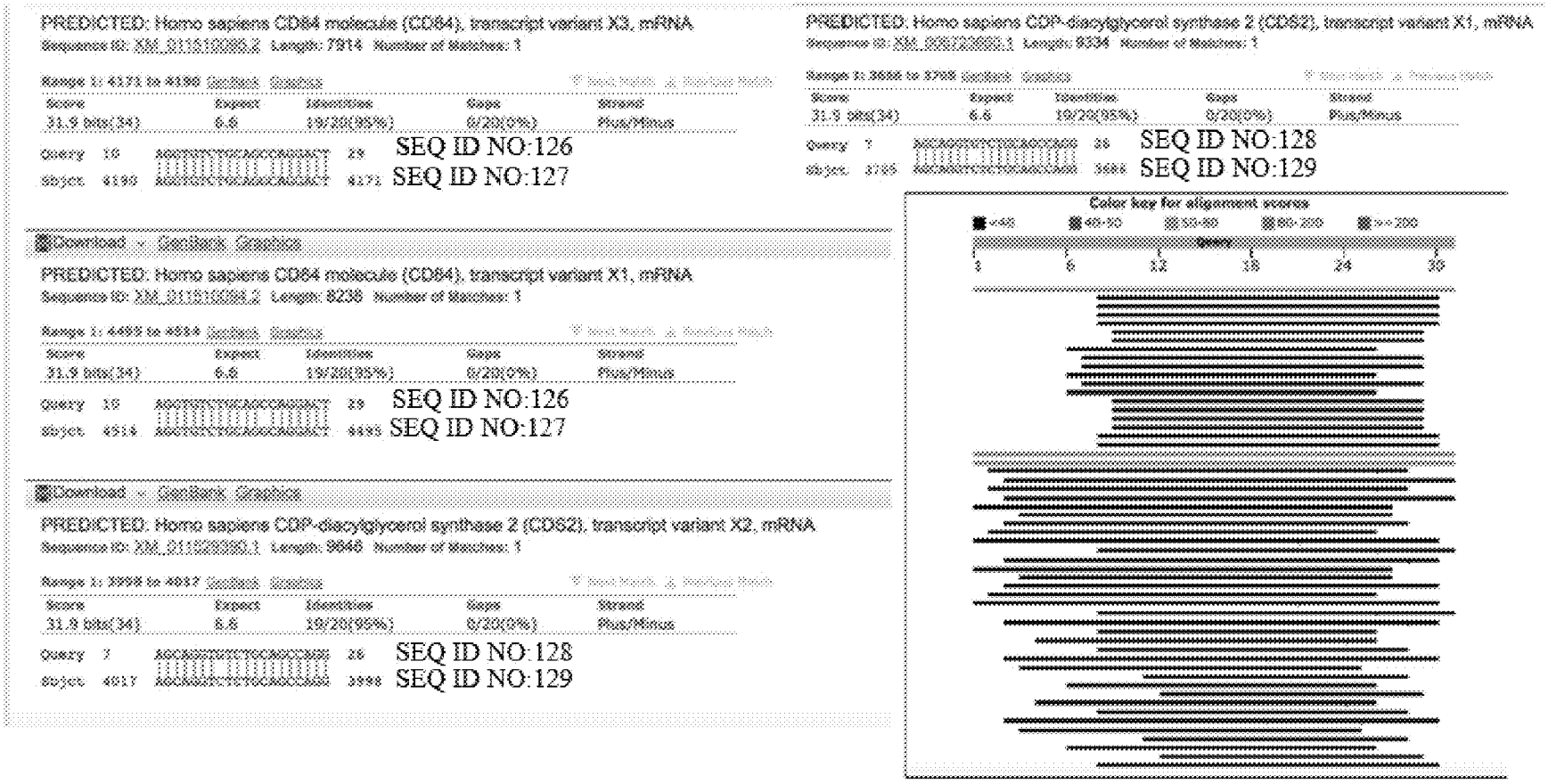

PREDICTED: Homo sapiens CD84 molecule (CD84), transcript variant X3, mRNA
Sequence ID: XM_011510285.2 Length: 7914 Number of Matches: 1
Range 1: 4171 to 4190 GenBank Graphics
Score Expect Identities Gaps Strand
31.9 bits(34) 6.6 19/20(95%) 0/20(0%) Plus/Minus
Query 10 29
Sbjct 4190 4171
SEQ ID NO:126
SEQ ID NO:127
PREDICTED: Homo sapiens CDP-diacylglycerol synthase 2 (CDS2), transcript variant X1, mRNA
Sequence ID: XM_005272600.1 Length: 9334 Number of Matches: 1
Range 1: 3698 to 3718 GenBank Graphics
Score Expect Identities Gaps Strand
31.9 bits(34) 6.6 19/20(95%) 0/20(0%) Plus/Minus
Query 7 26
Sbjct 3718 3698
SEQ ID NO:128
SEQ ID NO:129
Download GenBank Graphics
PREDICTED: Homo sapiens CD84 molecule (CD84), transcript variant X1, mRNA
Sequence ID: XM_011510284.2 Length: 8238 Number of Matches: 1
Range 1: 4493 to 4514 GenBank Graphics
Score Expect Identities Gaps Strand
31.9 bits(34) 6.6 19/20(95%) 0/20(0%) Plus/Minus
Query 10 29
Sbjct 4514 4493
SEQ ID NO:126
SEQ ID NO:127
Download GenBank Graphics
PREDICTED: Homo sapiens CDP-diacylglycerol synthase 2 (CDS2), transcript variant X2, mRNA
Sequence ID: XM_011526393.1 Length: 9846 Number of Matches: 1
Range 1: 3998 to 4017 GenBank Graphics
Score Expect Identities Gaps Strand
31.9 bits(34) 6.6 19/20(95%) 0/20(0%) Plus/Minus
Query 7 26
Sbjct 4017 3998
SEQ ID NO:128
SEQ ID NO:129
Color key for alignment scores
<40 40-50 50-80 80-200 >= 200
Score
1 6 12 18 24 30

FIG. 59

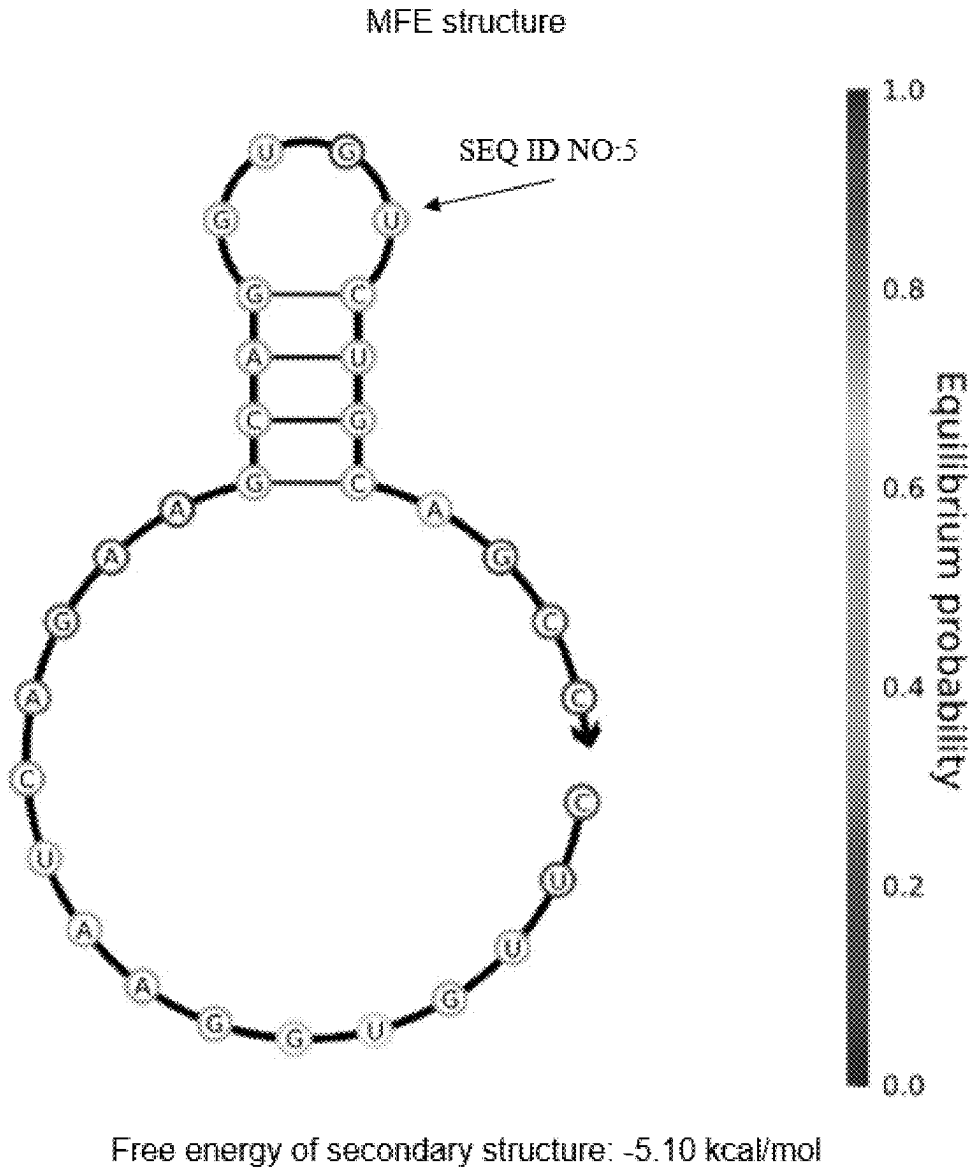

MFE structure
SEQ ID NO:5
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: -5.10 kcal/mol

FIG. 60

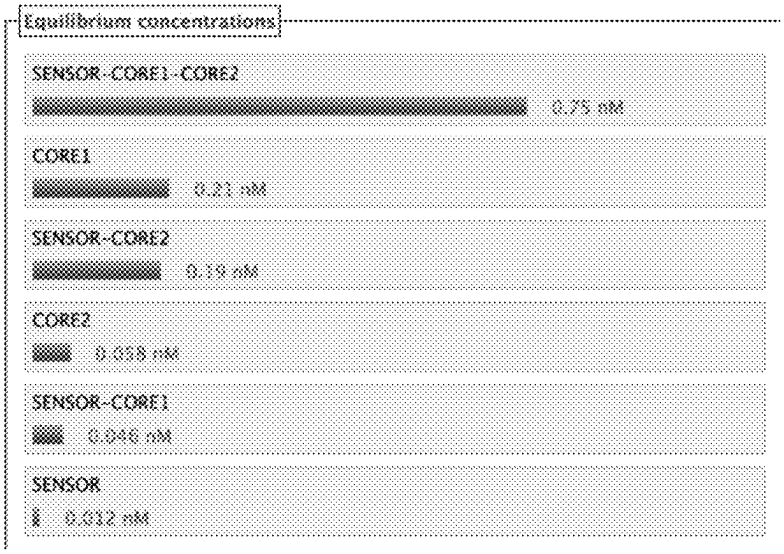
5′ CUUGUGGAAUCAGAAGCAGGUGU**CUGCAGCC** 3′ (SENSOR) (SEQ ID NO: 5)

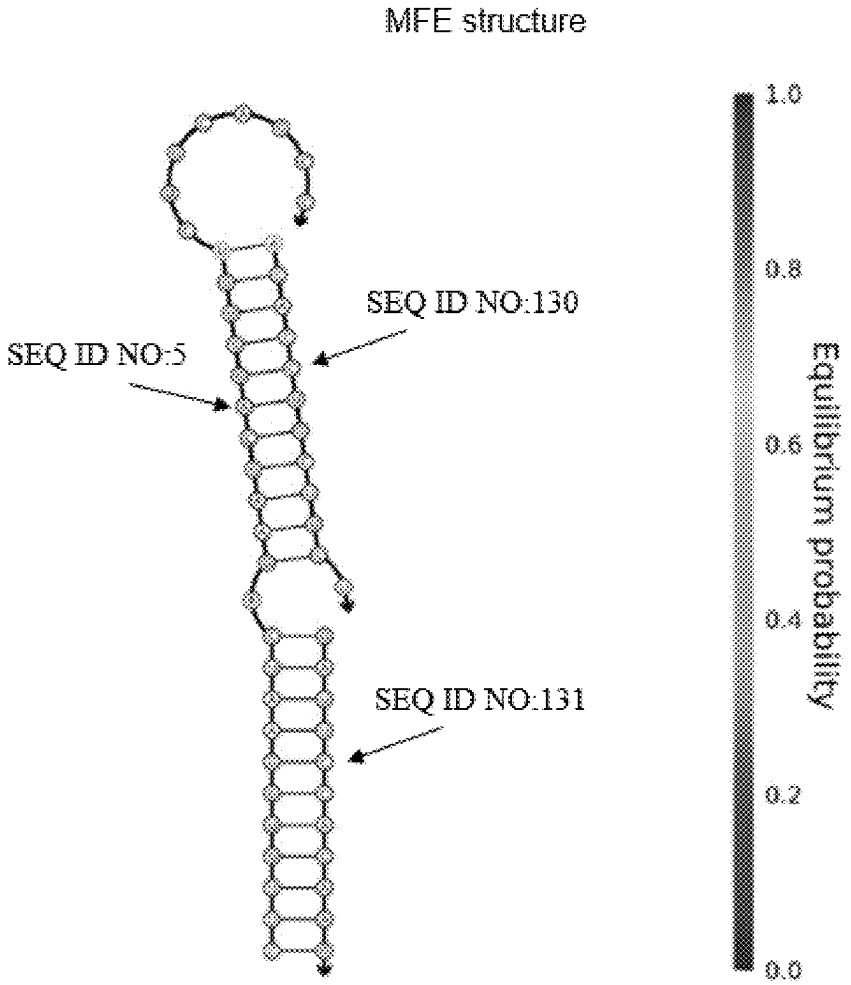
GAACACCUUAG 5′) (3′UCUUCGUCCACA (CORE W/NICK 12 BP FROM TOP)

ACGGUCAAUAACACCAGAUCUCG (CORE GUIDE) (SEQ ID NO: 22)

3′ **UUUGCCAGUUAUUGUGGUCUAGAGC** 5′ (GUIDE +2 U) (SEQ ID NO: 132)

FIG. 61A





Free energy of secondary structure: -41.56 kcal/mol

FIG. 61B

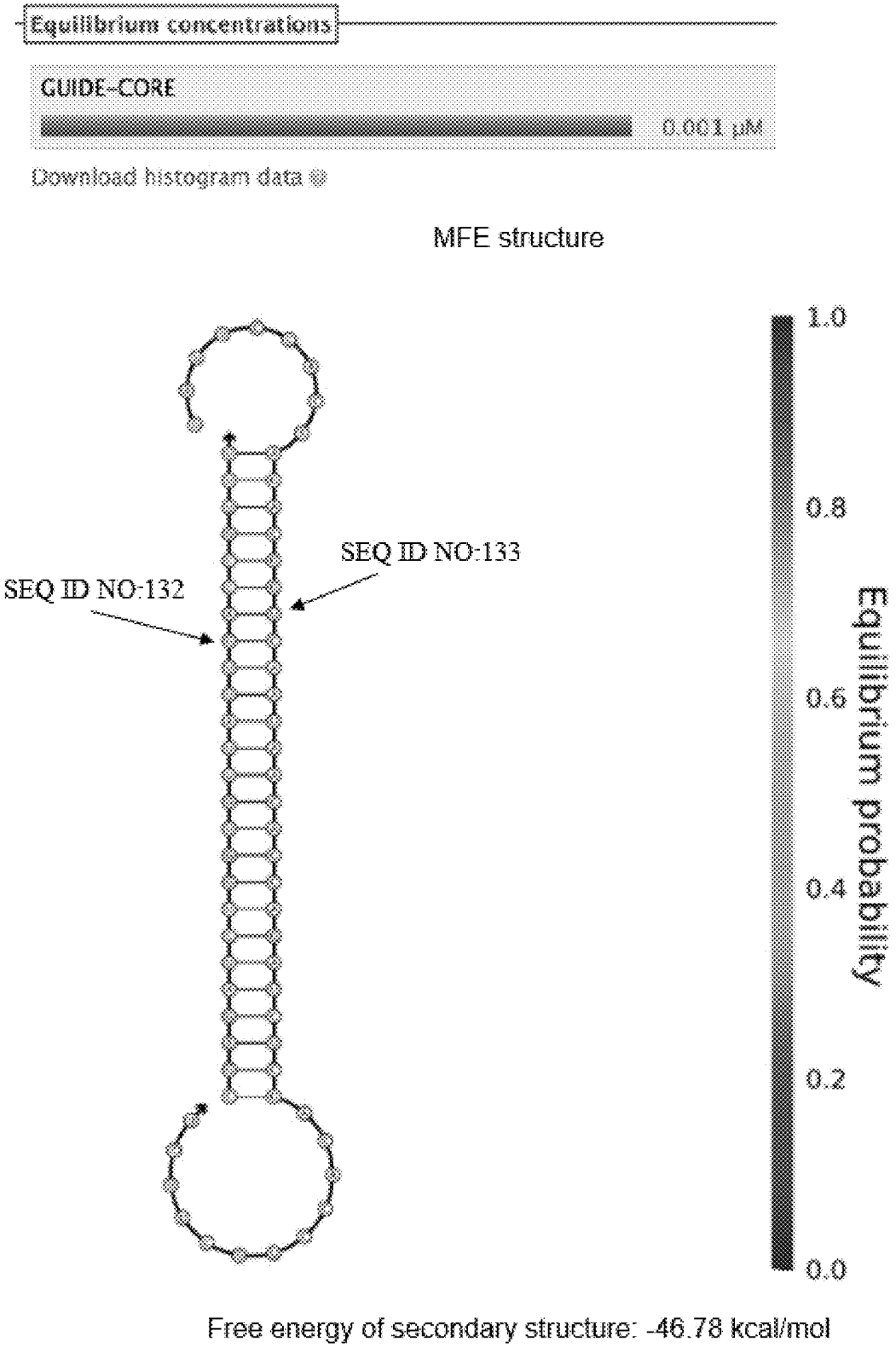

Equilibrium concentrations
GUIDE-CORE
0.001 μM
Download histogram data
MFE structure
SEQ ID NO:132
SEQ ID NO:133
1.0
0.8
0.6
0.4
0.2
0.0
Equilibrium probability
Free energy of secondary structure: -46.78 kcal/mol

FIG. 62

PREDICTED: Homo sapiens uncharacterized LOC105374714 (LOC105374714), ncRNA
Sequence ID: XR_[illegible] Length: 1622 Number of Matches: 1

Range 1: 476 to 491 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	18	16/16(100%)	0/16(0%)	Plus/Minus

Query 12 [illegible] 27
Sbjct 491 [illegible] 476

SEQ ID NO:134

Download GenBank Graphics

PREDICTED: Homo sapiens collagen type V alpha 2 (COL5A2), transcript variant X1, mRNA
Sequence ID: XM_[illegible] Length: 6110 Number of Matches: 1

Range 1: 99 to 114 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	18	16/16(100%)	0/16(0%)	Plus/Minus

Query 7 [illegible] 22
Sbjct 114 [illegible] 99

SEQ ID NO:135

Download GenBank Graphics

PREDICTED: Homo sapiens antizyme inhibitor 2 (AZIN2), transcript variant X22, misc_RNA
Sequence ID: XR_[illegible] Length: 2050 Number of Matches: 1

Range 1: 838 to 853 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	18	16/16(100%)	0/16(0%)	Plus/Minus

Query 14 [illegible] 29
Sbjct 853 [illegible] 838

SEQ ID NO:136

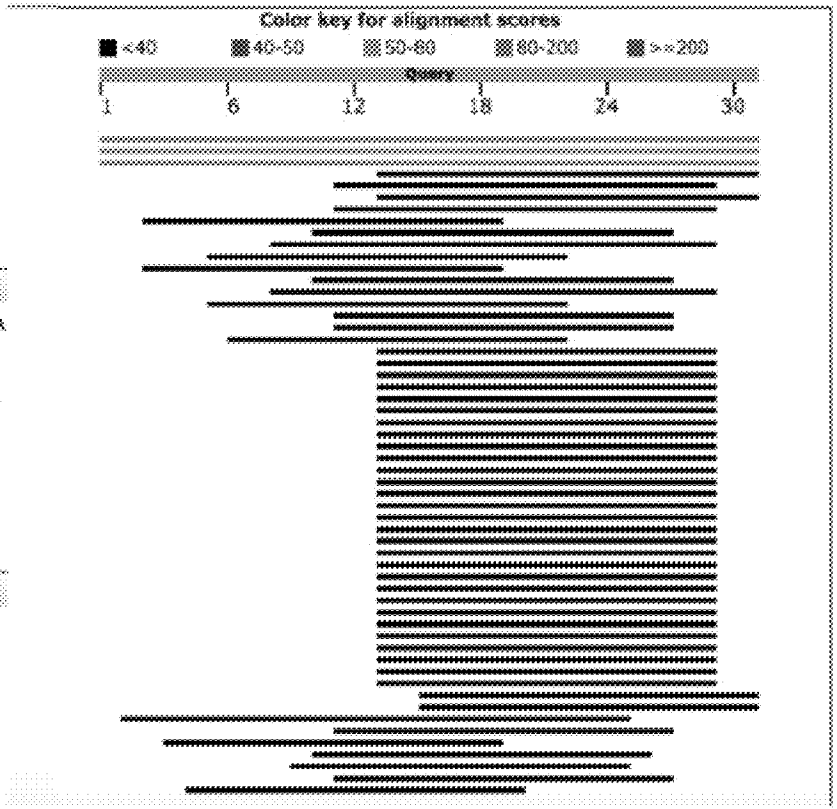


FIG. 62 (Cont'd)

Sensor vs NCBI human transcripts

PREDICTED: Homo sapiens tissue factor pathway inhibitor (TFPI), transcript variant X1, mRNA
Sequence ID: XM_011511707.2 Length: 4075 Number of Matches: 1

Range 1: 1806 to 1820 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	71	15/15(100%)	0/15(0%)	Plus/Minus

```
Query  9     ATCAGAAGCAGGTCT  23
             |||||||||||||||
Sbjct  1820  ATCAGAAGCAGGTCT  1806
```

SEQ ID NO:137

Download GenBank Graphics

PREDICTED: Homo sapiens zinc finger CCHC-type containing 2 (ZCCHC2), transcript variant X1, misc_RNA
Sequence ID: XR_001753205.1 Length: 4636 Number of Matches: 1

Range 1: 4310 to 4328 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	71	18/19(95%)	0/19(0%)	Plus/Minus

```
Query  13    GAAGCAGGTGTCTGCAGCC  31
             ||||||||||| |||||||
Sbjct  4328  GAAGCAGGTGCCTGCAGCC  4310
```

SEQ ID NO:138

SEQ ID NO:139

PREDICTED: Homo sapiens LLGL2, scribble cell polarity complex component (LLGL2), transcript variant X12, mRNA
Sequence ID: XM_017024632.1 Length: 2900 Number of Matches: 1

Range 1: 477 to 491 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	71	15/15(100%)	0/15(0%)	Plus/Minus

```
Query  3     TGTGGAATCAGAAGC  17
             |||||||||||||||
Sbjct  491   TGTGGAATCAGAAGC  477
```

SEQ ID NO:140

FIG. 63

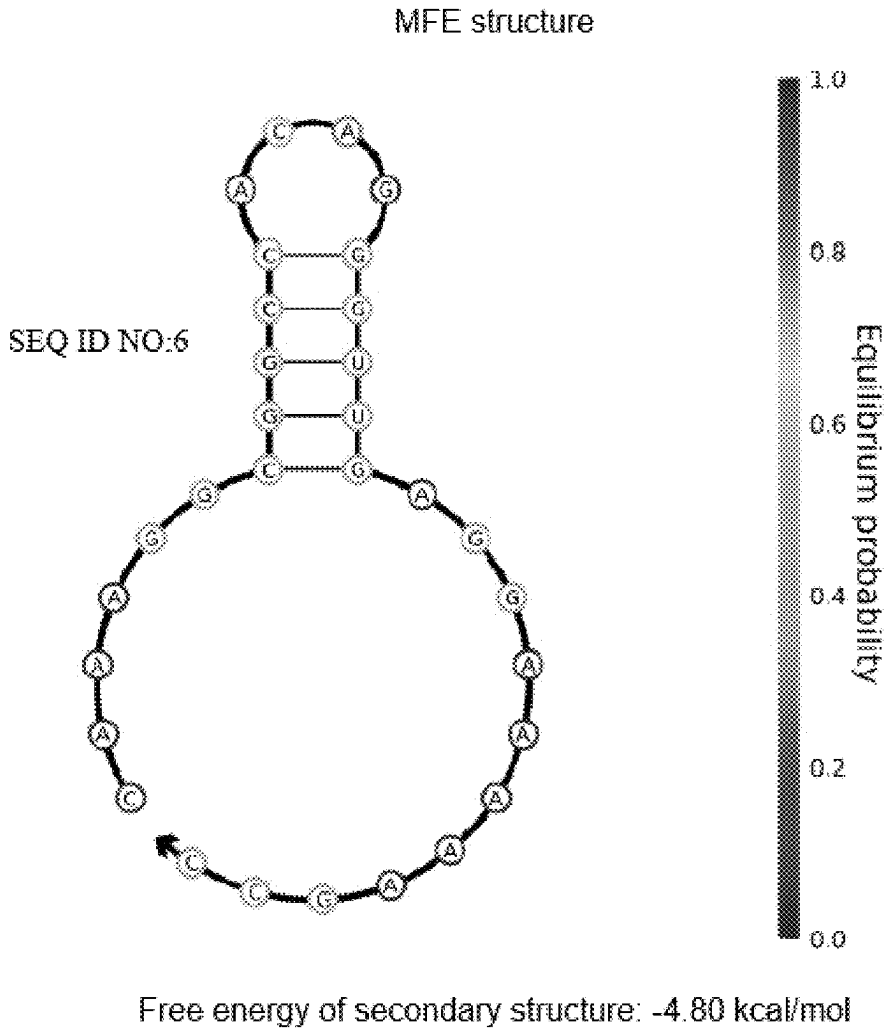

MFE structure
SEQ ID NO:6
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: -4.80 kcal/mol

FIG. 64

5′ CAAAGGCGGCCACAGGGUUGAGGAAAAAGCC 3′ (SENSOR) (SEQ ID NO: 6)

GUUUCCGCCGG 5′) (3′UGUCCCAACUCC (CORE NICK)

ACGGUCAAUAACACCAGAUCUCG (CORE GUIDE) (SEQ ID NO: 23)

3′ UUUGCCAGUUAUUGUGGUCUAGAGC 5′ (GUIDE +2 U) (SEQ ID NO: 132)

FIG. 65

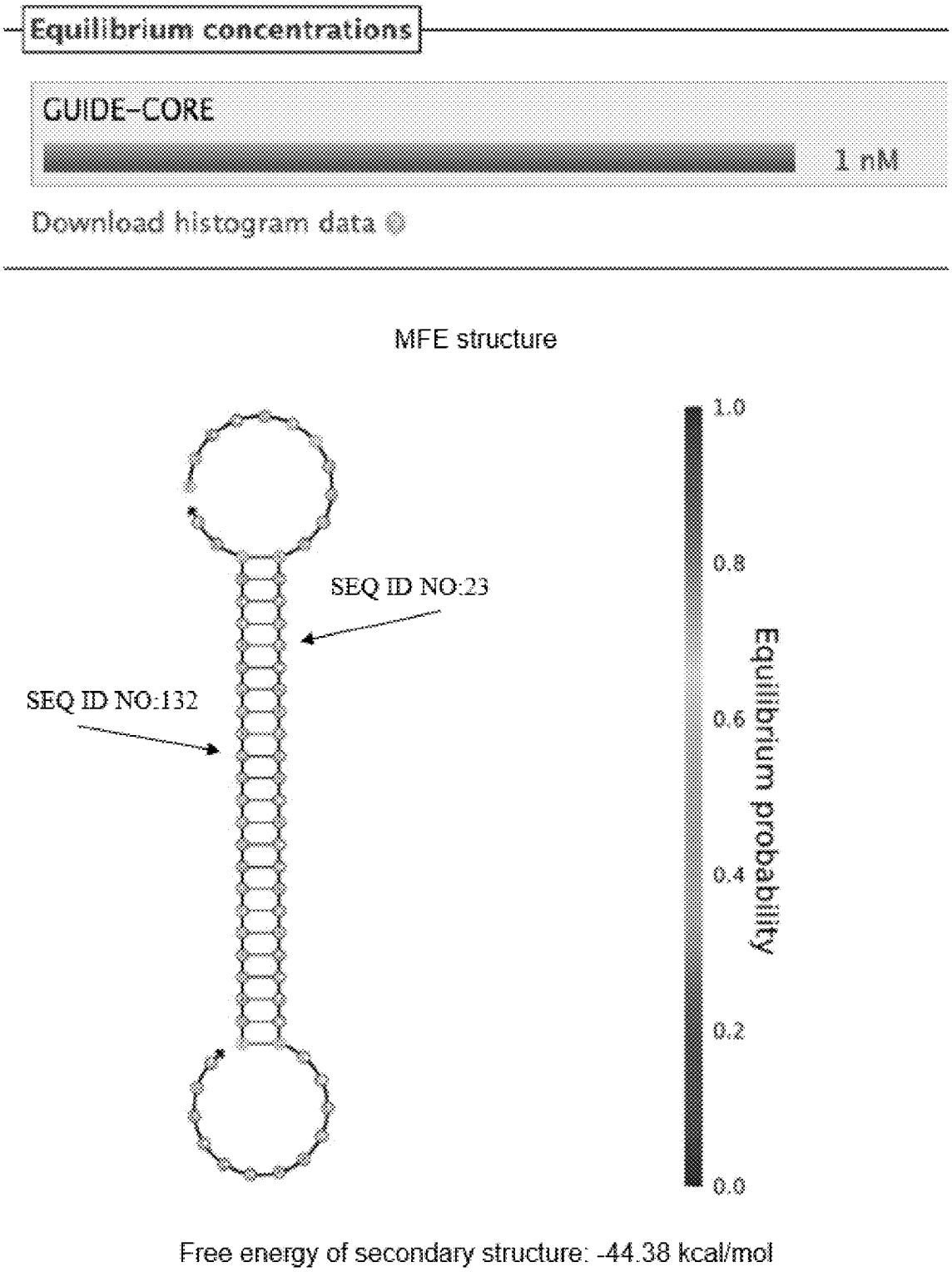

Equilibrium concentrations
GUIDE-CORE
1 nM
Download histogram data
MFE structure
SEQ ID NO:23
SEQ ID NO:132
1.0
0.8
0.6
0.4
0.2
0.0
Equilibrium probability
Free energy of secondary structure: -44.38 kcal/mol

FIG. 66

Sensor vs NCBI human transcripts

Download GenBank Graphics

PREDICTED: Homo sapiens uncharacterized LOC105379631 (LOC105379631), transcript varia

Sequence ID: XR_952252.2 Length: 9693 Number of Matches: 1

Range 1: 1473 to 1488 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	18	16/16(100%)	0/16(0%)	Plus/Minus

Query 8 GGCCACAGGGTTCAGG 23
Sbjct 1488 GGCCACAGGGTTCAGG 1473

SEQ ID NO:141

Download GenBank Graphics

PREDICTED: Homo sapiens zinc finger protein 93-like (LOC101929991), mRNA

Sequence ID: XM_011508848.2 Length: 1286 Number of Matches: 1

Range 1: 306 to 320 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	71	15/15(100%)	0/15(0%)	Plus/Minus

Query 14 AGGGTTGAGGAAAAA 28
Sbjct 320 AGGGTTGAGGAAAAA 306

SEQ ID NO:142

Download GenBank Graphics

Homo sapiens lens intrinsic membrane protein 2 (LIM2), transcript variant 1, mRNA

Sequence ID: NM_030657.3 Length: 1001 Number of Matches: 1

Range 1: 485 to 499 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	71	15/15(100%)	0/15(0%)	Plus/Minus

Query 14 AGGGTTGAGGAAAAA 28
Sbjct 499 AGGGTTGAGGAAAAA 485

SEQ ID NO:142

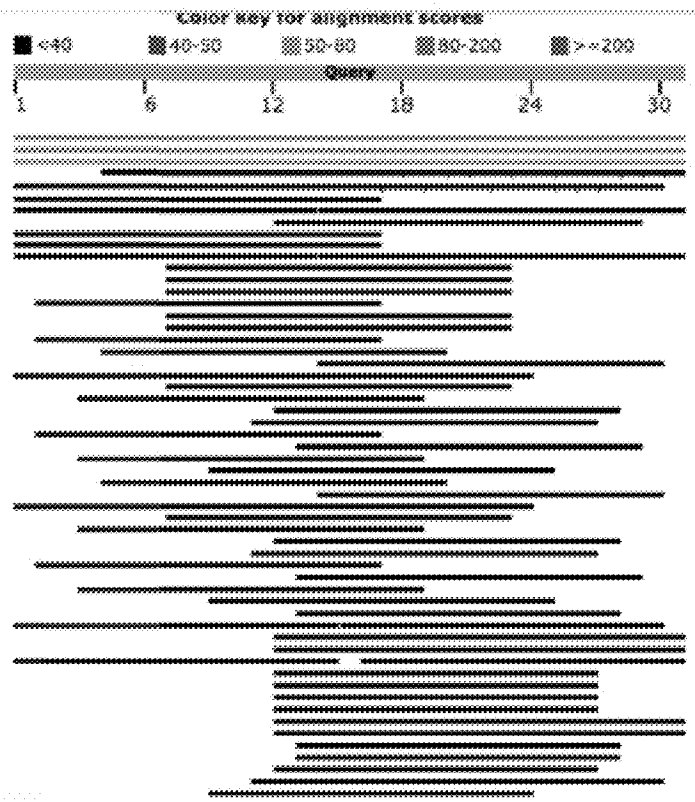


FIG. 66 (Cont'd)

Sensor vs NCBI human transcripts

PREDICTED: Homo sapiens tissue factor pathway inhibitor (TFPI), transcript variant X1, mRNA
Sequence ID: XM_011511707.2 Length: 4075 Number of Matches: 1

Range 1: 1806 to 1820 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	71	15/15(100%)	0/15(0%)	Plus/Minus

```
Query  9     ATCAGAAGCAGGTGT  23
             |||||||||||||||
Sbjct  1820  ATCAGAAGCAGGTGT  1806
```

SEQ ID NO:137

Download GenBank Graphics

PREDICTED: Homo sapiens zinc finger CCHC-type containing 2 (ZCCHC2), transcript variant X1, misc_RNA
Sequence ID: XR_001753205.1 Length: 4636 Number of Matches: 1

Range 1: 4310 to 4328 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	71	18/19(95%)	0/19(0%)	Plus/Minus

```
Query  13    GAAGCAGGTGTCTGCAGCC  31
             ||||||||||| |||||||
Sbjct  4328  GAAGCAGGTGCCTGCAGCC  4310
```

SEQ ID NO:138

PREDICTED: Homo sapiens LLGL2, scribble cell polarity complex component (LLGL2), transcript variant X12, mRNA
Sequence ID: XM_017024832.1 Length: 2900 Number of Matches: 1

Range 1: 477 to 491 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
30.2 bits(15)	71	15/15(100%)	0/15(0%)	Plus/Minus

```
Query  3     TGTCGAATCAGAAGC  17
             |||||||||||||||
Sbjct  491   TGTCGAATCAGAAGC  477
```

SEQ ID NO:140

FIG. 67

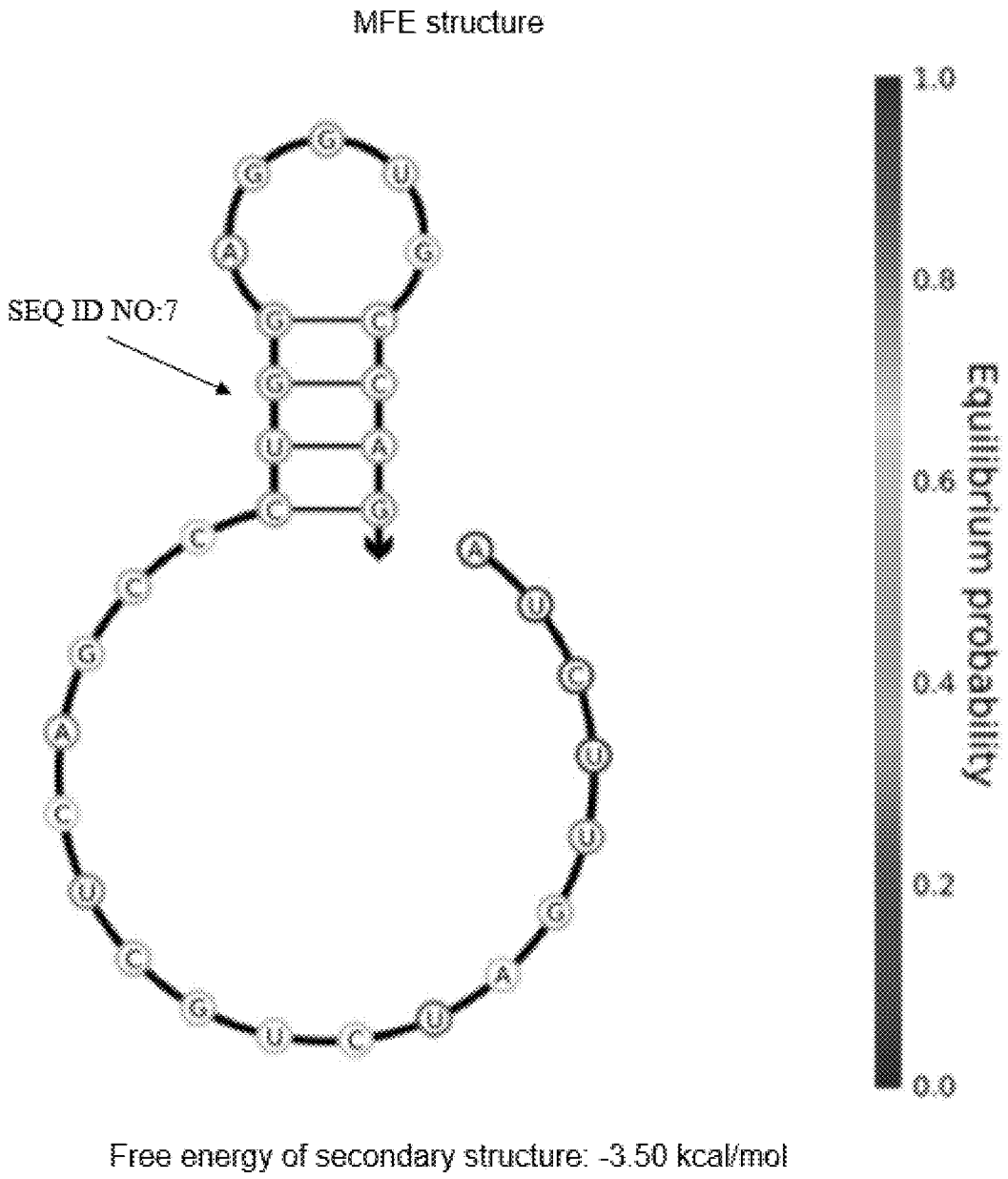

MFE structure
SEQ ID NO:7
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: -3.50 kcal/mol

FIG. 68

5′ AUCUUGAUCUGCUCAGCCCUGGAGGUGCCAG 3′ (SENSOR) (SEQ ID NO: 7)

UAGAACUAGACG 5′) (3′AGUCGGGACCU (CORE NICK)

ACGGUCAAUAACACCAGAUCUCG (CORE GUIDE) (SEQ ID NO. 24)

3′ UUUGCCAGUUAUUGUGGUCUAGAGC 5′ (GUIDE +2 U) (SEQ ID NO: 132)

FIG. 69A

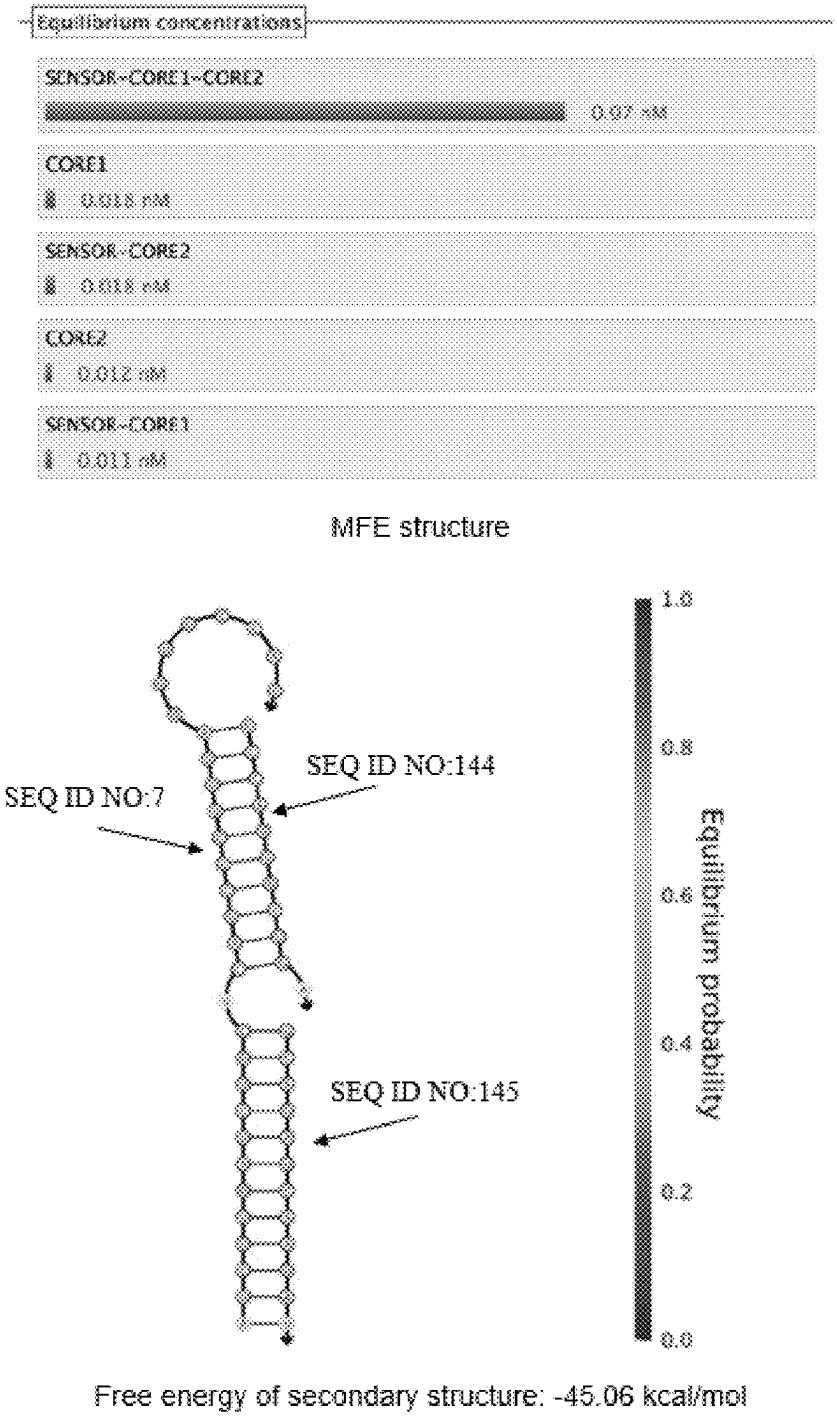
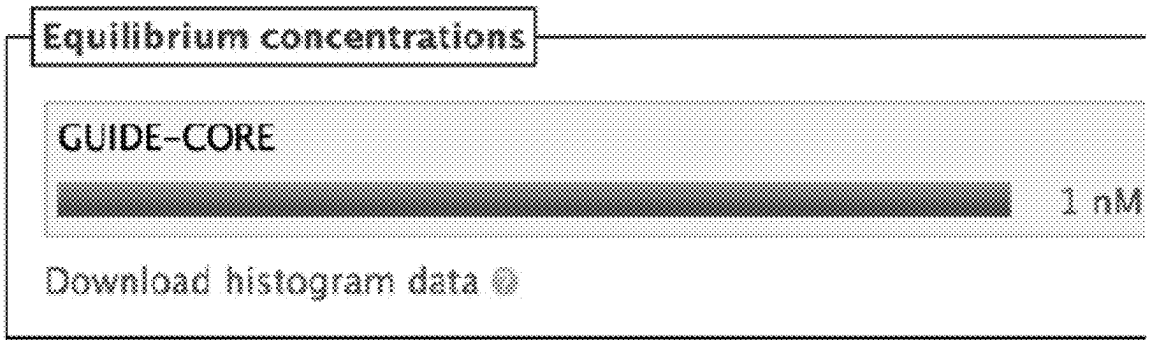
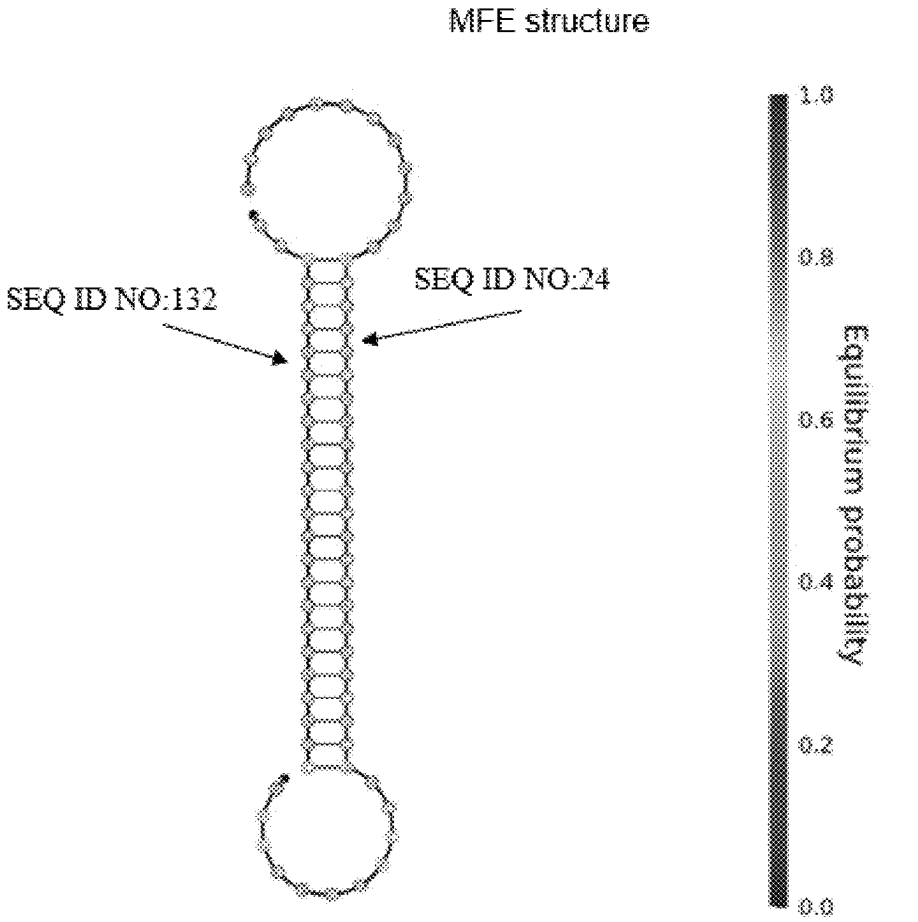

Equilibrium concentrations
SENSOR-CORE1-CORE2
0.07 nM
CORE1
0.018 nM
SENSOR-CORE2
0.018 nM
CORE2
0.012 nM
SENSOR-CORE1
0.011 nM
MFE structure
SEQ ID NO:144
SEQ ID NO:7
SEQ ID NO:145
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: -45.06 kcal/mol

FIG. 69B





Free energy of secondary structure: -44.38 kcal/mol

FIG. 70

Sensor vs NCBI human transcripts

Download ~ GenBank Graphics

PREDICTED: Homo sapiens calmodulin like 6 (CALML6), transcript variant X1, mRNA

Sequence ID: XM_[illegible]723.3 Length: 2223 Number of Matches: 1

Range 1: 1689 to 1704 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	18	16/16(100%)	0/16(0%)	Plus/Minus

Query 3 [illegible] 18
Sbjct 1704 [illegible] 1689

SEQ ID NO:123

Download ~ GenBank Graphics

Homo sapiens RAS guanyl releasing protein 2 (RASGRF2), transcript variant 5, mRNA

Sequence ID: NM_[illegible].1 Length: 2204 Number of Matches: 1

Range 1: 435 to 450 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	18	16/16(100%)	0/16(0%)	Plus/Minus

Query 3 [illegible] 18
Sbjct 450 [illegible] 435

SEQ ID NO:123

Download ~ GenBank Graphics

Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 2, mRNA

Sequence ID: NM_[illegible].4 Length: 3942 Number of Matches: 1

Range 1: 1153 to 1168 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
32.2 bits(16)	18	16/16(100%)	0/16(0%)	Plus/Minus

Query 3 ATCTTGATCTGCTCAG 18
Sbjct 1168 ATCTTGATCTGCTCAG 1153

SEQ ID NO:146

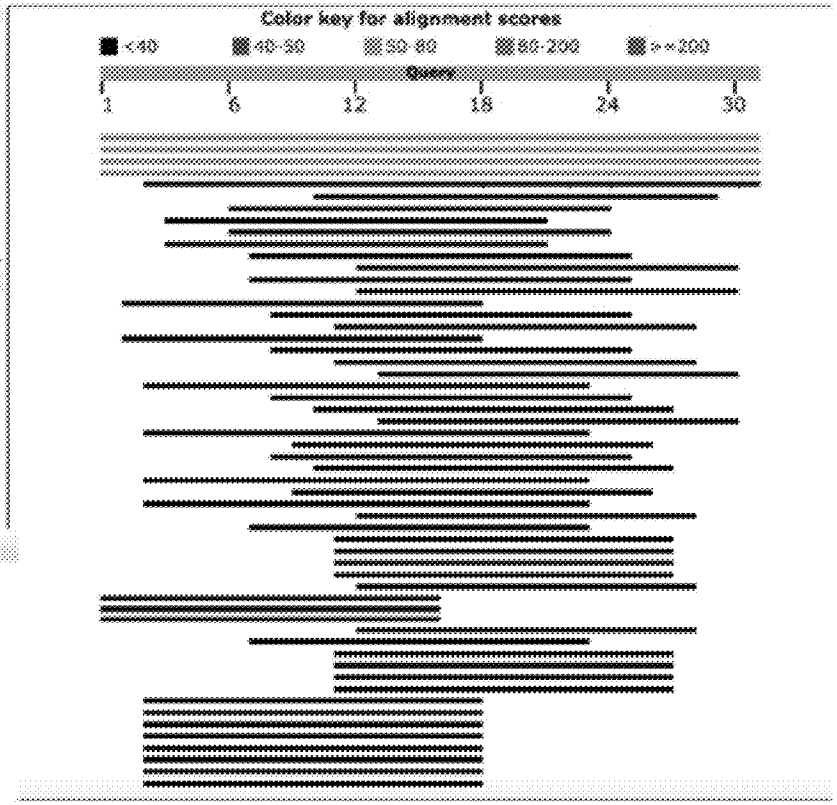
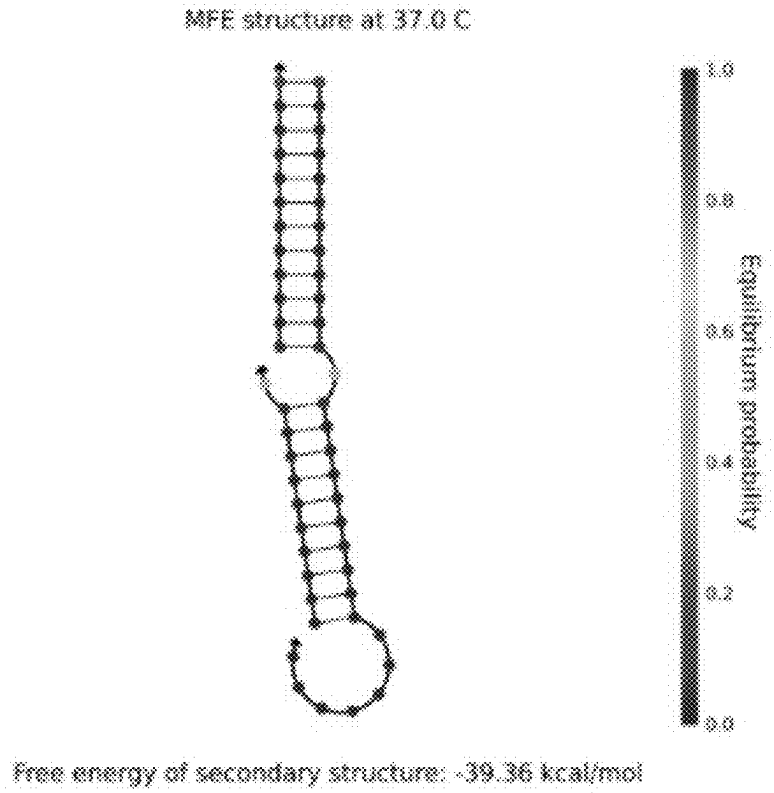


FIG. 71


MFE structure at 37.0 C
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: -39.36 kcal/mol

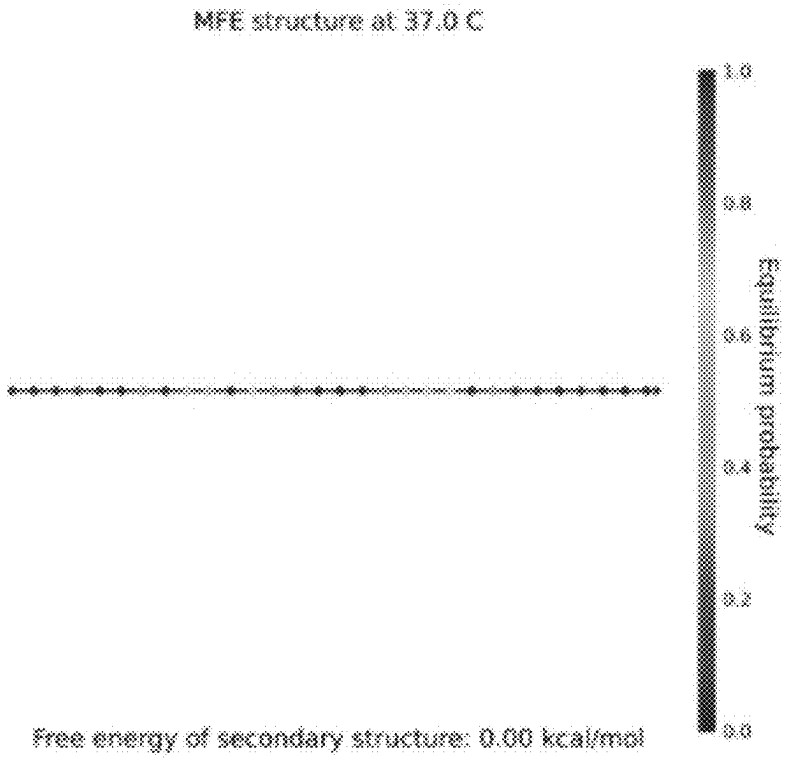
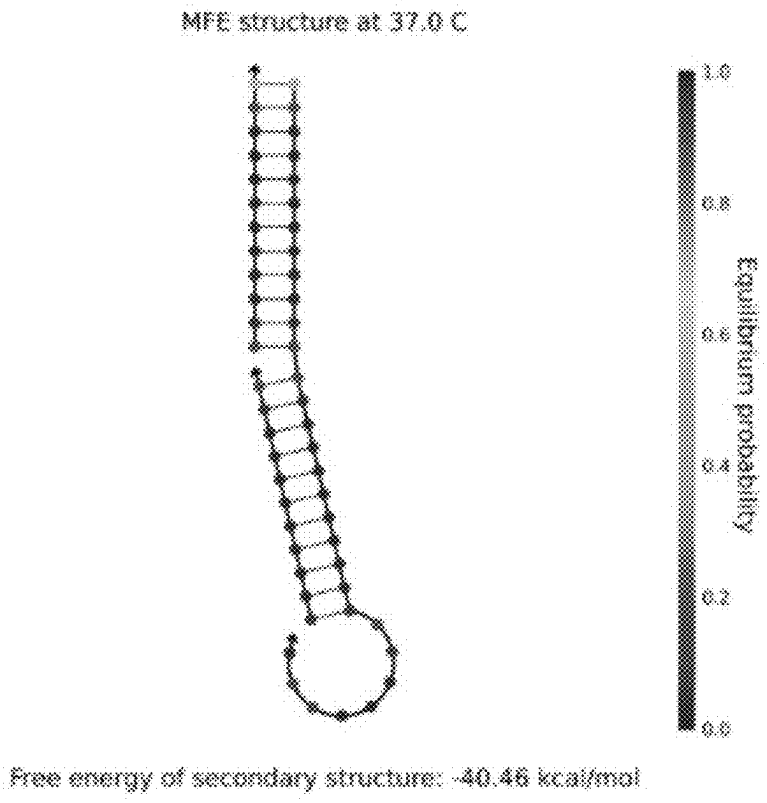

MFE structure at 37.0 C
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: 0.00 kcal/mol

FIG. 72


MFE structure at 37.0 C
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: -40.46 kcal/mol

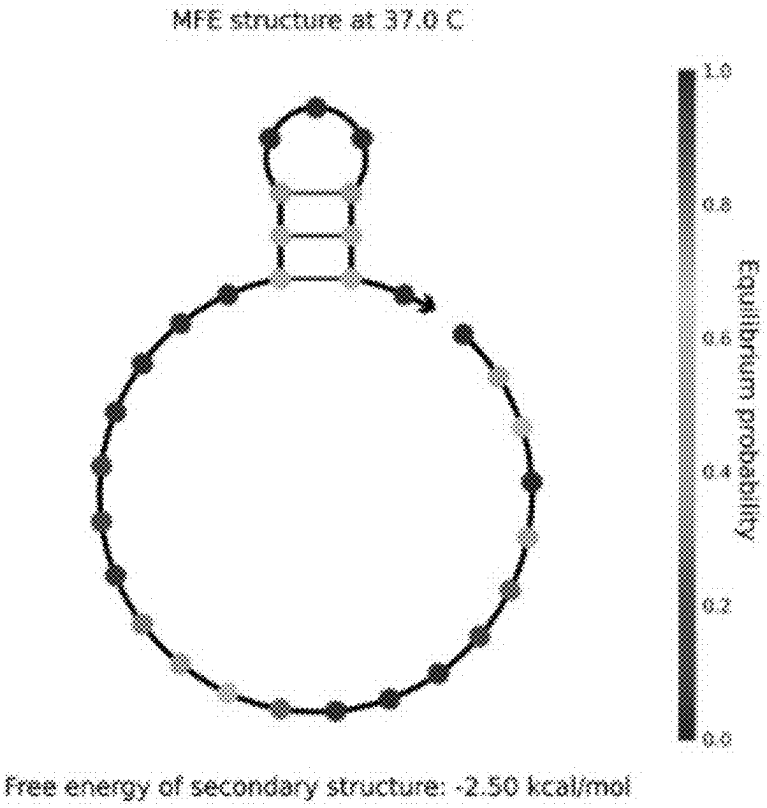
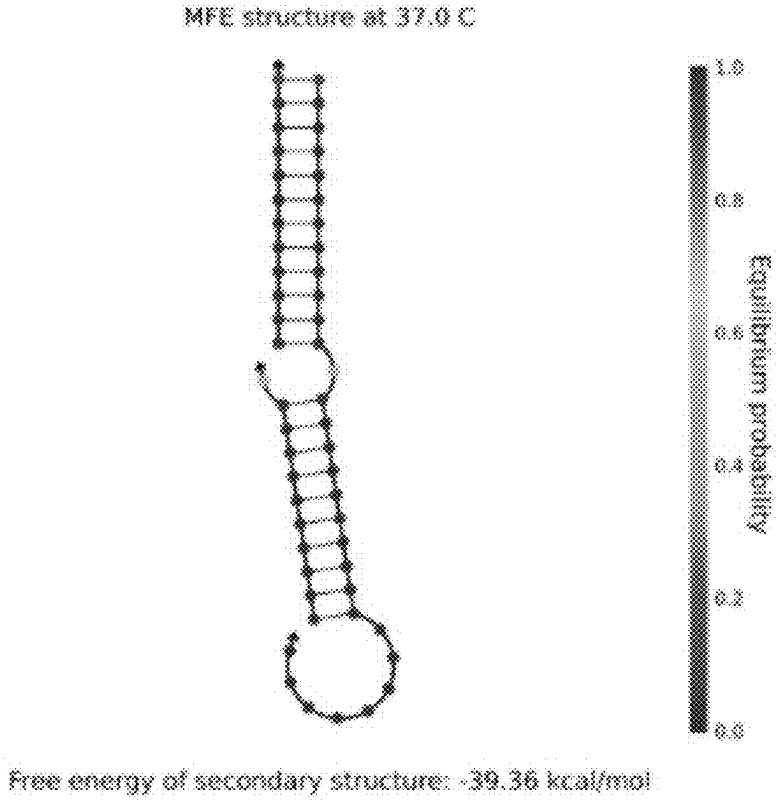
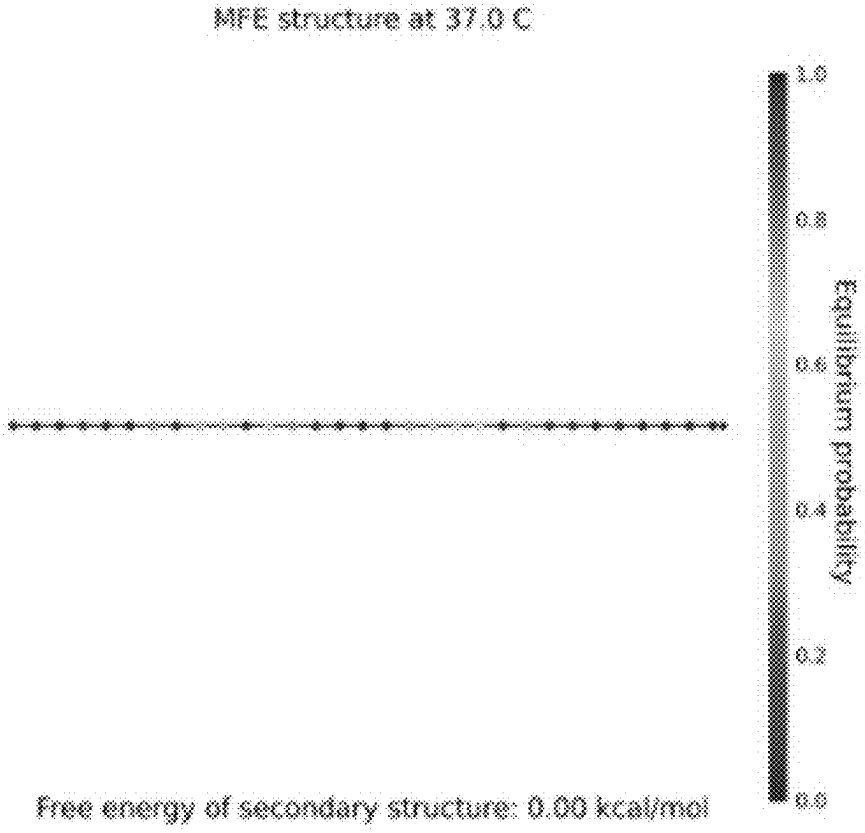

MFE structure at 37.0 C
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: -2.50 kcal/mol

FIG. 73


MFE structure at 37.0 C
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: -39.36 kcal/mol


MFE structure at 37.0 C
Equilibrium probability
1.0
0.8
0.6
0.4
0.2
0.0
Free energy of secondary structure: 0.00 kcal/mol

CONDITIONAL-SIRNAS AND USES THEREOF IN TREATING CARDIAC HYPERTROPHY

PRIORITY CLAIM

This application is a U.S. National Phase Application of International Application No. PCT/US2018/046379, filed Aug. 10, 2018, which claims priority to U.S. Provisional Patent Application No. 62/543,882, filed Aug. 10, 2017, the subject matter of which is hereby incorporated by reference in its entirety, as if fully set forth herein.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

This invention was made with government support under Grant Number 1332411, awarded by National Science Foundation through the Emerging Frontiers in Research and Innovation, Origami Design for Integration of Self-assembling Systems for Engineering Innovation (EFRI-ODISSEI), and Grant Number A1029329, awarded by National Institutes of Health (NIH). The government has certain rights to the invention.

SEQUENCE LISTING

This disclosure includes a sequence listing, which is submitted in ASCII format via EFS-Web, and is hereby incorporated by reference in its entirety. The ASCII copy, created Nov. 29, 2021, is named SubstituteSequenceListing.txt and is 252 kilobytes in size.

BACKGROUND

RNA interference (RNAi) is a sequence-specific mRNA degradation pathway mediated by siRNA duplexes, key for cellular immunity and developmental regulation. Researchers have utilized synthetic RNAi triggers for therapeutics by inhibiting a specific gene product found to be essential in disease driving pathways but non-essential for normal functioning.

Consider however that some genes essential in disease progression may have vital functions in normal cells and are dangerous to target. Meanwhile other upregulated genes are not essential for disease progression, but serve as effective indicators. Therefore, there is a need in the art to develop effective therapies to exploit this differential expression in various indications. The conditionally active siRNA complexes described below are candidates for investigation of treatments for those indications, such as cardiac hypertrophy.

Heart Failure (HF) is a chronic cardiac condition, affecting millions of people worldwide, and considered a major contributor to healthcare expenditure in the US. Compensatory cardiac hypertrophy is one of the initial hallmarks of pathological ventricular remodeling, which is characterized by an upregulation of a variety of genes and miRNA that mediate and regulate myocardial hypertrophy, and ultimately HF. Even though important advances have been done in the treatment of HF, no cardiac specific therapies with lack of adverse effects have been developed to date. Therefore, there is a need in the art to develop an effective therapy for HF.

BRIEF DESCRIPTION OF THE DRAWINGS

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

FIG. **1** shows a comparison of secondary and tertiary structure (from full atomistic MD simulations) of a Cond-siRNA construct according to one embodiment. Black arrows show corresponding features between the 2D and 3D representations.

FIG. **2** is a diagram showing the RNAi pathway.

FIG. **3** shows toehold mediated strand displacement process of conditional siRNA. In step I, c-siRNA meets RNA transcript with correct activation sequence (Input). In step II, an Input RNA binds to the toehold. Step III shows toehold mediated strand displacement. Step IV shows the sensor strand and input forming a waste duplex that separates from the pro-siRNA. In step V, XRN1, exosome and other cytosolic RNAses rapidly degrade unprotected overhangs, turning pro-siRNA into efficient Dicer substrate. In step VI, siRNA is processed by Dicer for incorporation into RISC. The basic biophysical process of toehold mediated strand displacement includes a fast 1 D random walk: uS to mS for each of N^2 steps. This results in sequence specificity from both toehold and duplexes. Thermodynamically stable chemical modifications are confined to sensor strand to avoid kinetic traps.

FIGS. **4**A-C: A) General construct design of cond-siRNA with green sensor strand designed reverse comp. to signal gene mRNA, red core strand with nick either 11 or 12 bp from toehold end on sensor side designed comp. to sensor and guide, and yellow guide strand designed reverse comp. to target gene mRNA. B) Model of cond-siRNA. C) Molecular simulation of cond-siRNA.

FIG. **5** shows an overview of the design process for Cond-siRNAs according to one embodiment.

FIG. **6** shows a hypothetical sensor duplex for mRNA used to check for thermodynamic stability of the sensor according to one embodiment.

FIG. **7** shows a structure calculation showing sensor strand with low internal secondary structure according to one embodiment.

FIG. **8** shows a histogram showing a 97% predicted formation of the hypothetical sensor duplex and correct secondary structure according to one embodiment.

FIG. **9** shows a hypothetical sensor duplex for miRNA used to check for thermodynamic stability of the sensor according to one embodiment.

FIG. **10** shows a structure of the RNAi targeting duplex according to one embodiment.

FIG. **11** is a schematic diagram of a signaling pathway involved in cardiac gene program regulating hypertrophy.

FIGS. **12**A-B show schematic depicting in vivo and in vitro screening approaches.

FIGS. **13**A-B: A) NuPack generated secondary structure of selected NPPB 31 bp sensor strand. Minimal secondary structure with approximately 40-50% probability of folding onto itself. B) NPPB sensor strand bound to 5' and 3' core overhangs 99% of the time.

FIGS. **14**A-B: A) NuPack generated secondary structure of selected MYH7 31 bp sensor strand. Minimal secondary structure with approximately 30% probability folding onto itself. B) NPPB sensor strand bound to 5' and 3' core overhangs 97% of the time.

FIGS. **15**A-B: A) NuPack generated secondary structure of HDAC2 25 bp guide strand. Significant secondary structure indicated by the equilibrium probabilities of binding. B) NuPack generated secondary structure of HDAC2 guide bound to core strand with the 5' and 3' overhangs that bind to the appropriate sensor strand. Although guide strand has

significant and strong secondary structure, when placed with core strand, guide binds to core 100%.

FIG. **16** shows test constructs detecting murine ANP mRNA and targeting murine Calcineurin according to certain embodiments.

FIG. **17** shows test constructs detecting murine and human mir-23a-3p and targeting murine Calcineurin according to certain embodiments.

FIG. **18** is a schematic depicting a site of injury that can be targeted for treatment according to methods of the present invention.

FIG. **19** is a series of bar graphs depicting experimental results of differential gene expression in tissues of wild-type mice in homeostasis.

FIG. **20**: Gene expression in NRVM under hypoxia.

FIG. **21**: Differential miRNA expression in NRVM under hypoxia.

FIG. **22**: Gene expression in NRVM after PE treatment.

FIG. **23**: Differential miRNA expression in NRVM after treatment with PE.

FIG. **24**: Gene expression in mice with non-ischemic (TAC) and ischemic (I/R) HF.

FIG. **25**: miRNA expression in mice with non-ischemic (TAC) and ischemic (I/R) HF.

FIG. **26** shows an equilibrium probability for an MFE structure.

FIG. **27** shows an equilibrium probability for an MFE structure.

FIG. **28** shows an equilibrium probability for an MFE structure.

FIG. **29** shows an equilibrium probability for an MFE structure.

FIG. **30** shows (ANP:calcineurin) and (mir-23a-3p:calcineurin) Cond-siRNAs on 10% non-denaturing PAGE gel in TBE. The correct assemblies are indicated in the green boxes.

FIG. **31** shows results of a dual luciferase assay of mir-23a-3p calcineurin Cond-siRNA according to certain embodiments.

FIG. **32** is a bar graph showing RNAi activity against Calcineurin in NRVM cells under PE stimulation according to one embodiment.

FIG. **33** shows images of NRVM cells with and without PE stimulation when treated with scrambled siRNA (negative control), (ANP:calcineurin) Cond-siRNA, and commercial calcineurin siRNA (positive control) according to one embodiment.

FIG. **34** shows results of cell size quantitation according to one embodiment.

FIG. **35**A shows Post-MI cardiac remodeling and left ventricular enlargement.

FIG. **35**B is a bar graph showing experimental results where patients with any of the patterns of LV remodeling post-MI had a greater risk of the composite of cardiovascular (CV) death, MI, heart failure (HF), stroke, or resuscitated cardiac arrest.

FIG. **36** is a flowchart accompanied by a corresponding schematic showing the RNA interference pathway starting with pri-miRNA processing in the nucleus.

FIG. **37** is a schematic showing post-MI remodeling.

FIG. **38** is a series of bar graphs depicting experimental results of differential miRNA expression in tissues of wild-type mice in homeostasis.

FIG. **39** is a table including candidate sensor strands for the 3' UTR of the human myh7 gene. Column abbreviations are as follows: BS is Bad Segments; 3LN is 3-Letteredness; NBP is Number Bad Points; P is Position.

FIG. **40** is a table including candidate sensor strands for the 3' UTR of the rat myh7 gene. Column abbreviations are as follows: BS is Bad Segments; 3LN is 3-Letteredness; NBP is Number Bad Points; P is Position.

FIG. **41** is a table including candidate sensor strands for the 3' UTR of the human nppa gene. Column abbreviations are as follows: BS is Bad Segments; 3LN is 3-Letteredness; NBP is Number Bad Points; P is Position.

FIG. **42** is a table including candidate sensor strands for the 3' UTR of the rat nppa gene. Column abbreviations are as follows: BS is Bad Segments; 3LN is 3-Letteredness; NBP is Number Bad Points; P is Position.

FIG. **43** is a table including candidate sensor strands for the 3' UTR of the human nppb gene. Column abbreviations are as follows: BS is Bad Segments; 3LN is 3-Letteredness; NBP is Number Bad Points; P is Position.

FIG. **44** is a table including candidate sensor strands for the 3' UTR of the rat nppb gene. Column abbreviations are as follows: BS is Bad Segments; 3LN is 3-Letteredness; NBP is Number Bad Points; P is Position.

FIG. **45** shows a top view of a 3D schematic of a Cond-siRNA construct according to one embodiment.

FIG. **46** shows the design of sensor miR-23-a-3p gene sequence.

FIG. **47** illustrates NCBI check for sensor strand.

FIG. **48** illustrates NCBI check for calcineurin and HDAC2 guide strand sequences.

FIG. **49** shows the secondary structure and MFE structure at 37° C. of the full miR-23a-3p sensor strand with toehold for calcineurin.

FIGS. **50**A-**50**D show that NuPack analyses were performed on core (FIG. **50**A), guide (FIG. **50**B), Sensor with two small overhangs of core: 97% (FIG. **50**C), and calcineurin guide with core: 100% (FIG. **50**D).

FIG. **51** shows NCBI check for calcineurin guide strand vs. human constructs.

FIGS. **52**A-**52**D show that NuPack analyses of miR-23a-3p sensor strand for HDAC2 were performed on core (FIG. **52**A), guide (FIG. **52**B), HDAC2 guide with core: 100% (FIG. **52**C), and sensor with core overhangs: 97% (FIG. **52**D).

FIG. **53** shows NCBI check for HDAC2 guide strand vs. human transcripts.

FIGS. **54**A-**54**B illustrate the check of guide vs. NCBI human transcripts and sequence alignment, respectively.

FIG. **55** shows the MFE structure of SEQ ID NO: 4.

FIG. **56** shows the BNP sensor sequence (SEQ ID NO: 4) together with core and guide sequences.

FIGS. **57**A and **57**B show Nupack analyses of BNP sensor (SEQ ID NO: 4) with overhangs, and guide with core, respectively.

FIG. **58** shows NCBI check of BNP sensor first candidate vs. human transcripts.

FIG. **59** shows the MFE structure of SEQ ID NO: 5.

FIG. **60** shows the BNP sensor sequence (SEQ ID NO: 5) together with core and guide sequences.

FIGS. **61**A and **61**B show Nupack analyses of BNP sensor (SEQ ID NO: 5) with overhangs, and guide with core, respectively.

FIG. **62** shows NCBI check of BNP sensor second candidate vs. human transcripts.

FIG. **63** shows the MFE structure of SEQ ID NO: 6.

FIG. **64** shows the BNP sensor sequence (SEQ ID NO: 6) together with core and guide sequences.

FIG. **65** shows Nupack analysis of guide with core for the third BNP candidate.

FIG. **66** shows NCBI check of BNP sensor third candidate vs. human transcripts.

FIG. **67** shows the MFE structure of SEQ ID NO: 7.

FIG. **68** shows the MYH7 sensor sequence (SEQ ID NO: 7) together with core and guide sequences.

FIGS. **69**A and **69**B show Nupack analyses of MYH7 sensor (SEQ ID NO: 7) with overhangs, and guide with core, respectively.

FIG. **70** shows NCBI check of MYH7 sensor vs. human transcripts.

FIG. **71** shows the MFE structure of NPPA HDAC2 construct #1.

FIG. **72** shows the MFE structure of NPPA HDAC2 construct #3.

FIG. **73** shows the MFE structure of NPPA calcineurin construct #1.

DETAILED DESCRIPTION

Overview of Conditional-siRNA

Described herein are conditional siRNA complexes (also referred to herein as Cond-siRNA, a conditional RNA-sensor, or an RNA-sensor) that include a therapeutic component (e.g., siRNA molecule) associated with a molecular sensor via a core molecule. The conditional siRNA complexes are inactive under normal conditions, but are activated upon interaction between the molecular sensor and a biomarker. Such molecules are synthetic riboswitch molecules that allow an input gene or RNA molecule to "switch on" an RNAi pathway against a target output gene.

An RNA-sensor molecule or complex includes sensor strand, a guide strand, and a core strand that bind to each other to form a multi-strand molecular complex having a dual duplex structure shown in FIGS. **1**, **45**. In certain embodiments, those three strands (core, sensor and guide) form two parallel oligonucleotide duplexes connected in a double crossover configuration. [14] (See FIG. **1**). In some aspects, the length of each of the oligonucleotide duplexes is sufficient to operate within the RNA interference (RNAi) pathway (See FIGS. **2**, **36**). For example, the duplexes may be between about 15 and 30 base pairs in length. In some embodiments, the duplexes are between 15 and 20 base pairs in length, between 20 and 25 base pairs in length, between 25 and 30 base pairs in length. In other embodiments, the duplexes are about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 25, 26, 27, 28, 29, 30, or more than 30 base pairs in length.

The double crossover configuration as shown in FIG. **1** represents the inactive or "OFF" state of the RNA-sensor complex wherein the sensor duplex inhibits RNAi loading of the siRNA duplex, serving as a "lock" on RNAi activity. In the OFF state, the guide strand binds a first portion (or "passenger" segment) of the core strand to form an siRNA duplex that serves as a pro-RNA molecule. The pro-RNA molecule operates in the RNAi pathway of a target cell to alter expression of a target gene or target RNA molecule associated with a pathological condition (i.e., the "therapeutic target molecule"). The second duplex is formed by the sensor strand binding to a second portion (or "protection" segment) of the core strand to form the sensor duplex. In some embodiments, the core strand has a third portion (or "protection" segment) that binds the sensor strand. In certain such embodiments, the core strand includes the passenger strand (P) that is joined to first and second protection segments (A, B) at each end by a linker (L1, L2) in the following configuration:

5' B-L2-P-L1-A 3'

The sequence of the core strand is determined by the sequences of the sensor and guide strands, and may be fully or complementary to the sensor strand, the guide strand, or both. Any suitable linker can be used in accordance with the embodiments described herein, including, but not limited to, an internal C3 spacer, a C6 linker, a tri-ethylene glycol linker.

The RNA-sensor complex is activated to the "ON" state upon interaction with a biomarker in the cell expressing a phenotype associated with the pathological condition targeted by the guide strand of the siRNA duplex. This activation is primarily due to the design of the sensor strand, which serves as the activation signal for RNAi activity. When this is the case, the RNA-sensor complex is said to detect the biomarker.

The sensor strand includes a nucleotide sequence designed to bind the biomarker associated with the pathological condition (i.e., "pathological biomarker"). Binding to the biomarker is initiated by the binding of at least one toehold segment (single stranded) to an input RNA strand that encodes at least a portion of the pathological biomarker, as shown in FIG. **3**. Upon displacement of the sensor strand, the sensor and input strands from a waste duplex that separates from the pro-siRNA molecule, allowing the pro-siRNA to be processed by the target cell's RNAi system. The structure and binding dynamics of the conditional-siRNAs described herein is explained further in U.S. Pat. No. 9,725,715, the content of which is incorporated herein by reference in its entirety.

The sequence of the sensor strand can be fully or partially complementary to an RNA sequence present in the pathological biomarker. In certain embodiments, the sensor strand is 100% complementary to the RNA sequence present in the pathological biomarker. Other embodiments may include a sensor strand that is largely complementary to the RNA sequence present in the pathological biomarker, for example, the sensor strand may be greater than 70% complementary, greater than 75% complementary, greater than 80% complementary, greater than 85% complementary, greater than 90% complementary, greater than 95% complementary, greater than 96% complementary, greater than 97% complementary, greater than 98% complementary, or greater than 99% complementary to the RNA sequence present in the pathological biomarker.

In some embodiments, the pathological biomarker is an RNA sequence that forms or encodes a molecule that is associated with the pathologic condition. In some aspects, the pathological biomarker is an RNA sequence that is present in the target cell under pathological conditions, but is substantially absent under normal conditions. Alternatively, the pathological biomarker is an RNA sequence that is upregulated in the target cell under pathological conditions as compared to normal conditions.

The guide strand includes a Dicer cleavage site near the 3' end. The sequence between the Dicer cleavage site and the 3' terminus of the guide strand is either fully or partially complementary to a nucleotide sequence found in the therapeutic target molecule (e.g., target gene, target mRNA or target miRNA). When this is the case, the Cond-siRNA is said to target the gene or RNA molecule. In certain embodiments, the guide strand is 100% complementary to the nucleotide sequence found in the therapeutic target molecule. Other embodiments may include a guide strand that is largely complementary to the nucleotide sequence found in the therapeutic target molecule, for example, the guide strand may be greater than 70% complementary, greater than 75% complementary, greater than 80% complementary,

greater than 85% complementary, greater than 90% complementary, greater than 95% complementary, greater than 96% complementary, greater than 97% complementary, greater than 98% complementary, or greater than 99% complementary to the nucleotide sequence found in the therapeutic target molecule.

A challenge of using oligonucleotides in vivo lies in preventing nuclease degradation of RNA nucleotides. Several chemical modifications in the sensor strand can be used to overcome this challenge. For example, Locked Nucleic Acids (LNAs) include a modification of RNA nucleotides with an extra bridge between the 2' O and 4' C increases thermal stability of RNA duplexes and allows for resistance to nucleases. 2' O-Methyl modifications confer stability, increase binding affinity to RNA nucleotides and prevent degradation by nucleases. And, phosphorothioate: modification by replacing one of the non-bridging oxygens in the phosphate linkage between bases with a sulfur that reduces nucleolytic degradation; however also lowers binding affinity.

Thus, in certain embodiments, the RNA-sensor complex includes one or more modifications to the nucleotide sequence of the sensor strand, the core strand, and/or the guide strand. Exemplary modifications that may be used include, but are not limited to, locked nucleic acids (LNA), peptide nucleic acids (PNA), 2'-O-methyl modifications, morpholino modifications, phosphorothioate modifications, terminal modifications, and other linker or backbone modifications or connections. Additional chemical modifications may be chosen according to methods described in U.S. Pat. No. 9,725,715B2, the disclosure of which is hereby fully incorporated herein.

The approach of designing a cond-siRNA sensor complex for use in treating a disease or other pathological condition using the cond-siRNA sensor complexes is advantageous in that it allows the complex to become biologically active only in diseased cells AND remain OFF in healthy cells. In addition, the approach allows for increased disease cell specificity and prevents toxicity from delivery to unintended off-targets. Further, the approach combines disease specificity from one gene with treatment efficacy from a second gene to create therapeutics that are precisely tailored to specific gene expression patterns. Still further, the approach is advantageous due to steric hindrance of the two RNA duplexes positioned in a parallel configuration (FIG. **4**). The sensor strand inhibits RNAi loading of siRNA and will only displace when activated in disease cells.

Overview of Methods for Designing a Conditional siRNA Complex

An siRNA complex is designed based on biomarkers and therapeutic target molecules that are specific to each cell type, pathological condition, and/or indication. According to certain embodiments, methods for designing and testing each conditional siRNA complex includes several steps, as described below.

FIG. **5** shows an overview of the design process. In certain embodiments methods for designing a conditional siRNA complex (the "design method") includes a step of determining a biomarker that will serve as an input for activation and a therapeutic target for RNAi inhibition. This step may include a determining one or more factors that are differentially expressed (i.e., upregulated or present in a diseased cell as compared to a normal cell) using methods known in the art.

The design method further includes a step of generating a list of candidate target segments of the biomarker (i.e., target mRNA sequence or target miRNA sequence) that can serve as a biomarker segment for binding the sensor strand, and then designing sensor strands for each biomarker.

The design method further includes a step of estimating the thermodynamic stability of the resulting sensor strand-biomarker duplexes (the sensor duplex) generated by the target segments and sensor strands by using secondary structure prediction tools used in the art [15].

The design method further includes a step of checking for the uniqueness of the binding site for the most stable sensor duplexes against the known transcriptome of the animal to which the conditional siRNA complex will be tested against.

The design method further includes a step of generating a list of guide strand sequences by using a protocol that may include, but is not limited to, standard siRNA design tools, literature references, or heuristic rules.

The design method further includes a step of creating a Dicer substrate from the chosen guide strand sequences.

The design method further includes a step of generating sequences for the core strand that connect the sensor strands to the guide strands.

The design method further includes a step of checking that the sensor: guide pairing does not create unwanted interactions.

The design method further includes a step of selecting a pattern of suitable chemical modifications as described herein, and optionally simulating the constructs using molecular simulation methods used in the art [16] to simulate the constructs (optional).

The design method may also include a method of synthesizing or purchasing the sensor, core, and guide strands from commercial vendors such as Qiagen, Dharmacon, or IDT, the constructs of which are then assembled, characterized, and purified using gel electrophoresis.

The design method further includes a step of conducting preliminary biological testing and validation of the construct function, and then optionally test in in vitro and in vivo models of pathological conditions, including, but not limited to, MI induced maladaptive hypertrophy as described below.

Additional embodiments related to designing the guide, the sensor and the core strands are explained below.

Method for Designing Sensor Strands for mRNA Biomarker

According to certain embodiments, methods for designing and testing sensor strands that target an mRNA biomarker includes an algorithm that includes several steps, as described below.

In certain embodiments, a method for designing a sensor strand for an mRNA biomarker (the "mRNA sensor design method") includes a step of identifying the 3' UTR for each messenger RNA biomarker.

The mRNA sensor design method further includes a step of generating all possible consecutive 31 base sequences for each 3' UTR identified above.

The mRNA sensor design method further includes a step of obtaining the prospective sensor strand sequence for each sequence segment from the previous step by identifying the reverse complement (full or partial) of each sequence

The mRNA sensor design method further includes a step of checking each sensor strand sequence for the following undesirable features: (i) three or more consecutive Gs, and (ii) four or more consecutive A or U bases.

The mRNA sensor design method further includes a step of checking each sensor strand sequence for the following desirable features: (i) higher than 50% G/C bases—this correlates with thermodynamic stability, (ii) "three lettedness," (iii) The first base at the 5' end of the sensor strand is a C or a G; and (iv) the 9th base from the 3' end of the sensor strand is a C or a G. According to the embodiments

described herein, "three letteredness" is defined as the proportion of the sequence comprising of the three most numerous bases (e.g., the extent to which sequence is mostly made of A, U, C; or C, G, A; or A, U, G). A higher three letteredness score correlates with lower internal secondary structure. Exemplar ranking tables can be seen in FIGS. **39-44**, which correspond to the genes or nucleotide sequences in Appendices C-H, submitted herewith.

The mRNA sensor design method further includes a step of ranking all possible sensor strands. Strands with the least number of features from 4 and the highest scores from 5 are ranked highest

The mRNA sensor design method further includes a step of generating hypothetical sensor duplexes using the pattern shown in FIG. **6**, starting from the highest ranked strands.

The RNA sensor design method further includes a step of using Nupack or similar secondary structure prediction codes to calculate the following, starting from the highest ranked strands: (i) the internal secondary structure of the sensor strand (lower amounts of internal secondary structure are desirable (FIG. **7**), (ii) the thermodynamic stability of the hypothetical duplex from 7. Ideally, at 1 nM strand concentration, Nupack should predict that >90% or >95% of component strands should form the hypothetical sensor duplex (FIG. **8**); and (iii) if sensor duplex is not stable, can adjust 1 to 5 bases at the 5' terminus of the sensor sequence to increase stability at the cost of reducing complementarity to the corresponding binding site on the putative biomarker.

The RNA sensor design method further includes a step of screening the sensor strand for thermodynamically stable duplexes using NCBI BLAST according to the following parameters: (i) use the "somewhat similar" search option, (ii) for sensor sequences, the 8 bases at the 3' terminus (constituting the 3' toehold) should have no more than 5 bases complementary to known transcripts in the target animal (eg, human or mouse) other than the intended biomarker, and (iii) if the first two criteria not met, broaden sequences considered in 1 to the coding region or the entirety of the mRNA.

Method for Designing Sensors for miRNA Biomarker

According to certain embodiments, methods for designing and testing sensor strands that target an miRNA biomarker includes an algorithm that includes several steps, as described below.

In certain embodiments, a method for designing a sensor strand for an miRNA biomarker (the "miRNA sensor design method") includes a step of identifying a guide sequence for each miRNA biomarker, to which the sensor strand is designed to bind (typically approximately 21 bases according to one aspect)

The miRNA sensor design method further includes a step of obtaining the reverse complement (full or partial) of the miRNA guide sequence.

The miRNA sensor design method further includes a step of adding 8 more bases to the 5' end of the sequence from the prior step.

The miRNA sensor design method further includes a step of generating hypothetical sensor duplexes using the pattern shown in FIG. **9**, starting from the sequence developed in the prior step.

The miRNA sensor design method further includes a step of using Nupack or similar secondary structure prediction codes to calculate the following: (i) the thermodynamic stability of the hypothetical duplex from the prior step. Ideally, at 1 nM strand concentration, Nupack should predict that >90% or >95% of component strands should form the hypothetical sensor duplex. (ii) if sensor duplex is not stable or the secondary structure is incorrect, determine whether the 8 terminal bases at the 5' end of the sensor strand, or the length of strand A or strand B can be altered or modified to optimize thermodynamic stability.

The miRNA sensor design method further includes a step of screening the sensor strand for thermodynamically stable duplexes in NCBI BLAST according to the following parameters: (i) use the "somewhat similar" search option, (ii) for sensor sequences, the 8 bases added at the 5' end of the sensor should not increase complementarity to transcripts other than the intended miRNA. If they do, adjust the sequence and start over from 4.

Methods for Designing a Guide Strand Sequence Against a Therapeutic Target Molecule

According to certain embodiments, methods for designing a guide strand sequence against a therapeutic target gene or RNA molecule (e.g., mRNA or miRNA) includes several steps, as described below.

In certain embodiments, a method for designing a guide strand sequence against a therapeutic target (the "guide strand design method") includes a step of obtaining one or more prospective guide strand sequences using at least one of the following methods: (i) find a published guide strand sequence for the intended target; (ii) find a known miRNA target site on the target gene, or (iii) use a published algorithm or design tool known in the art [17, 18].

The guide strand design method further includes a step of checking the guide sequence to make sure that the 6 bases at the 5' domain (FIG. **10**) is more AU rich than the 6 bases in the 3' domain (FIG. **10**). This will improve probability for correct strand loading [19]. Ideally, the 3' domain should be CG rich, and terminate in a CG base-pair.

The guide strand design method further includes a step of adding four terminal bases to the 5' end of the guide strand to complete the duplex. Those should be CG rich to improve thermodynamic stability.

The guide strand design method further includes a step of constructing the hypothetical RNAi targeting duplex as shown in FIG. **10**.

The guide strand design method further includes a step of checking that the guide strand has weak internal secondary structure and minimal tendency to bind to itself (no more than 10% at 1 nM strand concentration) using Nupack or similar standard secondary structure calculation tool. Adjust bases added in 3 as necessary.

Methods for Designing a Core Strand Sequence and Checking Compatibility of Pairing Sensor to Guide

According to certain embodiments, methods for designing a core strand sequence and checking compatibility of pairing sensor to guide includes several steps, as described below.

In certain embodiments, a method for designing a guide strand sequence against a therapeutic target (the "core strand design method") includes a step of choosing a suitable combination of sensor and guide strands, methods for designing those strands are discussed above and in the working examples, according to the embodiments described herein.

The core strand design method further includes a step of constructing the core strand by constructing a strand of the form 5'-B-C3-P-C3 A-3' where A and B are the sequence of complementary strand B from the hypothetical sensor duplex (FIG. **6** or **9**), P is the sequence of the passenger strand from the hypothetical RNAi duplex (FIG. **10**) and C3 are C3 linkers.

The core strand design method further includes a step of using Nupack or similar standard secondary structure calculation tool to check that the guide strand and core strand

base-pairing has the following properties: (i) >95% of strands are base-paired in the correct duplex at 1 nM strand concentration, (ii) the guide strand duplex has the correct conformation, with a ~23 base-pair duplex, a two base 3' guide strand overhang, and 10-12 base 5' and 3' core overhangs with minimal secondary structures, and (iii) If above criteria not met, choose new sensor or guide pairing.

Conditional siRNA Complexes for Treating Cardiac Hypertrophy

Disclosed herein is a therapeutic strategy that targets molecular pathways involved in cardiac hypertrophy (that often results after a myocardial infarction), with minimal off-target effects. A myocardial infarction (MI) is a heart attack. MIs can occur when a blood clot blocks a coronary artery, interrupting blood flow to the heart—a condition known as cardiac ischemia.

Heart muscles downstream of the blockage lose oxygen, leading to injury and death of the muscle cells. Post-MI, the hypoxia and tissue damage induces left ventricular remodeling (FIGS. **35**A, **37**). Cardiac reperfusion results in inflammation and oxidative damage. The injuries to cardiomyocytes during MI can cause a cascade of biological signaling events that leads cardiomyocytes to increase in volume and undergo proliferation in a specific way that compromises the functioning of the heart. This hypertrophic response is driven by a complex interplay of factors including a maladaptive regeneration gene program. During maladaptive regeneration, the heart undergoes changes that induce detrimental conditions to the patient (FIG. **35**B). The affected ventricle increases its volume, but the walls of the ventricle become thinner, and the ability of the heart to pump blood decreases over time. This can lead to a variety of serious problems, including heart failure, a second heart attack, or sudden death. Thus, this process is called maladaptive hypertrophy (as opposed to adaptive hypertrophy, which strengthens the heart in reaction to stimuli such as exercise).

Maladaptive cardiac hypertrophy can be ameliorated by drugs that inhibit calcineurin and histone deacetylase 2 (HDAC2), for example. However, these drugs can cause serious side effects in non-cardiac tissues. Therefore, it's necessary to have a method to restrict drug activity to the heart.

The specificity and versatility of the conditional small interfering RNAs (cond-siRNA) described herein offers a new class of therapeutics for a variety of diseases and cancers by hijacking the RNA interference (RNAi) pathway. Although current treatment options for post-MI cardiac hypertrophy alleviate the severity of the condition, it is necessary to target the internal maladaptive gene program that drives the hypertrophic responses. In particular, cond-siRNAs (FIG. **4**) are sequenced with a signal and target strand that due to steric hindrance, will only activate when the appropriate cardiac hypertrophy signal is present-thus only targeting disease cells through toehold-mediated strand displacement.

The Cond-siRNAs described herein can achieve this by using cardiac RNA biomarkers of MI as activation signals to switch ON RNAi silencing against calcineurin or HDAC2. Using this approach, RNAi silencing of the target genes are restricted to cardiomyocytes that express MI associated RNA biomarkers. This means that RNAi activity will NOT occur in other organs and tissues where inhibition of the targets can cause serious side effects. In one aspect, disclosed herein is a strand-displacement operated, programmable conditional-siRNA complex that can be activated by specific mRNA and miRNA transcripts expressed in the hypertrophied myocardium, to target unrelated pro-hypertrophic pathways by RNAi knockdown.

To design an effective Cond-siRNA for treating Cardiac Hypertrophy, in vivo and/or in vitro screening approaches for measuring relevant gene expression may be used in accordance with the embodiments described herein.

Certain genes are upregulated under pathological cardiac hypertrophic conditions, which may be candidate pathological biomarkers to guide a Cond-siRNA molecule to a population of target cells, and which can be used to displace the sensor strand of the Cond-siRNA. For example, certain signaling cascades are activated under hypertrophic stimulating conditions (see FIG. **11**). For example, genes and miRNAs that are upregulated in pathological cardiac hypertrophy were screened for differential gene expression in wild type (wt) mice as well as under various hypertrophic conditions to determine which genes are suitable candidates for use as a target for designing a sensor strand. See working examples below

In vitro screening approaches may include the use of a cardiomyocyte cell line (e.g., neonatal rat ventricular myocytes (NRVM), human cardiac myocytes (HCM)) cultured under hypoxic conditions or treated with phenylephrine. FIG. **12**A. In vivo approaches may also be used including, but not limited to, rat models for ischemic heart failure (HF) (e.g., ischemia/reperfusion model), or rat models for non-ischemic HF (e.g., thoracic aortic constriction (TAC) model). See FIG. **12**B.

Selection of RNA pathological biomarkers (input signals) for activation of Cond-siRNAs an important process for designing the cond-siRNA complexes described herein. The purpose of using pathological RNA biomarkers specific to the condition of cardiac hypertrophy for conditional RNAi activation is to ensure that RNAi activity is only active in cardiac tissues. Ideally, these biomarkers should be highly overexpressed in cardiac tissues affected by MI and not expressed in other tissues of the body. By comparing data gathered from in vitro and in vivo experiments on NRVM cell cultures and mice models with known organism wide expression patterns for the tested mRNAs and miRNAs (see working examples below), it was determined that at least three mRNAs and three miRNAs fit the criteria, including mRNAs that encode atrial naturetic peptide (ANP), B-type natriuretic peptide (BNP), and myosin heavy chain β (MHCP), and miRNAs that encode mir-23a-3p, mir-125-5p, and mir-199b-5p.

Thus therapeutic biomarkers that may be used to activate the conditional siRNA complexes in accordance with the embodiments described herein include, but are not limited to, mRNA biomarkers for MI affected cardiomyocytes, such as those described below.

In certain embodiments, a Cond-siRNA for treating cardiac hypertrophy includes a sensor strand designed to target a biomarker that is present and/or upregulated in heart cells (e.g., cardiac myocytes). Such biomarkers may include, but are not limited to, atrial naturetic peptide (ANP), B-type natriuretic peptide (BNP), myosin heavy chain β (MHCP), mir-23a-3p, mir-125-5p, and mir-199b-5p. In some aspects, the sensor strand detects an mRNA or an miRNA sequence that encodes the biomarker. And, in certain aspects, the sensor strand detects an mRNA sequence that encodes the biomarker by binding to the 3' UTR of the mRNA. Additional information regarding exemplary biomarkers is discussed below.

ANP (nppa) signal sensor strands. nppa (Natruiretic Peptide A) encodes for ANP protein that is overexpressed in hypertrophic conditions, thus is suitable as a biomarker for hypertrophy.

BNP (nppb) signal sensor strands. nppb (Natruiretic Peptide B) encodes for BNP protein that functions as a cardiac hormone and regulates natruiresis, diuresis, vasorelaxation and cardiovascular homeostasis. Low levels of BNP naturally found in the bloodstream in healthy individuals; high levels from cardiac ventricles. High concentrations of BNP in bloodstream indicates heart failure, and is a biomarker for hypertrophy. Thus, significant upregulation of BNP in induced cardiac hypertrophic conditions is indicative of effective sensor strand gene selection.

In some embodiments, a NPPB RH SSS v2.0 sensor was designed, wherein 31 bp sequence windows checked by hand through screening in entire 3' UTR of *Homo sapiens* mRNA based on A-U richness, hairpins, poly G tracts, and 8 bp toehold region. Three areas were found; NCBI Blast check for matches with other mRNAs and % yield of binding narrowed down options to chosen sensor (see NPPB sensor structures, FIG. **13**).

MHC3 (myh7) signal sensor strands. MYH7 (myosin heavy chain 7) encodes for the p-heavy chain subunit of cardiac myosin. Varying amounts of the encoded protein correlate with cardiac muscle fiber contractile velocity. myh7 is predominantly expressed in the ventricle and type I muscle fibers. Gene mutations are associated with hypertrophic cardiomyopathy, and mybh7 is upregulated in pathological cardiac hypertrophy. A significant upregulation of myh7 is seen in induced cardiac hypertrophic conditions, indicating that myh7 is another potential sensor strand gene selection.

In some embodiments, a myh7 RH SSS v2.0 sensor was designed, wherein 31 bp sequence windows checked by hand through screening of entire *Homo sapiens* mRNA. Because 3' UTR of mRNA is short with numerous poly G tracts, screening went into the coding region; however those contained secondary structure. Only 1 area found and chosen; checked NCBI Blast for matches with other mRNAs (see, e.g., myh7 sensor structures, FIG. **14**).

In some embodiments, the sensor strand is fully complementary to any of the biomarkers discussed above (i.e., 100% complementary). In some embodiments the sensor strand is partially complementary to any of the biomarkers discussed above. For example, the sensor strand may be at least 70% complementary to the biomarker, at least 70% complementary to the biomarker, at least 75% complementary to the biomarker, at least 80% complementary to the biomarker, at least 85% complementary to the biomarker, at least 90% complementary to the biomarker, at least 95% complementary to the biomarker, at least 96% complementary to the biomarker, at least 97% complementary to the biomarker, at least 98% complementary to the biomarker, or at least 99% complementary to the biomarker.

Further, the complementarity of the sensor strand to the biomarker may be matched to any 19-40 base segment of any variant of the mRNA sequence that encodes ANP (nppa), BNP (nppb), or MHCβ (myh7).

In other embodiments, the sensor strand includes one of the sequences in Table 1 below:

SEQ ID NO	STRAND	BIO-MARKER	SEQUENCE
1	SENSOR	MIR-23A-3P	5' CGAAGAACGGAAAUCCCUGGCAAUGTGAT 3'
2	SENSOR	MIR-23A-3P	5' CGAAGAACGGAAAUCCCTGGCAATGTGAU 3'
3	SENSOR	MIR-23A-3P	5' GGAGAAGAACGGAAAUCCCUGGC**AAUGUGAU** 3'
4	SENSOR	BNP	5' AUCAGAAGCAGGUGUCUGCAGCC**AGGACUUC** 3' (used with HDAC2 - 2) + 2 U
5	SENSOR	BNP	5' CUUGUGGAAUCAGAAGCAGGUGU**CUGCAGCC** 3'
6	SENSOR	BNP	5' CAAAGGCGGCCACAGGGUUGAGG**AAAAAGCC** 3'
7	SENSOR	MHCβ/myh7	5' AUCUUGAUCUGCUCAGCCCUGGA**GGUGCCAG** 3'
8	SENSOR	ANP	5' CAACAAGAUGACACAAAUGCAGCAGAGACCC 3'
9	SENSOR	ANP	5' AUGACACAAAUGCAGCAGAGACCCCAGGGGA 3'
10	SENSOR	ANP	5' CTUCACCACCUCUCAGTGGCAAUGCGACCAA 3'

In certain embodiments, a Cond-siRNA for treating cardiac hypertrophy includes a guide strand designed to target a therapeutic RNAi target that is present and/or upregulated in heart cells (e.g., cardiac myocytes) and known to the field to ameliorate post-MI maladaptive hypertrophy, but whose systemic inhibition or expression may lead to unwanted side effects. In certain embodiments, therapeutic targets that may be used to design guide strands of Cond-siRNAs include, but are not limited to, Calcineurin [7-10] (or a subunit thereof, e.g., PPP3Ca, PPP3CB, PPP3CC, PPP3R1, PPP3R2), and HDAC2 [11, 12] or HDAC2 [11, 12]. In some aspects, the guide strand binds to an mRNA or an miRNA sequence that encodes the therapeutic target.

HDAC2 guide strands. HDAC2 (Histone deacetylase 2) functions as a central regulator in transcriptional regulation, cell cycle progression and developmental pathways by modifying chromatin structure. HDAC2 inhibition represses the maladaptive regeneration program through a pathway involving GSK33, inhibiting the hypertrophic response. HDAC2 serves as a key cardiac hypertrophic regulator and a potential therapeutic target.

In some embodiments, an HDAC2 RH TGS v2.1 guide strand was designed, wherein a 23 base-pair sequence was taken from the HDAC2 *Homo sapiens* mRNA based on past research utilizing HDAC2-targeted siRNAs. Two U base pairs added to the 3' end. Four base pairs at 5' end purposefully changed to mismatch the mRNA in order to prevent potential improper Dicer cleavage and RISC complex loading incorporation. An NCBI Blast check was also done to check for matches with other mRNAs. See HDAC2 guide strand structures, FIG. **15**

Calcineurin guide strands. Calcineurin is a major promoter of cardiac hypertrophy, and inhibition of Calcineurin has been found to reduce hypertrophy. And, since it's always

present in ischemic cells, calcineurin is a good therapeutic target for the present invention.

In some aspects, the RNAi targeting segment of the guide strand (i.e., bases 1-21 from the 3' terminus) is fully complementary to any of the therapeutic targets discussed above (i.e., 100% complementary). In some aspects, the RNAi targeting segment of the guide strand (i.e., bases 1-21 from the 3' terminus) is partially complementary to any of the therapeutic targets discussed above. For example, the sensor strand may be at least 70% complementary to the biomarker, at least 70% complementary to the biomarker, at least 75% complementary to the biomarker, at least 80% complementary to the biomarker, at least 85% complementary to the biomarker, at least 90% complementary to the biomarker, at least 95% complementary to the biomarker, at least 96% complementary to the biomarker, at least 97% complementary to the biomarker, at least 98% complementary to the biomarker, or at least 99% complementary to any of the therapeutic targets discussed above. In other embodiments, bases 14-20 from the 3' terminus (the putative seed region of the guide strand) has at least 90% complementarity to the 3' UTR of an mRNA sequence that encodes at least a portion of a subunit of calcineurin (e.g., PPP3Ca, PPP3CB, PPP3CC, PPP3R1, PPP3R2) or HDAC2.

In certain embodiments, Cond-siRNAs that inhibit maladaptive hypertrophy are Cond-siRNAs that detect any biomarker from list A and target any member of list B in Table 2 below

TABLE 2

List A-cardiomyocytes biomarkers	List B-anti-maladaptive hypertrophy targets
ANP (nppa)	Calcineurin
BNP (nppb)	HDAC2
MHCβ (myh7)	
mir-23a-3p	
mir-125-5p	
mir-199b-5p	

Thus, according to some embodiments, the Cond-siRNA described herein may have a sensor strand that is mostly or completely complementary to a sequence of the RNA transcripts corresponding to biomarkers listed in A, and a guide strand that targets a member of list B in the manner described above.

In other embodiments, the sensor strand includes one of the sequences in Table 3 below:

SEQ ID NO	STRAND	THERAPEUTIC TARGET	SEQUENCE
11	GUIDE	CALCINEURIN	5' CGAGUGUUGUUUGGCUUUUCCUGUU 3' (green: change from C to G)
12	GUIDE	CALCINEURIN	5' CGAGUGUUGUUUGGCUUUUCCUGUU 3'
13	GUIDE	HDAC2	5' GCACUUAGAUUGAAACAACCCAGUU 3'
14	GUIDE	HDAC2	5' UGUUAUCUGGUGU UAUUGACCGU 3'
15	GUIDE	HDAC2	5' **CGAG**AUCUGGUGU UAUUGACCGU 3' (4 bp of 5' guide purposefully mismatched?)(used with BNP Sensor)
16	GUIDE	HDAC2	5' GCUCUUAGAUUGAAACAACCCAGUU3'

In other embodiments, a Cond-siRNA for treating cardiac hypertrophy includes a core strand designed to connect the sensor to the guide strand according a method described above. IN certain aspects the core strand includes one of the sequences in Table 4 below:

SEQ ID NO	STRAND	THERAPEUTIC TARGET	SEQUENCE
17	CORE	CALCINEURIN	5' **CGUUCUUCUC C-linker-**CAGGAAAAGCCAAACAACACUCG-linker-**GCCAGGGAUU UC** 3'
18	CORE	CALCINEURIN	5' GUCAUCUUGUUG-linker-CAGGAAAAGCCAAACAACACUCG-linker-GCUGCAUUUGU 3'
19	CORE	CALCINEURIN	5' AGGUGGUGAAG-linker-CAGGAAAAGCCAAACAACACUCG-linker-AUUGCCACUGAG 3'
20	CORE	HDAC2	5' CGUUC UUCUC C CUGGGUUGUUUCAAUCUAAGUGC GCCAG GGAUU UC 3'
21	CORE	HDAC2	5' CCUGCUUCUGAU-linker-ACGGUCAAUAACACCAGAUCUCG-linker-GGCUGCAGACA 3' (used with BNP Sensor)
22	CORE	HDAC2	5' GAUUCCACAAG-linker-ACGGUCAAUAACACCAGAUCUCG- linker-ACACCUGCUUCU 3'
23	CORE	HDAC2	5' GGCCGCCUUUG-linker-ACGGUCAAUAACACCAGAUCUCG-linker-CCUCAACCCUGU 3'

-continued

SEQ ID NO	STRAND	THERAPEUTIC TARGET	SEQUENCE
24	CORE	HDAC2	5' GCAGAUCAAGAU-linker-ACGGUCAAUAACACCAGAUCUCG-linker-UCCAGGGCUGA 3'
25	CORE	HDAC2	5' GUCAUCUUGUUGCUGGGUUGUUUCAAUCUAAGAGCGCUGCAUUUGU 3'
26	CORE	HDAC2	5' CAUUUGUGUCAUUGUUAGAUUGAAACAACCCAGGGUCUCUGCUG 3'

In some embodiments, the core strands above include 03 spacer linkers, where indicated, but any suitable linker may be used.

In certain embodiments, a Cond-siRNA for treating cardiac hypertrophy is a construct that includes a guide strand, core strand, and sensor strand as indicated in Table 5 below (also see FIGS. **16-17**):

	SENSOR	CORE	GUIDE
CONSTRUCT 1	BNP (SEQ ID NO: 4)	HDAC2 (SEQ ID NO 21)	HDAC2 (SEQ ID NO 15)
CONSTRUCT 2	BNP (SEQ ID NO: 5)	HDAC2 (SEQ ID NO 22)	HDAC2 (SEQ ID NO 15)
CONSTRUCT 3	BNP (SEQ ID NO 6)	HDAC2 (SEQ ID NO 23)	HDAC2 (SEQ ID NO 15)
CONSTRUCT 4	MHCp/myh7 (SEQ ID NO 7)	HDAC2 (SEQ ID NO 24)	HDAC2 (SEQ ID NO 15)
CONSTRUCT 5	ANP (SEQ ID NO 8)	HDAC2 (SEQ ID NO 25)	HDAC2 (SEQ ID NO 16)
CONSTRUCT 6	ANP (SEQ ID NO 9)	HDAC2 (SEQ ID NO 26)	HDAC2 (SEQ ID NO 16)
CONSTRUCT 7	ANP (SEQ ID NO 8)	Calcineurin (SEQ ID NO 18)	Calcineurin (SEQ ID NO 11)
CONSTRUCT 8	ANP (SEQ ID NO 10)	Calcineurin (SEQ ID NO 19)	Calcineurin (SEQ ID NO 12)
CONSTRUCT 9	MIR-23A-3P (SEQ ID NO: 1)	Calcineurin (SEQ ID NO 19)	Calcineurin (SEQ ID NO 12)
CONSTRUCT 10	MIR-23A-3P (SEQ ID NO. 2)	Calcineurin (SEQ ID NO 19)	Calcineurin (SEQ ID NO 12))

In other embodiments, the conditional siRNA complex may comprise any combination of one sensor strand, one guide strand, and one core strand selected from Tables 1, 3, and 4, respectively. Additional embodiments of the conditional siRNA complex showing the full complex may be found in Appendix A, which is attached hereto.

Further, as described in the examples below, several mRNA and miRNA transcripts were screened under different pro-hypertrophic conditions both in vivo and in vitro, to assist with designing cond-siRNA complex strands.

Methods of Treatment

The cond-siRNA complexes described above may be used in methods to treat cardiac hypertrophy. Thus, in some embodiments, a method for treating cardiac hypertrophy is disclosed herein, wherein the method includes a step of administering to a subject a therapeutically effective amount of one or more of the cardiac hypertrophy-related cond-siRNAs described above. As disclosed herein, the subject may be any human or other animal suffering from post-MI cardiac hypertrophy, or any other type of cardiac hypertrophy.

"Treating" or "treatment" of a condition may refer to preventing the condition, slowing the onset or rate of development of the condition, reducing the risk of developing the condition, preventing or delaying the development of symptoms associated with the condition, reducing or ending symptoms associated with the condition, generating a complete or partial regression of the condition, or some combination thereof.

The methods for treating cardiac hypertrophy include administering a therapeutically effective amount of a therapeutic composition. An "effective amount," "therapeutically effective amount" or "effective dose" is an amount of a composition (e.g., a therapeutic composition or agent) that produces a desired therapeutic effect in a subject, such as preventing or treating a target condition or alleviating symptoms associated with the condition. The precise therapeutically effective amount is an amount of the composition that will yield the most effective results in terms of efficacy of treatment in a given subject. This amount will vary depending upon a variety of factors, including but not limited to the characteristics of the therapeutic compound (including activity, pharmacokinetics, pharmacodynamics, and bioavailability), the physiological condition of the subject (including age, sex, disease type and stage, general physical condition, responsiveness to a given dosage, and type of medication), the nature of the pharmaceutically acceptable carrier or carriers in the formulation, and the route of administration. One skilled in the clinical and pharmacological arts will be able to determine a therapeutically effective amount through routine experimentation, namely by monitoring a subject's response to administration of a compound and adjusting the dosage accordingly. For additional guidance, see Remington: The Science and Practice of Pharmacy 21st Edition, Univ. of Sciences in Philadelphia (USIP), Lippincott Williams & Wilkins, Philadelphia, PA, 2005.

In some embodiments, one or more cond-siRNAs may be used alone or as part of a pharmaceutical composition for treating cardiac hypertrophy. Thus, in some embodiments, a pharmaceutical composition comprising any one or more of the cardiac hypertrophy-related Cond-siRNAs described above is disclosed. The therapeutic compositions may also include one or more pharmaceutically acceptable carriers. A

"pharmaceutically acceptable carrier" refers to a pharmaceutically acceptable material, composition, or vehicle that is involved in carrying or transporting a compound of interest from one tissue, organ, or portion of the body to another tissue, organ, or portion of the body. For example, the carrier may be a liquid or solid filler, diluent, excipient, solvent, or encapsulating material, or some combination thereof. Each component of the carrier must be "pharmaceutically acceptable" in that it must be compatible with the other ingredients of the formulation. It also must be suitable for contact with any tissue, organ, or portion of the body that it may encounter, meaning that it must not carry a risk of toxicity, irritation, allergic response, immunogenicity, or any other complication that excessively outweighs its therapeutic benefits.

The therapeutic compositions described herein may be administered by any suitable route of administration. A route of administration may refer to any administration pathway known in the art, including but not limited to aerosol, enteral, nasal, ophthalmic, oral, parenteral, rectal, transdermal (e.g., topical cream or ointment, patch), or vaginal. "Transdermal" administration may be accomplished using a topical cream or ointment or by means of a transdermal patch. "Parenteral" refers to a route of administration that is generally associated with injection, including infraorbital, infusion, intraarterial, intracapsular, intracardiac, intradermal, intramuscular, intraperitoneal, intrapulmonary, intraspinal, intrasternal, intrathecal, intrauterine, intravenous, subarachnoid, subcapsular, subcutaneous, transmucosal, or transtracheal. In one embodiment the cardiac hypertrophy-related cond-siRNAs or therapeutic compositions thereof is administered by intracardial injection (FIG. **18**) to ensure local delivery to the heart tissue.

Having described the invention with reference to the embodiments and illustrative examples, those in the art may appreciate modifications to the invention as described and illustrated that do not depart from the spirit and scope of the invention as disclosed in the specification. The examples are set forth to aid in understanding the invention but are not intended to, and should not be construed to limit its scope in any way. The examples do not include detailed descriptions of conventional methods. Such methods are well known to those of ordinary skill in the art and are described in numerous publications. Further, all references cited above and in the examples below are hereby incorporated by reference in their entirety, as if fully set forth herein. All appendices A-E submitted herewith constitute part of the complete disclosure.

EXAMPLES

Example 1: Prohypertrophic Gene and miRNA Expression Screening for Selection of Sensor Candidates for Treatment of Cardiac Hypertrophy

Genes and miRNA that are upregulated under pathological cardiac hypertrophic conditions were screened for differential expression in mice and in NRVM under various conditions to determine which molecules are suitable candidates for use as a biomarker target for designing a sensor strand.

Differential gene expression in tissues of wild type mice in homeostasis. Suitable pathological biomarker candidates should be differentially expressed in the heart as compared to other tissues to minimize off target effects. Several genes that are upregulated in pathological cardiac hypertrophy (DDiT4L, MYH7, ANP, BNP), as well as transcription factors that control their expression (MEF2C, Myocardin), were measured in normal heart, liver, lung, kidney, skeletal muscle, and brains of wt mice. FIG. **19**. Several miRNA were also measured, as shown in 38

Differential gene and miRNA expression in NRVM under hypoxic conditions. Suitable pathological biomarker candidates (ANP, BNP, MYH7, MEF2C, Myocardin, DDiT4L, and miRNAs) were screened in NRVM for differential expression under hypoxic conditions as shown in FIGS. **20-21**.

This experiment mimics oxygen deprivation (hypoxia) during myocardial infarction (MI). NRVM cells were prepared cultured on standard petri dish substrates using techniques known to those who are skilled in the art [1,2]. Cultured NRVM cells are then exposed to hypoxic conditions (0.2% 02 atmosphere) for 24 hours at 37 C. This was followed by incubation for 12 hours under normal oxygen conditions (95% ambient air/5% CO2).

Following incubation, NRVM cells were harvested and total RNA was extracted using protocols and kits standard in the art [3]. The messenger RNAs ANP, BNP, Myh7, MEF2C, Myocardin, DDiT4L, and the microRNAs mir-23a-3p, mir-125b-5p, mir-199b-5p, mir-208 and mir-195 were quantified by quantitative RT-PCR using standard methods appropriate for mRNAs4 and miRNAs [5].

Results are presented in FIGS. **20-21** as fold change in copy numbers of mRNA or miRNA present in NRVM cells exposed to hypoxia compared to those incubated for 36 hours under normal oxygen conditions.

The results of this experiment show that ANP, BNP, DDiT4L, mir-23a-3p, and mir-199b-5p, were over expressed by more than 4× under hypoxic conditions.

Differential gene and miRNA expression in NRVM after phenylephrine treatment. Expression of miRNAs, and of ANP, BNP, MYH7, MEF2C, Myocardin, DDiT4L was measured in phenylephrine (PE) treated as compared to untreated NRVM.

Phenylephrine stimulation is a standard method for studying hypertrophy in cardiomyocytes [6,7]. In this experiment, NRVM cells were prepared by standard protocols. Phenylephrine was then added to the culture media to 50 μM concentration for 24 hours. After 24 hours, cells were harvested for RNA isolation and analysis as described above.

The results of the experiment show that ANP, BNP, Myh7, myocardin mRNA were overexpressed by more than 10× after PE stimulation (FIG. **22**), and that miRNAs, mir-23a-3p, mir-125b-5p, and mir-199b-5p were overexpressed by more than 4× after PE stimulation (FIG. **23**).

Differential gene expression in mouse models of heart failure. Expression of ANP, BNP, MYH7, MEF2C, Myocardin, DDiT4L was measured in heart tissue of mice with non-ischemic heart failure in a thoracic aortic constriction (TAC) model and of mice with ischemic heart failure in an ischemia/reperfusion (I/R) model as compared to sham-treated mice.

In experiments related to the ischemia/reperfusion (I/R) model, mice underwent procedures to simulate ischemic (deprivation of blood flow) heart failure. At day zero, mice were subject to ischemic heart failure via surgical clamping of a coronary artery for 20 min, followed by reperfusion. After 28 days, the experimental mice were sacrificed. Heart tissue was harvested and RNA was isolated using standard protocols as described above. mRNA and miRNAs were quantified using RT-PCR as described above. The mRNA and miRNA in the treated mice were compared with those found in control mice who were subjected to a sham

procedure that did not involve clamping of the coronary artery to induce ischemia/reperfusion.

The results show that all mRNAs tested were overexpressed by more than 10× in mice with ischemic HF (FIG. **24**). ANP and myh7 were overexpressed by more than 1000× (FIG. **24**). And for miRNAs, only mir-23a-3p was significantly overexpressed, by ~15× (FIG. **25**).

In experiments related to the non-ischemic HF model (TAC), mice underwent thoracic aortic constriction (TAC) procedures to induce non-ischemic heart failure. Briefly the upper thorax of mice constricted to reduce blood flow through the aorta for 28 days. This induced non-ischemic heart failure. After 28 days, the animals were sacrificed and heart tissue was harvested. RNA was isolated using standard protocols as described above. mRNA and miRNAs were quantified using RT-PCR as described above. The mRNA and miRNA in the treated mice were compared with those found in control mice who were subjected to a sham procedure that did not involve aortic constriction.

The results show that all mRNAs tested were overexpressed by more than 20× in the constricted mice (FIG. **24**). ANP and myh7 were overexpressed by more than 1000× (FIG. **24**). For miRNAs, all tested miRNAs were overexpressed by more than 10×. (FIG. **25**). And, mir-23a-3p was overexpressed by ~80× (FIG. **25**).

Example 2: Design of ANP:Calcineurin Cond-siRNA

The 5' UTR and coding sequences of messenger RNAs are frequently occupied by mRNA binding proteins or transiting ribosomes. In mammals, miRNAs commonly bind at 3' UTR sites to regulate mRNAs. Thus, binding sites in the 3' UTR may be more accessible than sites in the 5' UTR and the coding sequence of region of mRNAs.

When designing sensors to detect mRNAs, it is desirable to start with sites in the 3' UTR. If such sites cannot be found or there are other reasons (such as the need to detect a particular important sequence in the coding region or the 5' UTR), then sensors can be designed to those sites.

ANP 3'UTR sequencing results. Murine models were used to test the ability of ANP:Calcineurin Cond-siRNAs to inhibit phenylephrine induced cardiomyocytes hypertrophy. Thus, an ANP sensor was designed to target rat ANP.

To design the ANP sensor, the 3' UTR of ANP mRNA found in neonatal rat ventricular cardiomyocytes cells was sequenced by extracting RNA using standard procedures, amplifying the 3' UTR via RT-PCR, and submitting the amplified DNA for sequencing by the Massachusetts General Hospital's DNA sequencing core.

The sequenced DNA is as follows (N indicates indetermined base)

ANP 3'UTR sequencing results from CCIB DNA Core (MGH)
293387-293389_D10_1_074_nppa_3_UTR_Ane.seq
this is the forward sequence:

(SEQ ID NO: 27)
TCAGCCANNNNNNNNNGAGCAGATCGCAAAAGATCCCAAGGCCTTGCG

GTGTGTCACACAGCTTGGTCGCATTGCCACTGAGAGGTGGTGAATACCC

TCCTGGAGCTGCAGCTTCCTGTCTTCATCTATCACGATCGATGTTAAGTG

-continued

TAGATGAGTGGTTTAGTGAGGCCTTACCTCTCCCACTCTGCATATTAAGG

TAGATCCTCACCCNNNNANNANNNNCNNNNNNNNNNNNNNNNNNNNNNN

NNNNNNNN

Using NCBI BLAST, it was determined that the central sequence

(SEQ ID NO: 28)
GAGCAGATCGCAAAAGATCCCAAGGCCTTGCGGTGTGTCACACAGC**TTGG**

TCGCATTGCCACTGAGAGGTGGTGAATACCCTCCTGGAGCTGCAGCTTCC

TGTCTTCATCTATCACGATCGATGTTAAGTGTAGATGAGTGGTTTAGTGA

GGCCTTACCTCTCCCACTCTGCATATTAAGGTAGATCCTCACCC

Is 99% homologous to *Rattus norvegicus* nppa mRNA 3' UTR and 92% homologous to *Mus musculus* nppa mRNA 3' UTR.

Generation of Sensor Candidates:

To generate candidate sensor strands, the reverse complement of the above sequence was determined.

(SEQ ID NO: 29)
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGNNNNTNNTNNNNGGGTGAG

GATCTACCTTAATATGCAGAGTGGGAGAGGTAAGGCCTCACTAAACCACT

CATCTACACTTAACATCGATCGTGATAGATGAAGACAGGAAGCTGCAGCT

CCAGGAGGGTATTCACCACCTCTCAGTGGCAATGCGACCAAGCTGTGTGA

CACACCGCAAGGCCTTGGGATCTTTTGCGATCTGCTCNNNNNNNNNTGGC

TGA

Then, a Python script was used to generate all possible consecutive 31 nt segments (8 nt for toehold, plus 23 nt for duplex region) of the central bold sequence (rat nppa 3 prime utr sensor.xlsx). These are the initial possible sensor sequences for this region (T needs to be converted to U). The python script is attached herewith as Appendix B.

The Python code that was generated performed following analyses for each sensor sequence: (i) add one demerit point for each occurrence of three or more consecutive Gs (eg: GGG, GGGG, GGGGG); (ii) add one demerit point for each occurrence of four or more consecutive A/Ts (eg: ATAT, AAAA, TTTT, TTAT, etc), (iii) calculate the percent of the sequence composed of G or Cs; and (iv) calculate the percent of the sequence accounted for by the most numerous three bases (e.g., out of A, G, C, T, if A, G and T are the most numerous in the sequence, what percent of bases are A, G or T).

Then the list of possible sensors were ranked by the following criteria, in order of importance: (i) least number of demerit points, preferably 0' (ii) highest 3 letteredness; and (iii) highest GC content (see, e.g., FIGS. **41-42**)

The sequences on the ranked list were screened one by one for two qualities: (i) the hypothetical sensor duplex has high stability and correctness according to standard RNA secondary structure prediction codes; and (ii) the sensor strand has few significant matches to RNA transcripts other than nppa mRNA in rats and mice that extends from the toehold region (8 bases at 3') into more than 50% of the duplex region (bases 9 to 31 from the 3').

The following sensor sequence was identified as favorable:

(SEQ ID NO: 30)
ATTCACCACCTCTCAGTGGCAATGCGACCAA

To further improve the thermodynamic stability of the sensor, the first base was changed at the 5' from an A to a C. This gives the following sensor sequence:

Sensor (mutated base underlined):
(SEQ ID NO: 31)
CUUCACCACCUCUCAGUGGCAAUGCGACCAA

On nupack, the hypothetical sensor duplex constructed from this sequence showed 8 thermodynamic stability, with an equilibrium concentration of 0.97 nM. Also see FIG. **26**.

NCBI BLAST of the sensor sequence using "somewhat similar" settings showed no significant sequence matches other than to mouse and rat ANP (nppa) mRNA.

Calcineurin is a heterodimer composed of one of three catalytic isozymes (PPP3CA, PPP3CB, PPP3CC) and one of two regulatory subunits (PPP3R1 and PPP3R2). To target Calcineurin, a guide sequence against the PPP3CA subunit of Calcineurin was identified that targets a widely conserved target site present in human, rat, and mice: UGUUGU UUGGCUU UUCCUG UU (SEQ ID NO:32)

The segment CGAG was then added to the 5' end to create a 23 nt guide strand, and then generated the core strand according to the previous stated rules. Those sequences are shown below:

Guide:
(SEQ ID NO: 11)
CG AG UGUUGU UUGGC UU UUCCUG UU

Sensor (mutated base underlined):
(SEQ ID NO: 33)
CUUCACCACCU CUCAGUGGCAAU GCGACCAA

Core:
(SEQ ID NO: 19)
AGGUGGUGAAG-linker-CAGGAAAAGCCAAACAACACUCG-linker-AUUGCCACUGAG

The guide strand plus the core strand showed good thermodynamic stability as predicted by Nupack (FIG. **27**)

Then, chemical modifications were added according to schemes previously disclosed in U.S. Pat. No. 9,725,715, the subject matter of which is incorporated by reference herein. The final sequences are shown below:

Sensor:
(SEQ ID NO: 34)
/5Sp9/mC*+T*mU*mC*+A*mC*mC*+A*mC*+C*mU*mC*mU*+C*mA*mG*+T*mG*+G*mC*mA*+A*mU*mG*mC*+G*mA*mC*mC*+A*mA*/3AmMO/

Guide:
(SEQ ID NO: 35)
/5AmMC6/+C*+G rArG rUrGrUrUrGrU rUrUrGrGrC rUrU rUrUrCrCrUrG rUrU

-continued

Core:
(SEQ ID NO: 36)
mArGmGrUrGrGrUrGrArArG/iSpC3/mC*+A*mGrGrArArArArGrCrCrArArArCrArArCrArCrUrC*mG/iSpC3/rArUrUrGrCrCrArCrUrGrAmG

The nucleotides and modifications are indicated as follows: (1)+A, +T, +C, +G are LNA; (2) mA, mU, mC, mG are 2'-O-methyl; (3) rA, rU, rC, rG are RNA; (4) * denotes phosphorothioate backbone connection; (5) /5Sp9/ is a triethylene glycol linker; (6) /iSpC3/ is an internal C3 spacer; (7) /5AmMC6/ is a 5' primary amine modification on a C6 linker; (8) /3AmMO/ is a 3' primary amine modification.

Example 3: Design of mir-23a-3p:Calcineurin Cond-siRNA

An mir-23a-3p sensor was designed as follows. The mir-23a entry for miRbase is found at the following URL: http://www.mirbase.org/cgi-bin/mirna entry.pl?acc=M10000079

The sequence of mir-23a-3P sequence, 5'-3' is:

>hsa-miR-23a-3p MIMAT0000078
(SEQ ID NO: 37)
AUCACAUUGCCAGGGAUUUCC

The reverse complement of mir-23a-3p is GGAAAUCCCUGGCAAUGUGAU (SEQ ID NO:38)

The Cond-siRNA sensor to sense a microRNA input is that the microRNA guide strand is usually only 21 nt long, whereas the Cond-siRNA sensor's duplex region is usually 23 nucleotides long and the toehold is usually 5 to 8 nucleotides long. This means that a microRNA guide strand is not long enough to completely displace the sensor strand from the core strand.

This issue was solved by configuring the sensor strand so that the guide strand will displace the sensor from base-pairing with the 3' overhang of the core strand and the last few bases at the 5' terminus of 5' overhang of the core strand.

This way, the 3' overhang of the core strand becomes unprotected and is degraded. The 5' terminus of the 5' overhang also becomes unprotected and subject to degradation, leading to eventual degradation of the entire 5' overhang. This then allows the sensor strand to completely dissociate from the RNAi region.

Thus, assuming a 21 nt miRNA guide strand, some of the possible geometries for the sensor strand, starting from the 3' end, are shown in Table 6 below:

Scheme	Toehold length	Length bound to 3' core strand overhang	Length bound to 5' core strand overhang
A	6	11	12
B	7	11	12
C	7	10	13
D	6	10	13
E	6	10	12
F	7	11	11

In Table 6, scheme A gives a 23 bp sensor duplex and allows the miRNA to displace up to 4 terminal bases of the 5' core strand segment, scheme B, 23 bp sensor, 3 terminal bases displaced, scheme C, 23 bp sensor, 4 terminal bases displaced, scheme D, 23 bp sensor, 5 terminal bases displaced, scheme E, 22 bp sensor, 5 terminal bases displaced, and scheme F, 22 bp sensor, 3 terminal bases displaced

Calcineurin Sensor Design:

Scheme F from Table 6 was used to design the following calcineurin sensor:

```
                                        (SEQ ID NO: 39)
5' CGAAGAACGGAAAUCCCUGGCAAUGUGAU 3'
```

A sequence: CGAAGAAC (SEQ ID NO:40) is added to the 5' of the sensor. This sequence is designed to improve thermodynamic stability of the sensor duplex, minimize secondary structure in the sensor strand, and minimize overlap with non-mir23a-3p transcripts.

According to NCBI BLAST, the sensor has no significant unintended matches to human RNA transcripts, and there are only a few significant unintended matches to mouse RNA transcripts.

The same Calcineurin PPP3CA siRNA guide identified for the ANP: Calcineurin construct above was used and the core strand sequence was generated using the algorithms described herein.

```
Core:
                                        (SEQ ID NO: 41)
UCCGUUCUUCG-linker-CAGGAAAAGCCAAACAACACUCG-linker-

UGCCAGGGAUU
```

The guide strand plus the core strand showed good thermodynamic stability as predicted by Nupack (FIG. **28**), as did the hypothetical sensor duplex (FIG. **29**).

Thus, the final fully modified sequences are as follows:

```
Calcineurin guide:
                                        (SEQ ID NO: 42)
C6Amine+C*+GrArG rUrGrUrUrGrU rUrUrGrGrC rUrU

rUrUrCrCrUrG rUrU

Mir-23a-3p sensor using a 22 bp sensor duplex
with LNA pattern:
                                        (SEQ ID NO: 43)
/5Sp9/mC*+G*mA*+A*mG*mA+A*mC *+G*mG*mA*+A*mA*mU*

mC*mC*+C*mU*mG*+G*mC*mA*+A*mU*mG*+T*mG*+A*+T*/

3AmMO/

Core strand:
                                        (SEQ ID NO: 44)
mUrCrCrGrUrUrCrUrUrCrG/iSpC3/mC*+A*mGrGrArArArArGr

CrCrArArArCrArArCrArCrUrC*mG/iSpC3/rUrGrCrCrArGrGr

G mA rU mU
```

The nucleotides and modifications are indicated as follows: (1)+A, +T, +C, +G are LNA; (2) mA, mU, mC, mG are 2'-O-methyl; (3) rA, rU, rC, rG are RNA; (3) * denotes phosphorothioate backbone connection; (4) /5Sp9/ is a triethylene glycol linker; (5) /iSpC3/ is an internal C3 spacer; (6) /5AmMC6/ is a 5' primary amine modification on a C6 linker; (7) /3AmMO/ is a 3' primary amine modification.

Example 4: Synthesis and Testing of Cond-siRNA Constructs

To demonstrate use of Cond-siRNAs to inhibit hypertrophy of cardiomyocytes, Cond-siRNAs were designed and synthesized to detect murine ANP or mir-23a-3p and inhibit calcineurin. The constructs are shown in FIGS. **16** and **17**. All strands were purchased from a commercial oligonucleotide vendor (Exiqon Inc, now a part of Qiagen).

Assembly and purification. Sensor, core, and guide strands were mixed at 1.0:1.1:1.0 ratios at 50 nM to 1 uM strand concentrations and underwent thermal annealing in 1×PBS buffer (80 C for 30 seconds followed by constant temperature incubation at 50 C to 60 C for ~1 hour followed by cooling to room temperature).

Where purification was desired, constructs were annealed at 500 nM, loaded at 20 uL per well in 10% non-denaturing PAGE. Run in 1×TBE buffer at 120V for 90 min. The correct bands were excised. The Cond-siRNA constructs were then extracted via the crush and soak method using standard RNA isolation kits.

FIG. **30** shows an example gel where Cond-siRNAs were assembled and purified.

Dual luciferase assays of mir-23a-3p:calcineurin Cond-siRNA (FIG. **31**). For this assay, the Cond-siRNA described above was assessed for its ability of to keep RNAi activity OFF in the absence of the correct biomarker and switching RNAi ON in the presence of RNA transcripts bearing the mir-23a-3p sequence. For this test, unpurified mir-23a-3p: calcineurin Cond-siRNAs was co-transfected at the indicated concentrations into human Hek 293 cells, along activator and dual luciferase plasmids.

The activator plasmids expressed either a null transcript, a transcript with an incorrect activator, the 21 base mir-23a-3p sequence, or a longer sequence that was complementary to the entire sensor strand.

The dual luciferase plasmid encoded Firefly luciferase as the control and a Renilla luciferase with the calcineurin target site in its 3' UTR as the target of RNAi.

The results show that this Cond-siRNA had significantly increased RNAi activity against the calcineurin target when either the mir-23a-3p sequence or the fully matching sequence was expressed. FIG. **31**. Thus, this construct should be able to activation RNAi activity against calcineurin in the presence of mir-23a-3p.

in vitro experiment for purified ANP:calcineurin Cond-siRNA in NRVM cells under PE stimulation. For this experiment, it was tested whether the murine ANP calcineurin Cond-siRNA could detect overexpression of ANP upon phenylephrine (PE) stimulation, and activate RNAi knockdown against calcineurin.

The biological effects of ANP:calcineurin against murine biomarkers and targets is tested because there are no suitable human models to test against. The biological effect of this murine oriented Cond-siRNA should be representative of biological effects that Cond-siRNA configured for humans would have.

For this experiment, NRVM cells were incubated using standard protocols under normal conditions (95% air, 5% CO2, 37 C). The purified ANP: calcineurin Cond-siRNA was transfected at 20 nM concentration into NRVM cells using RNAiMax. The transfected cells were incubated for 24 hours. PE was then added to the media to 50 μM final concentration. After a further 48 hours, cells were harvested and stained or processed for RNA isolation.

The results for RT-PCR quantitation of calcineurin mRNA are shown in FIG. **32**. For each cohort (untreated and PE treated cells), the level of calcineurin mRNA observed in cells transfected with scrambled siRNA (negative control) was normalized to 1.0. In the untreated cohort, cells transfected with ANP:Calcineurin Cond-siRNA had no detectable knockdown of calcineurin. This means that, as intended, the Cond-siRNA has very little RNAi activity in normal cells.

In cells treated with PE, the Cond-siRNA activated RNAi, and reduced calcineurin mRNA levels by ~ 50% compared with levels seen in cells transfected with the scrambled siRNA control. This shows that the ANP:calcineurin Cond-siRNA can detect overexpression of ANP mRNA, and respond with RNAi inhibition of calcineurin as intended.

The results of imaging of the treated and untreated cells by fluorescence microscopy are shown in FIG. **33**. The results show that cells treated with purified ANP:calcineurin Cond-siRNAs underwent less hypertrophy than cells treated with scrambled siRNA. Furthermore, the effects of treatment with Cond-siRNAs was similar to treatment with the positive control (commercial, non-conditional calcineurin siRNA).

The results of cell size quantitation using fluorescence microscopy are shown in FIG. **34**. The results show that PE stimulation resulting in the increase in the average cell size from ~750 μm2 to ~1300 μm2 in cells treated with the negative control scrambled siRNA. However, in cells treated with the Cond-siRNA, average cell size increased from ~750 μm2 to ~900 μm2, and was not statistically significant. This result is similar to the non-conditional, commercial calcineurin siRNA.

The above results show that the ANP:Calcineurin Cond-siRNA has low background RNAi activity, can detect and respond to PE stimulation of NRVM cells, and has significant biological effects on reducing hypertrophy of NRVM cells.

Example 5: Exemplary Guide and Sensor Strand Sequences

Below are examples of automatically generating core strand sequences from guide and sensor strand sequences. These have 23 bp sensor duplexes with 8 base toeholds

Example 5a, randomly chosen human/rat PPP3CA mRNA guide paired with randomly chosen human NPPA sensor

```
Cond-siRNA Guide:
                                        (SEQ ID NO: 45)
CCAC UUUACCAGCAUCUCAGUCAUU

Cond-siRNA Sensor:
                                        (SEQ ID NO: 46)
GGAGAGGCGAGGAAGUCACCAUCAAACCACU

Core is:
                                        (SEQ ID NO: 47)
CUCGCCUCUCC UGACUGAGAUGCUGGUAAAGUGGGAUGGUGACUUC
```

Example 5b, human/rat PPP3CA mRNA guide above paired with randomly chosen human NPPB sensor

```
Cond-siRNA Guide:
                                        (SEQ ID NO: 45)
CCAC UUUACCAGCAUCUCAGUCAUU

Cond-siRNA Sensor:
                                        (SEQ ID NO: 48)
GGAAUCAGAAGCAGGUGUCUGCAGCCAGGAC

Core is:
                                        (SEQ ID NO: 49)
CUUCUGAUUCC UGACUGAGAUGCUGGUAAAGUGGUGCAGACACCUG
```

Example 5c, human/rat PPP3CA mRNA guide above paired with randomly chosen human Myh7 sensor

```
Cond-siRNA Guide:
                                        (SEQ ID NO: 45)
CCAC UUUACCAGCAUCUCAGUCAUU

Cond-siRNA Sensor:
                                        (SEQ ID NO: 50)
CCAAGGAGCUGUUACACAGGCUCCAGCAUGG

Core is:
                                        (SEQ ID NO: 51)
CAGCUCCUUGG UGACUGAGAUGCUGGUAAAGUGGGAGCCUGUGUAA
```

Example 5d, randomly chosen human/rat HDAC2 mRNA guide paired with human NPPA sensor from example 1

```
Cond-siRNA Guide:
                                        (SEQ ID NO: 52)
CCAC UUCAUCACAAGCUAUCCGCUU

Cond-siRNA Sensor:
                                        (SEQ ID NO: 46)
GGAGAGGCGAGGAAGUCACCAUCAAACCACU

Core is:
                                        (SEQ ID NO: 53)
CUCGCCUCUCC GCGGAUAGCUUGUGAUGAAGUGGGAUGGUGACUUC
```

Example 5e, randomly chosen human/rat HDAC2 mRNA guide above paired with human NPPB sensor from example 2

```
Cond-siRNA Guide:
                                        (SEQ ID NO: 52)
CCAC UUCAUCACAAGCUAUCCGCUU

Cond-siRNA Sensor:
                                        (SEQ ID NO: 48)
GGAAUCAGAAGCAGGUGUCUGCAGCCAGGAC

Core is:
                                        (SEQ ID NO: 54)
CUUCUGAUUCC GCGGAUAGCUUGUGAUGAAGUGGUGCAGACACCUG
```

Example 5f, randomly chosen human/rat HDAC2 mRNA guide above paired with human Myh7 sensor from example 3

```
Cond-siRNA Guide:
                                        (SEQ ID NO: 52)
CCAC UUCAUCACAAGCUAUCCGCUU

Cond-siRNA Sensor:
                                        (SEQ ID NO: 50)
CCAAGGAGCUGUUACACAGGCUCCAGCAUGG

Core is:
                                        (SEQ ID NO: 55)
CAGCUCCUUGG GCGGAUAGCUUGUGAUGAAGUGG

GAGCCUGUGUAA
```

In the next examples, we reuse the guide from examples 1-6, but choose miRNA sensors. The sensors are configured as 22 bp duplexes with 7 base overhangs and symmetric 11 base core strand overhangs

Example 5g, randomly chosen human/rat PPP3CA mRNA guide paired with mir-23a-3p sensor

```
Cond-siRNA Guide:
                                (SEQ ID NO: 45)
CCAC UUUACCAGCAUCUCAGUCAUU

Cond-siRNA Sensor:
                                (SEQ ID NO: 39)
CGAAGAAC GGAAAUCCCUGGCAAUGUGAU

Core is:
                                (SEQ ID NO: 56)
UCCGUUCUUCG UGACUGAGAUGCUGGUAAAGUGG

UGCCAGGGAUU
```

Example 5h, human/rat PPP3CA mRNA guide above paired with mir-125b-5p sensor

```
Cond-siRNA Guide:
                                (SEQ ID NO: 45)
CCAC UUUACCAGCAUCUCAGUCAUU

Cond-siRNA Sensor:
                                (SEQ ID NO: 57)
CGACAGU UCACAAGUUAGGGUCUCAGGGA

Core is:
                                (SEQ ID NO: 58)
GUGAACUGUCG UGACUGAGAUGCUGGUAAAGUGG

GACCCUAACUU
```

Example 5i, human/rat PPP3CA mRNA guide above paired with mir-195b-5p sensor

```
Cond-siRNA Guide:
                                (SEQ ID NO: 45)
CCAC UUUACCAGCAUCUCAGUCAUU

Cond-siRNA Sensor:
                                (SEQ ID NO: 59)
CCUGAA GAACAGAUAGUCUAAACACUGGG

Core is:
                                (SEQ ID NO: 60)
UGUUCUUCAGG UGACUGAGAUGCUGGUAAAGUGG

UUUAGACUAUC
```

Example 5j, randomly chosen human/rat HDAC2 mRNA guide paired with mir-23a-3p sensor

```
Cond-siRNA Guide:
                                (SEQ ID NO: 52)
CCAC UUCAUCACAAGCUAUCCGCUU

Cond-siRNA Sensor:
                                (SEQ ID NO: 39)
CGAAGAAC GGAAAUCCCUGGCAAUGUGAU

Core is:
                                (SEQ ID NO: 61)
AACAGCUCCUUGG GCGGAUAGCUUGUGAUGAAGUGG

GGAGCCUGUGU
```

Example 5k, randomly chosen human/rat HDAC2 mRNA guide above paired with mir-125b-5p sensor

```
Cond-siRNA Guide:
                                (SEQ ID NO: 52)
CCAC UUCAUCACAAGCUAUCCGCUU

Cond-siRNA Sensor:
                                (SEQ ID NO: 57)
CGACAGU UCACAAGUUAGGGUCUCAGGGA

Core is:
                                (SEQ ID NO: 62)
UCCGUUCUUCG GCGGAUAGCUUGUGAUGAAGUGG

UGCCAGGGAUU
```

Example 5l, randomly chosen human/rat HDAC2 mRNA guide above paired with mir-195b-5p sensor

```
Cond-siRNA Guide:
                                (SEQ ID NO: 52)
CCAC UUCAUCACAAGCUAUCCGCUU

Cond-siRNA Sensor:
                                (SEQ ID NO: 59)
CCUGAA GAACAGAUAGUCUAAACACUGGG

Core is:
                                (SEQ ID NO: 63)
UGUUCUUCAGG GCGGAUAGCUUGUGAUGAAGUGG

UUUAGACUAUC
```

Example 6: Exemplar siRNAs Designed by a Commercial siRNA Automated Design Website

From: http://dharmacon.horizondiscovery.com/design-center/

For each category below, the design tool was tasked with designing siRNAs targeting the protein coding region of both the human and the rat mRNA. The top three candidates are shown. Cond-siRNA guides are made by adding 4 G/C rich bases to the 5' of the antisense strand.

Candidate siRNA guide strands sequences (antisense) and corresponding target sites (sense) targeting both Human (NM_000944) and Rat (NM_017041) PPP3CA mRNA

```
Sense:
                                (SEQ ID NO: 64)
5' G.A.A.C.A.A.G.A.U.C.C.G.A.G.C.A.A.U.A.U.U 3'

Antisense:
                                (SEQ ID NO: 65)
5' U.A.U.U.G.C.U.C.G.G.A.U.C.U.U.G.U.U.C.U.U 3'

Cond-siRNA Guide:
                                (SEQ ID NO: 66)
5' CGACU.A.U.U.G.C.U.C.G.G.A.U.C.U.U.G.U.U.C.U.U

3'

Sense:
                                (SEQ ID NO: 67)
5' U.G.A.C.U.G.A.G.A.U.G.C.U.G.G.U.A.A.A.U.U 3'

Antisense:
                                (SEQ ID NO: 68)
5' U.U.U.A.C.C.A.G.C.A.U.C.U.C.A.G.U.C.A.U.U 3'
```

-continued

Cond-siRNA Guide:
(SEQ ID NO: 69)
5' CGACU.U.U.A.C.C.A.G.C.A.U.C.U.C.A.G.U.C.A.U.U 3'

Sense:
(SEQ ID NO: 70)
5' G.G.U.C.A.G.A.A.G.A.A.G.A.U.G.G.A.U.U.U.U 3'

Antisense:
(SEQ ID NO: 71)
5' A.A.U.C.C.A.U.C.U.U.C.U.U.C.U.G.A.C.C.U.U 3'

Cond-siRNA Guide:
(SEQ ID NO: 72)
5' CCACA.A.U.C.C.A.U.C.U.U.C.U.U.C.U.G.A.C.C.U.U 3'

Candidate siRNA guide strands sequences (antisense) and corresponding target sites (sense) targeting both Human (NM_001142353) and Rat (NM_017042) PPP3CB mRNA

Sense:
(SEQ ID NO: 73)
5' G.C.U.A.U.A.G.A.A.U.G.U.A.C.A.G.A.A.A.U.U 3'

Antisense:
(SEQ ID NO: 74)
5' U.U.U.C.U.G.U.A.C.A.U.U.C.U.A.U.A.G.C.U.U 3'

Cond-siRNA Guide:
(SEQ ID NO: 75)
5' CGACU.U.U.C.U.G.U.A.C.A.U.U.C.U.A.U.A.G.C.U.U

Sense:
(SEQ ID NO: 76)
5' C.C.U.U.U.A.A.G.C.A.G.G.A.A.U.G.U.A.A.U.U 3'

Antisense:
(SEQ ID NO: 77)
5' U.U.A.C.A.U.U.C.C.U.G.C.U.U.A.A.A.G.G.U.U 3'

Cond-siRNA Guide:
(SEQ ID NO: 78)
5' GGACU.U.A.C.A.U.U.C.C.U.G.C.U.U.A.A.A.G.G.U.U

Sense:
(SEQ ID NO: 79)
5' G.C.A.A.U.U.G.G.C.A.A.G.A.U.G.G.C.A.A.U.U 3'

Antisense:
(SEQ ID NO: 80)
5' U.U.G.C.C.A.U.C.U.U.G.C.C.A.A.U.U.G.C.U.U 3'

Cond-siRNA Guide:
(SEQ ID NO: 81)
5' CCACU.U.G.C.C.A.U.C.U.U.G.C.C.A.A.U.U.G.C.U.U

Candidate siRNA guide strands sequences (antisense) and corresponding target sites (sense) targeting both Human (NM_001243974) and Rat (NM_134367) PPP3CB mRNA

Sense:
(SEQ ID NO: 82)
5' G.U.A.U.A.G.A.G.U.G.U.G.U.G.C.U.G.U.A.U.U 3'

Antisense:
(SEQ ID NO: 83)
5' U.A.C.A.G.C.A.C.A.C.A.C.U.C.U.A.U.A.C.U.U 3'

Cond-siRNA Guide:
(SEQ ID NO: 84)
5' CCACU.A.C.A.G.C.A.C.A.C.A.C.U.C.U.A.U.A.C.U.U 3'

-continued

Sense:
(SEQ ID NO: 85)
5' A.G.U.A.U.U.U.G.A.G.A.A.U.G.G.G.A.A.A.U.U 3'

Antisense:
(SEQ ID NO: 86)
5' U.U.U.C.C.C.A.U.U.C.U.C.A.A.A.U.A.C.U.U.U 3'

Cond-siRNA Guide:
(SEQ ID NO: 87)
5' CCACU.U.U.C.C.C.A.U.U.C.U.C.A.A.A.U.A.C.U.U.U 3'

Sense:
(SEQ ID NO: 88)
5' C.U.A.U.G.U.G.G.A.C.A.G.A.G.G.C.U.A.U.U.U 3'

Antisense:
(SEQ ID NO: 89)
5' A.U.A.G.C.C.U.C.U.G.U.C.C.A.C.A.U.A.G.U.U 3'

Cond-siRNA Guide:
(SEQ ID NO: 90)
5' CCACA.U.A.G.C.C.U.C.U.G.U.C.C.A.C.A.U.A.G.U.U 3'

Candidate siRNA guide strands sequences (antisense) and corresponding target sites (sense) targeting both Human (NM_001527) and Rat (NM_053447) HDAC2 mRNA

Sense:
(SEQ ID NO: 91)
5' G.C.G.G.A.U.A.G.C.U.U.G.U.G.A.U.G.A.A.U.U 3'

Antisense:
(SEQ ID NO: 92)
5' U.U.C.A.U.C.A.C.A.A.G.C.U.A.U.C.C.G.C.U.U 3'

Cond-siRNA Guide:
(SEQ ID NO: 52)
5' CCACU.U.C.A.U.C.A.C.A.A.G.C.U.A.U.C.C.G.C.U.U 3'

Sense:
(SEQ ID NO: 93)
5' G.G.A.U.A.U.U.G.G.U.G.C.U.G.G.A.A.A.A.U.U 3'

Antisense:
(SEQ ID NO: 94)
5' U.U.U.U.C.C.A.G.C.A.C.C.A.A.U.A.U.C.C.U.U 3'

Cond-siRNA Guide:
(SEQ ID NO: 95)
5' CCACU.U.U.U.C.C.A.G.C.A.C.C.A.A.U.A.U.C.C.U.U 3'

Sense:
(SEQ ID NO: 96)
5' A.A.G.C.A.G.A.U.G.C.A.G.A.G.A.U.U.U.A.U.U 3'

Antisense:
(SEQ ID NO: 97)
5' U.A.A.A.U.C.U.C.U.G.C.A.U.C.U.G.C.U.U.U.U 3'

Cond-siRNA Guide:
(SEQ ID NO: 98)
5' CCACU.A.A.A.U.C.U.C.U.G.C.A.U.C.U.G.C.U.U.U.U 3'

Example 7: Example Designs for miRNA Sensor Strands

Example designs for miRNA sensor strands are shown below.

miRNAs have highly conserved sequences across mammalian species. Therefore, we can design a single miRNA sensor for all test animals, including humans.

For each sequence, we first take the reverse complement of the guide sequence, then add 8 bases to create a 29 nt sensor.

```
>hsa-miR-23a-3p MIMAT0000078
                                (SEQ ID NO: 37)
AUCACAUUGCCAGGGAUUUCC

> reverse complement
                                (SEQ ID NO: 38)
GGAAAUCCCUGGCAAUGUGAU

> Sensor, add 8 bases to make 29 mer
                                (SEQ ID NO: 39)
CGAAGAAC GGAAAUCCCUGGCAAUGUGAU
```

Nupack shows minimum secondary structure and no self-self base-pairing accept

```
>hsa-miR-125b-5p MIMAT0000423
                                (SEQ ID NO: 99)
UCCCUGAGACCCUAACUUGUGA

> reverse complement
                               (SEQ ID NO: 100)
UCACAAGUUAGGGUCUCAGGGA

> Sensor, add 7 bases to make 29 mer,
                                (SEQ ID NO: 57)
CGACAGU UCACAAGUUAGGGUCUCAGGGA
```

Use secondary structure prediction codes make sure that the secondary structure is relatively open. If not, change the added bases and try again

```
>hsa-miR-199b-5p MIMAT0000263
                               (SEQ ID NO: 101)
CCCAGUGUUUAGACUAUCUGUUC

> reverse complement
                              (SEQ ID NO:  102)
GAACAGAUAGUCUAAACACUGGG

> Sensor, add 6 bases to make 29 mer,
                                (SEQ ID NO: 59)
CCUGAA GAACAGAUAGUCUAAACACUGGG
```

Acceptably Low Secondary Structure

Example 8: miRNAs

Additional miRNAs are shown below:

```
>rno-miR-23a-3p MIMAT0000792
                                (SEQ ID NO: 37)
AUCACAUUGCCAGGGAUUUCC

>hsa-miR-23a-3p MIMAT0000078
                                (SEQ ID NO: 37)
AUCACAUUGCCAGGGAUUUCC
```

-continued

```
>rno-miR-23a-3p MIMAT0000792
                                (SEQ ID NO: 37)
AUCACAUUGCCAGGGAUUUCC

>mmu-miR-125b-5p MIMAT0000136
                                (SEQ ID NO: 99)
UCCCUGAGACCCUAACUUGUGA

>hsa-miR-125b-5p MIMAT0000423
                                (SEQ ID NO: 99)
UCCCUGAGACCCUAACUUGUGA

>rno-miR-125b-5p MIMAT0000830
                                (SEQ ID NO: 99)
UCCCUGAGACCCUAACUUGUGA

>hsa-miR-199b-5p MIMAT0000263
                               (SEQ ID NO: 101)
CCCAGUGUUUAGACUAUCUGUUC

>mmu-miR-199b-5p MIMAT0000672
                               (SEQ ID NO: 103)
CCCAGUGUUUAGACUACCUGUUC
```

Example 9: Design Review for Sensor Strand miR-23a-3p with Calcineurin and HDAC2 Targets

FIG. **46** illustrates the design of sensor miR-23a-3p. FIG. **47** illustrates that the sequence of the sensor strand was checked against NCBI by blast. FIG. **48** illustrates that calcineurin and HDAC2 guide strand sequences are checked against NCBI by blast as well. FIG. **49** illustrates the secondary structure and MFE structure at 37° C. of the full miR-23a-3p sensor strand with toehold for calcineurin or HDAC2. The sensor has the following sequence, with toe hold shown in bold and underlined:

```
                                        (SEQ ID NO: 3)
5' GGAGA AGAAC G (nick) GAAA UCCCU GGCAA UGUGAU 3'

(31 bp).
```

The Nupack analysis was performed on the sensor strand. The exiqon code with LNA modifications is shown as follows:

```
                                       (SEQ ID NO: 109)
  5' G + GA + GA + AG + AA + C G G + AA + A TC +

  CCT + GGC + AA + TGT + G + A + T 3'.
```

Calcineurin is a protein phosphatase and is composed of two subunits: PPP3CA (catalytic) and PPP3R1 (regulatory). Thermo Fisher has an siRNA for this protein (PPP3CA) beginning at base pair 1549 (www.thermofisher.com/order/genome-database/browse/sirna/keyword/s72075). The guide and core strand sequences are as follows:

Guide (calcineurin target of 19 bp), starting from 1549: 5' CGAG UGUUG UUUGG CUUUU CCUG UU 3' (SEQ ID NO: 11, mutation from C to G is shown in bold and underlined);

```
Core strand:
                                       (SEQ ID NO: 17)
5' CGUUC UUCUC C CAGGA AAAGC CAAAC AACAC UCG GCCAG

GGAUU UC 3'.
```

FIG. **50** shows that NuPack analyses of miR-23a-3p sensor strand for calcineurin were performed on core (FIG.

50A), guide (FIG. 50B), Sensor with two small overhangs of core: 97% (FIG. 50C), and calcineurin guide with core: 100% (FIG. 50D).

FIG. 51 shows NCBI check for calcineurin guide strand vs. human constructs. The matches of primary concern include: *Homo sapiens* poly(ADP-ribose) polymerase family member 14 (PARP14), transcript variant X2, mRNA (20/21 plus/minus match); *Homo sapiens* uncharacterized LOC105374732 (LOC105374732), ncRNA (15 bp plus/minus match); *Homo sapiens* zinc finger FYVE-type containing 16 (ZFYVE16), transcript variant X19, mRNA (15 bp plus/minus match); and *Homo sapiens* GC-rich promoter binding protein 1 (GPBP1), transcript variant X11, misc_RNA (15 bp plus/minus match).

The guide of HDAC2 was from S100434959 (www.qiagen.com/us/shop/rnai/flexitube-sirna/?catno=S100434952#orderinginformation), having the following sequence: 5' GC ACUUA GAUUG AAACA ACCCA GUU 3' (25 bp) (SEQ ID NO: 13). The core with HDAC2 target has the following sequence, with short overhangs shown in bold and underlined: 5' CGUUC UUCUC C CUGGGUU-GUUUCAAUCUAAGUGC GCCAG GGAUU UC 3' (SEQ ID NO: 20).

FIG. 52 shows that NuPack analyses of miR-23a-3p sensor strand for HDAC2 were performed on core (FIG. 52A), guide (FIG. 52B), HDAC2 guide with core: 100% (FIG. 52C), and sensor with core overhangs: 97% (FIG. 52D).

FIG. 53 shows NCBI check for HDAC2 guide strand vs. human transcripts. The matches of primary concern include: *Homo sapiens* solute carrier family 35 member F5 (SLC35F5), transcript variant X6, mRNA (15 bp plus/minus match); and PREDICTED: *Homo sapiens* aquaporin 12B (AQP12B), transcript variant X16, misc_RNA (14 bp plus/minus match).

Example 10: Design Review for HDAC2 Targeted Conditional siRNA Constructs with Signals of BNP and MYH7

HDAC2 target guide sequence was designed as follows. HDAC2 siRNA was disclosed in published literature: www.nature.com/cddis/journal/v8/n3/extref/cddis201749x1.docx. The sequence was checked against the HDAC2 mRNA sequence from NCBI: www.ncbi.nlm.nih.gov/nuccore/NM_001527.3. A given DNA sequence was made into an RNA sequence, and then taken the reverse complement for the guide strand, starting at bp 518 on HDAC2 mRNA:

(SEQ ID NO: 111)
5' ACG GTCAATAAGA CCAGATAACA 3';

(SEQ ID NO: 112)
5' ACG GUCAAUAACA CCAGAUAACA 3';

Guide target HDAC2: 5' UGU UAUCUGGUGU UAUUGACCGU 3' (SEQ ID NO: 14); and then 4 bp of 5' guide were purposefully mismatched: 5' CGAG AUCUG-GUGU UAUUGACCGU 3' (SEQ ID NO: 15).

FIG. 54 illustrates the check of guide vs. NCBI human transcripts and sequence alignment.

Three BNP candidates were selected. The first BNP candidate had an mRNA sequence source from www.ncbi.nlm.nih.gov/nuccore/83700236. The sequence starting from 3' UTR of BNP mRNA is as follows, with the 31 bp sequence used for reference for sensor strand shown in bold and underlined:

(SEQ ID NO: 121)
GAG**GAAGUCCUGGCUGCAGACACUGCUUCUGAU**UCCACAAGGGGCUUUUU CCUCAACCCUGUGCCGCCUUUGAAGUGACUCAUUUUUUUAAUGUAUUUAU GAUUUAUUUGAUUGUUUUAUAUAAGAUGGUUUCUUACCUUUGAGCACAAA AUUUCCACGGGAAAUAAAGUCAACAUUAU AAGCUUUAAAAAAAAAAA.

The BNP sensor was designed by taking the reverse complement of the bold and underlined portion of SEQ ID NO: 121. The sequence is as follows, with the 8 bp toehold shown in bold and underlined:

(SEQ ID NO: 4)
AUCAGAAGCAGGUGUCUGCAGCC**AGGACUUC**.

The Nupack assessment was performed (www.nupack.org/partition/histogram_detail/1166536?token=PcTqQEaZRt&strand_id=0) and the MFE structure of SEQ ID NO: 4 is shown in FIG. 55.

FIG. 56 shows the BNP sensor sequence (SEQ ID NO: 4) together with core and guide sequences. FIGS. 57A and 57B show Nupack analyses of BNP sensor (SEQ ID NO: 4) with overhangs, and guide with core, respectively. The revised guide strand with the first 4 bp of 5' end with CGAG to provide mismatching in case of incorrect Dicer cleavage and RISC complex loading. The modified guide has 2 U overhang: 5' CGAG AUCUGGUGUU AUUGACCGUUU 3' (SEQ ID NO: 4). The modified core has the following sequence: CCUGCUUCUGAUACGGUCAAUAACACC-AGAUCUCGGGCUGCAGACA (SEQ ID NO: 122). FIG. 58 shows NCBI check of BNP sensor vs. human transcripts.

The design of the second BNP candidate was similar to the first except that the 31 bp sequence used for reference for sensor strand was a different portion from SEQ ID NO: 121 shown in bold and underlined:

(SEQ ID NO: 121)
GAGGAAGUCCU**GGCUGCAGACACUGCUUCUGAUUCCACAAG**GGGCUUUUU CCUCAACCCUGUGCCGCCUUUGAAGUGACUCAUUUUUUUAAUGUAUUUAU GAUUUAUUUGAUUGUUUUAUAUAAGAUGGUUUCUUACCUUUGAGCACAAA AUUUCCACGGGAAAUAAAGUCAACAUUAU AAGCUUUAAAAAAAAAAA.

The sequence of the second BNP sensor is as follows, with the 8 bp toehold shown in bold and underlined:

(SEQ ID NO: 5)
CUUGUGGAAUCAGAAGCAGGUGU**CUGCAGCC**.

The Nupack assessment was performed (www.nupack.org/partition/histogram_detail/1166628?token=wqLsVGJXbN&strand_id=0) and the MFE structure of SEQ ID NO: 5 is shown in FIG. 59. FIG. 60 shows the BNP sensor sequence (SEQ ID NO: 5) together with core and guide sequences. FIGS. 61A and 61B show Nupack analyses of BNP sensor (SEQ ID NO: 5) with overhangs, and guide with core, respectively. FIG. 62 shows NCBI check of BNP sensor second candidate vs. human transcripts.

Likewise, the design of the third BNP candidate was similar to the first and second except that the 31 bp sequenceused for reference for sensor strand was a different portion from SEQ ID NO: 121 shown in bold and underlined:

(SEQ ID NO: 121)

GAGGAAGUCCUGGCUGCAGACACUGCUUCUGAUUCCACAAGG**GGCUUUUU**

CCUCAACCCUGUGGCCGCCUUUGAAGUGACUCAUUUUUUUAAUGUAUUUA

UGAUUUAUUUGAUUGUUUUAUAUAAGAUGGUUUCUUACCUUUGAGCACAA

AAUUUCCACGGGAAAUAAAGUCAACAUUAU AAGCUUUAAAAAAAAAAA.

The sequence of the third BNP sensor is as follows, with the 8 bp toehold shown in bold and underlined:

(SEQ ID NO: 6)

CAAAGGCGGCCACAGGGUUGAGG**AAAAAGCC**.

The Nupack assessment was performed (www.nupack.org/partition/histogram_detail/1166638?token=wZSopNPdBt&strand_id=0) and the MFE structure of SEQ ID NO: 6 is shown in FIG. **63**. FIG. **64** shows the BNP sensor sequence (SEQ ID NO: 6) together with core and guide sequences. FIG. **65** shows Nupack analysis of guide with core for the third BNP candidate. FIG. **66** shows NCBI check of BNP sensor third candidate vs. human transcripts.

Myosin heavy chain 7 (MYH7) encodes for a heavy chain subunit of cardiac myosin-contractile velocity of cardiac muscle. Myosin has 2 heavy chains, 2 alkali light chains, and 2 regulatory light chains. It is expressed in normal human ventricles as well as type 1 (slow twitch) muscle fibers. Mutations in this gene result in hypertrophic cardiomyopathy, myosin storage myopathy, and numerous other cardiac diseases. See www.genecards.org/cgi-bin/carddisp.pl?gene=MYH7.

The MYH7 candidate had an mRNA sequence source from www.ncbi.nlm.nih.gov/nuccore/NM_000257.3. The sequence starting from 3' UTR of MYH7 mRNA is as follows, with the 31 bp sequence used for reference for sensor strand shown in bold and underlined:

(SEQ ID NO: 143)

UUUUUUUUUU UUUUUCUCGG CUUCAAGGAA AAUUGCUUUA

UUCUGCUUCC UCCCAAGGAG CUGUUACACA GGCUCCAGCA

UGGGGCUUUG **CUGGCACCUC CAGGGCUGAG CAGAUCAAGA**

UGUGGCAAAG.

The MYH7 sensor was designed by taking the reverse complement of the bold and underlined portion of SEQ ID NO: 143. The sequence is as follows, with the 8 bp toehold shown in bold and underlined:

(SEQ ID NO: 7)

AUCUUGAUCUGCUCAGCCCUGGA**GGUGCCAG**.

The Nupack assessment was performed (www.nupack.org/partition/histogram_detail/1167009?token=OyDl4ywh0J&strand_id=0) and the MFE structure of SEQ ID NO: 7 is shown in FIG. **67**.

FIG. **68** shows the MYH7 sensor sequence (SEQ ID NO: 7) together with core and guide sequences. FIGS. **69**A and **69**B show Nupack analyses of MYH7 sensor (SEQ ID NO: 7) with overhangs, and guide with core, respectively. FIG. **70** shows NCBI check of MYH7 sensor vs. human transcripts.

Example 11: Design Review of Conditional siRNAs in Cardiac Ischemia

NPPA (aka: ANP, ANF, ANH, or CDD), if overexpressed in heart cells, inhibits, maladaptive cardiac hypertrophy. High levels of NPPB (aka: BNP) serve as a biomarker for heart failure in ischemic patients. Overexpression or mutation of MYH7 (aka: CMD1S, C1, MYHCB, SPMD, or SPMM) can cause cells to die prematurely and increase cardiac fibrosis. This design uses NPPA, NPPB or MYH7 as sensor, and HDAC2 and calcineurin as targets. Inhibition of HDAC2 or calcineurin causes reduced cardiac hypertrophy.

Examples of NPPA HDAC2 designs are illustrated as follows. Construct #1 (best, MPE structure shown in FIG. **71**) (www.nupack.org/partition/histogram_detail/1157307?temperature=37.0&token=gYZWv2FATz&permutation_id=2&complex_id=23) was designed with the following sequences:

Core: 5' GUCAUCUUGUUGCUGGGUUGUUUCAAUCUAAGAGCGCUGCAUUUGU

3' (SEQ ID NO: 25);

Sensor: 5' CAACAAGAUGACACAAAUGCAGCAGAGACCC 3' (SEQ ID NO: 8)

Modified sensor (SEQ ID NO: 147):
CA + ACA + AG + ATG + AC + ACA + AA + TGC + AGC + AG + AGA + C + C + C
s1-s1: 28 S1: 24 DNA ™: 87 RNA ™: 92;
and

Guide: 5' GCUCUUAGAUUGAAACAACCCAGUU 3' (SEQ ID NO: 16)

Construct #3 (MPE structure shown in FIG. **72**) (www.nupack.org/partition/show/1169058?time_refresh=1.0&token=OXLbgX6bBo) was designed with the following sequences:

Core: 5' CAUUUGUGUCAUUGUUAGAUUGAAACAACCCAGGGUCUCUGCUG 3'

(SEQ ID NO: 26);

Sensor: 5' AUGACACAAAUGCAGCAGAGACCCCAGGGGA 3' (SEQ ID NO: 9)

-continued

```
Modified sensor (SEQ ID NO: 148):
A + TG + AC + ACA + AA + TGC + AGC + A + G + A + G + ACCCC + AG + GGG + A
s1-s1: 40 s1: 33 DNA ™: 95 RNA ™: 100
and

Guide: 5' GCUCUUAGAUUGAAACAACCCAGUU 3' (SEQ ID NO: 16).
```

An example of NPPA calcineurin design is illustrated as follows. Construct #1 (best, MPE structure shown in FIG. **73**) (www. www.nupack.org/partition/show/1169063? time_refresh=1.0&to ken=RnEIROmvsz) was designed with the following sequences:

```
Core: 5' GUCAUCUUGUUGCAGGAAAAGCCAAACAACACUCGGCUGCAUUUGU

3' (SEQ ID NO: 149);

Sensor: 5' CAACAAGAUGACACAAAUGCAGCAGAGACCC 3' (SEQ ID NO: 8)

Modified sensor (SEQ ID NO: 147):
Modified sensor: CA + ACA + AG + ATG + AC + ACA + AA + TGC +
AGC + AG + AGA + C + C + C
s1-s1: 28 s1: 24 DNA ™: 87 RNA ™: 92
and

Guide: 5' CGAGUGUUGUUUGGCUUUUCCUGUU 3' (SEQ ID NO: 12).
```

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APPENDIX B

```
import re
def check_sequence(seq, n, filename, exclude = ['CCC', 'GGG', '[A, U, T]{4}']):
 '"This will check through a sequence and see if it meets a set of requirements"'
 nseq = len(seq)
 assert nseq >= n
 excludereg = [ ]
 for i in exclude:
   exclude_reg.append(re.compile(i))
 # make everything upper case
 seq = seq.upper( )
 lines = [ ]
 for i in range(nseq-n+1):
  bad=0
  excluded = [ ]
    seg = seq[i:i+n]
  gcau = (seg.count('G'), seg.count('C'), seg.count('A'), seg.count('U')+seg.count('T'))
  assert (gcau[0]+gcau[1]+ gcau[2] + gcau[3]) == n
  gc_percent = float((gcau[0]+gcau[1]))/n
  for pat in exclude reg:
    x = pat.findall(seg)
    bad += len(x)
    excluded, append(x)
    threeletter = 1-float(min(gcau))/n
    lines.append((seg, excluded, gc_percent, threeletter, bad, i))
  f = open(filename, 'w')
  f.write('Sequence \t Bad Segments\t GCness\t 3-letteredness\t Number bad points\t
position\n')
  for i in lines:
   for j in i:
   fwrite(repr(j)+'\f')
  f.write('\n')
 f.close()
 return lines
def reverse_complement_RNA(input):
 output ="
 input=input.upper()
 for i in range(len(input)):
  x = input[i]
  if x== 'A':
   output += U
  elif x == 'a'
   output += 'u'
  elif x == U or x=T':
   output += 'A'
  elif x == 'u':
   output += 'a'
  elif x == 'G':
   output += 'C'
  elif x == 'g':
   output += 'c'
  elif x == 'C':
   output += 'G'
  elif x == 'c':
   output += 'g'
 return output[::-1]
# generate 31 nt sensor candidates for human myh7 3' utr
hmyh7 =
'gctttgccacatcttgatctgctcagccctggaggtgccagcaa
```

```
agccccatgctggagcctgtgtaacagctccttgggaggaagca

gaataaagcaattttccttgaagccgag' (SEQ ID NO: 150)

chmyh7 = reverse_complement_RNA(hmyh7)
print(chmyh7)
print('\n')
check_sequence(chmyh7, 31, 'myh7 human.tsv')
# generate 31 nt sensor candidates for human nppa 3' utr
hnppa ='"agata acagccaggg aggacaagca gggctgggcc tagggacaga ctgcaagagg ctcctgtccc

ctggggtctc tgctgcattt gtgtcatctt gttgccatgg agttgtgatc atcccatcta

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atggtgactt cctcgcctct cccaccccat gcattaaatt ttaaggtaga acctcacctg

ttactgaaag tggtttgaaa gtgaataaac ttcagcacca tggacagaag ac"' (SEQ ID NO: 151)

chnppa = reverse_complement_RNA(hnppa)
print(chnppa)
printin')
check_sequence(chnppa, 31, 'nppa human.tsv')
# generate 31 nt sensor candidates for human nppb 3' utr
hnppb = '"gag gaagtcctgg ctgcagacac ctgcttctga ttccacaagg

ggctttttcc tcaaccctgt ggccgccttt gaagtgactc atttttttaa tgtatttatg

tatttatttg attgttttat ataagatggt ttcttacctt tgagcacaaa atttccacgg

tgaaataaag tcaacattat aagcttf"' (SEQ ID NO: 152)

chnppb = reversecomplementRNA(hnppb)
print(chnppb)
print('\n')
check_sequence(chnppb, 31, 'nppb human.tsv')
# generate 31 nt sensor candidates for rat myh7 3' utr
rmyh7 = '"atct

tgtgctaccc aaccctaagg atgcctgtga agccctgaga cctggagcct ttgaaacagc

accttaggca gaaacacaat aaagcaattt tccttcaagc c"' (SEQ ID NO: 153)

crmyh7 = reverse_complement_RNA(rmyh7)
print(crmyh7)
print('\n')
check_sequence(crmyh7, 31, 'myh7 rat.tsv')
# generate 31 nt sensor candidates for rat nppa 3' utr
rnppa = '"cagcc
aaatctgctc gagcagatcg caaaagatcc caagcccttg cggtgtgtca cacagcttgg

tcgcattgcc actgagaggt ggtgaatacc ctcctggagc tgcagcttcc tgtcttcatc

tatcacgatc gatgttaagt gtagatgagt ggtttagtga ggccttacct ctcccactct

gcatattaag gtagatcctc accccttttca gaaagcagtt ggaaaaaaat aaatccgaat

aaacttcagc accacggaca gacgctgagg cctg"' (SEQ ID NO: 154)

crnppa = reversecomplementRNA(rnppa)
print(crnppa)
print('\n')
check_sequence(crnppa, 31, 'nppa rat.tsv')
# generate 31 nt sensor candidates for rat nppa 3' utr
rnppb = '"gaagacc tcctggctgc agactccggc ttctgactct gcctgcggct cttctttccc

cagctctggg accacctctc aagtgatcct gtttatttat ttgtttattt atttattttt

atgttgctga ttttctacaa gactgtttct tatcttccag cacaaacttg ccacagtgta

ataaacatag cctatttctt gcttttgg"' (SEQ ID NO: 155)

crnppb = reversecomplementRNA(rnppb)
print(crnppb)
print('\n')
check_sequence(crnppa, 31, 'nppb rat.tsv')
```

APPENDIX C

Homo sapiens myosin heavy chain 7 (MYH7), mRNA
NCBI Reference Sequence: NM_000257.3
FASTA Graphics
Go to:

```
LOCUS           NM_0002576069 bp mRNA linear PRI 17-JUN-2018
DEFINITION      Homo sapiens myosin heavy chain 7 (MYH7), mRNA.
ACCESSION       NM_000257 XM_005267696
VERSION         NM_000257.3
KEYWORDS        RefSeq.
SOURCE          Homo sapiens (human)

ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
                Catarrhini; Hominidae; Homo.

REFERENCE       1 (bases 1 to 6069)
AUTHORS         Feng X, He T, Wang JG and Zhao P.
TITLE           Asn391Thr Mutation of beta-Myosin Heavy Chain in a Hypertrophic
                 Cardiomyopathy Family
JOURNAL         Int Heart J 59 (3), 596-600 (2018)
PUBMED          29743414
REMARK          GeneRIF: Asn391Thr mutation of MYH7 is a malignant mutation for
                hypertrophic cardiomyopathy and that mutation carriers should get
                effective treatment to prevent sudden death.

REFERENCE       2 (bases 1 to 6069)
AUTHORS         Viswanathan SK, Sanders HK, McNamara JW, Jagadeesan A, Jahangir A,
                Tajik AJ and Sadayappan S.
TITLE           Hypertrophic cardiomyopathy clinical phenotype is independent of
                gene mutation and mutation dosage
JOURNAL         PLoS ONE 12 (11), e0 187948 (2017)
PUBMED          29121657
REMARK          GeneRIF: Data provide evidence that MYH7 mutations contributed to
                24.4% MYBPC3 mutations of hypertrophic cardiomyopathy (HCM) cases,
                that MYBPC3 constitute the preeminent cause of HCM and that both
                mutations are phenotypically indistinguishable.
                Publication Status: Online-Only

REFERENCE       3 (bases 1 to 6069)
AUTHORS         Wang B, Guo R, Zuo L, Shao H, Liu Y, Wang Y, Ju Y, Sun C, Wang L,
                Zhang Y and Liu L.
TITLE           [Analysis of genotype and phenotype correlation of MYH7-V878A
                mutation among ethnic Han Chinese pedigrees affected with
                hypertrophic cardiomyopathy]
JOURNAL         Zhonghua Yi Xue Yi Chuan Xue Za Zhi 34 (4), 514-518 (2017)
PUBMED          28777849
REMARK          GeneRIF: MYH7-V878A is a hot spot among ethnic Han Chinese with a
                high penetrance.

REFERENCE       4 (bases 1 to 6069)
AUTHORS         OldforsA.
TITLE           Hereditary myosin myopathies
JOURNAL         Neuromuscul. Disord. 17 (5), 355-367 (2007)
PUBMED          17434305
REMARK          Review article

REFERENCE       5 (bases 1 to 6069)
AUTHORS         Cirino, A.L. and Ho, C.
TITLE           Hypertrophic Cardiomyopathy Overview
JOURNAL         (in) Adam MP, Ardinger HH, Pagon RA, Wallace SE, Bean LJH, Stephens
                K and Amemiya A (Eds.);
                GENEREVIEW S((R));
                (1993)
PUBMED          20301725

REFERENCE       6 (bases 1 to 6069)
AUTHORS         Lamont, P. and Laing, N.G.
TITLE           Laing Distal Myopathy
JOURNAL         (in) Adam MP, Ardinger HH, Pagon RA, Wallace SE, Bean LJH, Stephens
                K and Amemiya A (Eds.);
                GENEREVIEW S((R));
                (1993)
PUBMED          20301606

REFERENCE       7 (bases 1 to 6069)
AUTHORS         Hershberger, R.E. and Morales, A.
TITLE           Dilated Cardiomyopathy Overview
JOURNAL         (in) Adam MP, Ardinger HH, Pagon RA, Wallace SE, Bean LJH, Stephens
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                K and Amemiya A (Eds.);
                GENEREVIEW S((R));
                (1993)
PUBMED          20301486

REFERENCE       8 (bases 1 to 6069)
AUTHORS         DeChene, E.T., Kang, P.B. and Beggs, A.H.
TITLE           Congenital Fiber-Type Disproportion
JOURNAL         (in) Adam MP, Ardinger HH, Pagon RA, Wallace SE, Bean LJH, Stephens
                K and Amemiya A (Eds.);
                GENEREVIEW S((R));
                (1993)
PUBMED          20301436

REFERENCE       9 (bases 1 to 6069)
AUTHORS         Warlick CA, Ramachandra S, Mishra S and Donis-Keller H.
TITLE           Dinucleotide repeat polymorphism at the human cardiac beta-myosin
                heavy chain gene (HMSYHCO1) locus
JOURNAL         Hum. Mol. Genet. 1 (2), 136 (1992)
PUBMED          1301151

REFERENCE       10 (bases 1 to 6069)
AUTHORS         Fougerousse F, Dufour C, Roudaut C and Beckmann JS.
TITLE           Dinucleotide repeat polymorphism at the human gene for cardiac
                beta-myosin heavy chain (MYH6)
JOURNAL         Hum. Mol. Genet. 1 (1), 64 (1992)
PUBMED          1301139
                COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff The
                reference sequence was derived from BF834726.1, EU747717.1,
                M58018.1 andBC112173.L
                On or before Jun. 20, 2014 this sequence version replaced
                XM_005267696.1, NM_000257.2.

                Summary: Muscle myosin is a hexameric protein containing 2 heavy
                chain subunits, 2 alkali light chain subunits, and 2 regulatory
                light chain subunits. This gene encodes the beta (or slow) heavy
                chain subunit of cardiac myosin. It is expressed predominantly in
                normal human ventricle. It is also expressed in skeletal muscle
                tissues rich in slow-twitch type I muscle fibers. Changes in the
                relative abundance of this protein and the alpha (or fast) heavy
                subunit of cardiac myosin correlate with the contractile velocity
                of cardiac muscle. Its expression is also altered during thyroid
                hormone depletion and hemodynamic overloading. Mutations in this
                gene are associated with familial hypertrophic cardiomyopathy,
                myosin storage myopathy, dilated cardiomyopathy, and Laing
                early-onset distal myopathy, [provided by RefSeq, Jul 2008].

                Publication Note: This RefSeq record includes a subset of the
                publications that are available for this gene. Please see the Gene
                record to access additional publications.

                ##Evidence-Data-START ##
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                [ECO:0000350]
                ##Evidence-Data-END##
                COMPLETENESS: complete on the 3' end.
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1832-3501	BC112173.1	1756-3425
3502-6053	M58018.1	3457-6008
6054-6069	EU747717.1	6029-6044

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5701 acaggaaaaa cctgctgcgg ctgcaggacc tggtagacaa gctgcagcta aaggtcaagg
5761 cctacaagcg ccaggccgag gaggcggagg agcaagccaa caccaacctg tccaagttcc
5821 gcaaggtgca gcacgagctg gatgaggcag aggagcgggc ggacatcgcc gagtcccagg
5881 tcaacaagct gcgggccaag agccgtgaca ttggcacgaa gggcttgaat gaggagtagc
5941 tttgccacat cttgatctgc tcagccctgg aggtgccagc aaagccccat gctggagcct
6001 gtgtaacagc tccttgggag gaagcagaat aaagcaattt tccttgaagc cgagaaaaaa
6061 aaaaaaaaa (SEQ ID NO: 157)
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APPENDIX D

Homo sapiens natriuretic peptide A (NPPA), mRNA
NCBI Reference Sequence: NM_006172.3
FASTA Graphics
Go to:
LOCUS NM_006172 858 bp mRNA linear PRI 29-JUL.-2018
DEFINITION *Homo sapiens* natriuretic peptide A (NPPA), mRNA.
ACCESSION NM_006172
VERSION NM_006172.3
KEYWORDS RefSeq.
SOURCE *Homo sapiens* (human)
ORGANISM *Homo sapiens*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 858)
AUTHORS Cannone V., Scott C. G., Decker P. A., Larson N. B., Palmas W, Taylor K. D.,
Wang T. J., Gupta D. K., Bielinski S. J. and Burnett J. C. Jr.
TITLE A favorable cardiometabolic profile is associated with the G allele
of the genetic variant rs5068 in African Americans: The
Multi-Ethnic Study of Atherosclerosis (MESA)
JOURNAL PLoS ONE 12 (12), e0189858 (2017)
PUBMED 29253899
REMARK GeneRIF: the G allele of the genetic variant rs5068 in African
Americans is associated with lower prevalence of metabolic syndrome

and lower triglycerides values
Publication Status: Online-Only

REFERENCE 2 (bases 1 to 858)
AUTHORS Salo, P. P., Havulinna, A. S., Tukiainen, T., Raitakari, O., Lehtimaki, T., Kahonen, M., Kettunen, J., Mannikko, M., Eriksson, J. G., Jula, A., Blankenberg, S., Zeller, T., Salomaa, V., Kristiansson, K. and Perola, M.
TITLE Genome-Wide Association Study Implicates Atrial Natriuretic Peptide Rather Than B-Type Natriuretic Peptide in the Regulation of Blood Pressure in the General Population
JOURNAL Circ Cardiovasc Genet 10 (6) (2017)
PUBMED 29237677
REMARK GeneRIF: Data indicate the blood pressure-lowering effect of atrial natriuretic peptide (ANP) in the general population.

REFERENCE 3 (bases 1 to 858)
AUTHORS Wakula P., Neumann B., Kienemund J., Thon-Gutschi E., Stojakovic T., Manninger M., Scherr D., Schamagl H., Kapi M., Pieske B. and Heinzel F. R.
TITLE CHA2DS2-VASc score and blood biomarkers to identify patients with atrial high-rate episodes and paroxysmal atrial fibrillation
JOURNAL Europace 19 (4), 544-551 (2017)
PUBMED 28431065
REMARK GeneRIF: TIMP-4, NT-proANP, NT-proBNP were strongest associated with PAF and AHRE. The discriminatory performance of CHADS2-VASc for PAF was increased by addition of selected biomarkers.

REFERENCE 4 (bases 1 to 858)
AUTHORS Bartus K., Podolec J., Lee R. J., Kapelak B., Sadowski J., Bartus M., Oles K., Ceranowicz P., Trabka R. and Litwinowicz R.
TITLE Atrial natriuretic peptide and brain natriuretic peptide changes after epicardial percutaneous left atrial appendage suture ligation using LARIAT device
JOURNAL J. Physiol. Pharmacol. 68 (1), 117-123 (2017)
PUBMED 28456775
REMARK GeneRIF: In summary, there were no significant differences in ANP and BNP levels after percutaneous epicardial left atrial appendage suture ligation using LARIAT device 3 months after procedure.

REFERENCE 5 (bases 1 to 858)
AUTHORS Suga S., Nakao K., Hosoda K., Mukoyama M., Ogawa Y., Shirakami G., Arai H., Saito Y., Kambayashi Y., Inouye K. et al.
TITLE Receptor selectivity of natriuretic peptide family, atrial natriuretic peptide, brain natriuretic peptide, and C-type natriuretic peptide
JOURNAL Endocrinology 130 (1), 229-239 (1992)
PUBMED 1309330

REFERENCE 6 (bases 1 to 858)
AUTHORS Bennett B. D., Bennett G. L., Vitangcol R. V., Jewett J. R., Burnier J., Henzel W. and Lowe D. G.
TITLE Extracellular domain-IgG fusion proteins for three human natriuretic peptide receptors. Hormone pharmacology and application to solid phase screening of synthetic peptide antisera
JOURNAL J. Biol. Chern. 266 (34), 23060-23067 (1991)
PUBMED 1660465

REFERENCE 7 (bases 1 to 858)
AUTHORS Koller K. J, Lowe D. G., Bennett G. L., Minamino N., Kangawa K., Matsuo H. and Goeddel D. V.
TITLE Selective activation of the B natriuretic peptide receptor by C-type natriuretic peptide (CNP)
JOURNAL Science 252 (5002), 120-123 (1991)
PUBMED 1672777

REFERENCE 8 (bases 1 to 858)
AUTHORS Yang-Feng, T. L., Floyd-Smith, G., Nemer, M., Drouin, J. and Francke, U.
TITLE The pronatriodilatin gene is located on the distal short arm of human chromosome 1 and on mouse chromosome 4
JOURNAL Am. J. Hum. Genet. 37 (6), 1117-1128 (1985)
PUBMED 2934979

REFERENCE 9 (bases 1 to 858)
AUTHORS Zivin, R. A., Condra, J. H., Dixon, R. A., Seidah, N. G., Chretien, M., Nemer, M., Chamberland, M. and Drouin, J.
TITLE Molecular cloning and characterization of DNA sequences encoding rat and human atrial natriuretic factors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81 (20), 6325-6329 (1984)

-continued

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PUBMED 6238331

REFERENCE 10 (bases 1 to 858)
AUTHORS Oikawa, S., Imai, M., Ueno, A., Tanaka, S., Noguchi, T., Nakazato, H.,
Kangawa, K., Fukuda, A. and Matsuo, H.
TITLE Cloning and sequence analysis of cDNA encoding a precursor for
human atrial natriuretic polypeptide
JOURNAL Nature 309 (5970), 724-726 (1984)
PUBMED 6203042

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff The
reference sequence was derived from BC005893.1 and AA779538.1.
This sequence is a reference standard in the RefSeqGene project.
On Jun. 13, 2009 this sequence version replaced NM_006172.2.

Summary: The protein encoded by this gene belongs to the
natriuretic peptide family. Natriuretic peptides are implicated in
the control of extracellular fluid volume and electrolyte
homeostasis. This protein is synthesized as a large precursor
(containing a signal peptide), which is processed to release a
peptide from the N-terminus with similarity to vasoactive peptide,
cardiodilatin, and another peptide from the C-terminus with
natriuretic-diuretic activity. Mutations in this gene have been
associated with atrial fibrillation familial type 6. This gene is
located adjacent to another member of the natriuretic family of
peptides on chromosome 1. [provided by RefSeq, October 2015].

Publication Note: This RefSeq record includes a subset of the
publications that are available for this gene. Please see the Gene
record to access additional publications.

##Evidence-Data-START ##
Transcript exon combination :: BC005893.1, ERR279837.2678.1
[ECO: 0000332]
RNAseq introns :: single sample supports all introns
SAMEA2154361, SAMEA2155550
[ECO: 0000348]
##Evidence-Data-END##
COMPLETENESS: complete on the 3'end.
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PRIMARY COMP	REFSEQ_SPAN	PRIMARY_IDENTIFIER	PRIMARY_SPAN
1-552	BC005893.1	1-552	
553-858	AA779538.1	1-306 c	

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FEATURES      Location/Qualifiers

source          1 . . . 858
              /organism = "Homo sapiens"
              /mol_type = "mRNA"
              /db_xref = "taxon: 9606"
              /chromosome = "1"
              /map = "1p36.22"

gene            1 . . . 858
              /gene = "NPPA"
              /gene_synonym = "ANF; ANP; ATFB6; ATRST2; CDD; CDD-ANF; CDP;
              PND"
              /note = "natriuretic peptide A"
              /db_xref = "GeneID: 4878"

              /db_xref = "HGNC :HGNC: 7939"
              /db_xref = "MIM: 108780"

exon            1 . . . 222
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              /gene_synonym = "ANF; ANP; ATFB6; ATRST2; CDD; CDD-ANF; CDP;
              PND"
              /inference = "alignment: Splign: 2.1.0"

CDS           100 . . . 555
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              /gene_synonym = "ANF; ANP; ATFB6; ATRST2; CDD; CDD-ANF; CDP;
              PND"
              /note = "cardiodilatin-related peptide; cardionatrin;
              atriopeptin; prepronatriodilatin; natriuretic peptide
              precursor A variant 1"
              /codon_start = 1
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             /db_xref = "CCDS: CCDS139.1"
             /db_xref = "GeneID: 4878"
             /db_xref = "HGNC: HGNC: 7939"
             /db_xref = "MIM: 108780"

/translation = "MSSFSTTTVSFLLLLAFQLLGQTRANPMYNAVSNADLMDFKNLL
DHLEEKMPLEDEVVPPQVLSEPNEEAGAALSPLPEVPPWTGEVSPAQRDGGALGRGP
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DSSDRSALLKSKLRALLTAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY"
(SEQ ID NO: 158)

sig_peptide  100 . . . 174
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             /gene_synonym = "ANF; ANP; ATFB6; ATRST2; CDD; CDD-ANF; CDP;
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             /inference = "COORDINATES: ab initio prediction:SignalP: 4.0"

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             /gene_synonym = "ANF; ANP; ATFB6; ATRST2; CDD; CDD-ANF; CDP;
             PND"
             /experiment= "experimental evidence, no additional details
             recorded"
             /note = "Cleavage, by CORIN. {ECO: 0000269|PubMed: 10880574};
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             site"

mat_peptide  469 . . . 552
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             /gene_synonym = "ANF; ANP; ATFB6; ATRST2; CDD; CDD-ANF; CDP;
             PND"
             /product = "Atrial natriuretic factor.
             {ECO: 0000269|PubMed: 10880574, ECO: 0000269|PubMed:6230082}"
             /experiment = "experimental evidence, no additional details
             recorded"
             /note = "propagated from UniProtKB/Swiss-Prot (P01160.1)"

misc_feature 487 . . . 492
             /gene = "NPPA"
             /gene_synonym = "ANF; ANP; ATFB6; ATRST2; CDD; CDD-ANF; CDP;
             PND"
             /experiment = "experimental evidence, no additional details
             recorded"
             /note = "Cleavage, by MME. {ECO: 0000269|PubMed: 2972276};
             propagated from UniProtKB/Swiss-Prot (P01160.1); cleavage
             site"

exon         223 . . . 549
             /gene = "NPPA"
             /gene_synonym = "ANF; ANP; ATFB6; ATRST2; CDD; CDD-ANF; CDP;
             PND"
             /inference = "alignment: Splign: 2.1.0"

STS          354 . . . 604
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             /db_xref = "UniSTS: 156242"

STS          367 . . . 548
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             PND"
             /standard_name = "NPPA"
             /db_xref = "UniSTS: 253991"

exon         550 . . . 855
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             /gene_synonym = "ANF; ANP; ATFB6; ATRST2; CDD; CDD-ANF; CDP;
             PND"
             /inference = "alignment: Splign: 2.1.0"

STS          588 . . . 847
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             /gene_synonym = "ANF; ANP; ATFB6; ATRST2; CDD; CDD-ANF; CDP;
             PND"
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             /db_xref = "UniSTS: 87961"

STS          595 . . . 762
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             /db_xref = "UniSTS: 43068"

regulatory   824 . . . 829
             /regulatory_class = "polyA_signal_sequence"
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             /gene_synonym = "ANF; ANP; ATFB6; ATRST2; CDD; CDD-ANF; CDP;
             PND"

polyA_site   855
             /gene = "NPPA"
             /gene_synonym = "ANF; ANP; ATFB6; ATRST2; CDD; CDD-ANF; CDP;
             PND"

   ORIGIN
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      61     agagcagcaa gcagtggatt gctccttgac gacgccagca tgagctcctt ctccaccacc
     121     accgtgagct tcctcctttt actggcattc cagctcctag gtcagaccag agctaatccc
     181     atgtacaatg ccgtgtccaa cgcagacctg atggatttca agaatttgct ggaccatttg
     241     gaagaaaaga tgcctttaga agatgaggtc gtgcccccac aagtgctcag tgagccgaat
     301     gaagaagcgg gggctgctct cagccccctc cctgaggtgc ctccctggac cggggaagtc
     361     agcccagccc agagagatgg aggtgccctc gggcggggcc cctgggactc ctctgatcga
     421     tctgccctcc taaaaagcaa gctgagggcg ctgctcactg cccctcggag cctgcggaga
     481     tccagctgct tcgggggcag gatggacagg attggagccc agagcggact gggctgtaac
     541     agcttccggt actgaagata acagccaggg aggacaagca gggctgggcc tagggacaga
     601     ctgcaagagg ctcctgtccc ctggggtctc tgctgcattt gtgtcatctt gttgccatgg
     661     agttgtgatc atcccatcta agctgcagct tcctgtcaac acttctcaca tcttatgcta
     721     actgtagata aagtggtttg atggtgactt cctcgcctct cccaccccat gcattaaatt
     781     ttaaggtaga acctcacctg ttactgaaag tggtttgaaa gtgaataaac ttcagcacca
     841     tggacagaag acaaaaaa (SEQ ID NO: 159)
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APPENDIX E

Homo sapiens natriuretic peptide B (NPPB), mRNA
NCBI Reference Sequence: NM_002521.2
FASTA Graphics
Go to:
LOCUS NM_002521 708 bp mRNA linear PRI 22-JUL.-2018
DEFINITION *Homo sapiens* natriuretic peptide B (NPPB), mRNA.
ACCESSION NM_002521
VERSION NM_002521.2
KEYWORDS RefSeq.
SOURCE *Homo sapiens* (human)
ORGANISM *Homo sapiens*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 708)
AUTHORS Hex C., Smeets M., Penders J., Van Hoof V., Verbakel J., Buntinx F. and
Vaes B.
TITLE Accuracy, user-friendliness and usefulness of the Cobas h232
point-of-care test for NT-proBNP in primary care
JOURNAL J. Clin. Pathol. 71 (6), 539-545 (2018)
PUBMED 29263170
REMARK GeneRIF: Report usefulness of point-of-care test for NT-proBNP in
primary care for the diagnosis of heart failure.

REFERENCE 2 (bases 1 to 708)
AUTHORS Drozdz T., Kwinta P., Kordon Z., Sztefko K., Rudzinski A., Zachwieja K.,
Miklaszewska M., Czarnecka D. and Drozdz D.
TITLE [B-type natriuretic peptide as a marker of cardiac dysfunction in
children with chronic kidney disease]
JOURNAL Pol. Merkur. Lekarski 44 (262), 171-176 (2018)
PUBMED 29775443
REMARK GeneRIF: In children with chronic kidney disease, BNP is an
indicator of heart failure correlating with renal function
parameters and left ventricular mass index.

REFERENCE 3 (bases 1 to 708)
AUTHORS Fernandez-Susavila H, Rodriguez-Yanez M., Dopico-Lopez A., Arias S., Santamaria M., Avila-Gomez P., Doval-Garcia J. M., Sobrino T., Iglesias-Rey R., Castillo J. and Campos F.
TITLE Heads and Tails of Natriuretic Peptides: Neuroprotective Role of Brain Natriuretic Peptide
JOURNAL J Am Heart Assoc 6 (12), e007329 (2017)
PUBMED 29203579
REMARK GeneRIF: Suggest potential role for BNP as a protective endogenous factor against cerebral ischemia.
Publication Status: Online-Only

REFERENCE 4 (bases 1 to 708)
AUTHORS Legaz-Arrese A., Carranza-Garcia L. E., Navarro-Orocio R., Valadez-Lira A., Mayolas-Pi C., Munguia-Izquierdo D., Reverter-Masia J. and George K.
TITLE Cardiac Biomarker Release after Endurance Exercise in Male and Female Adults and Adolescents
JOURNAL J. Pediatr. 191, 96-102 (2017)
PUBMED 29173327
REMARK GeneRIF: An exercise-associated increase in hs-cTnT and NT-proBNP occurred in response to a 60-minute maximal swimming test that was independent of pubertal status/adolescent vs adults. The present data also suggests that baseline and postexercise hs-cTnT values are higher in male compared with female, with no sex differences in NT-proBNP values.

REFERENCE 5 (bases 1 to 708)
AUTHORS Krause A., Liepke C., Meyer M., Adermann K., Forssmann W. G. and Maronde E.
TITLE Human natriuretic peptides exhibit antimicrobial activity
JOURNAL Eur. J. Med. Res. 6 (5), 215-218 (2001)
PUBMED 11410403
REMARK GeneRIF: Brain-type natriuretic peptide (hBNP-32) is an antimicrobial peptide active against Gram-positive and Gram-negative bacteria and yeast.

REFERENCE 6 (bases 1 to 708)
AUTHORS Arden K. C., Viars C. S., Weiss S., Argentin S. and Nemer M.
TITLE Localization of the human B-type natriuretic peptide precursor (NPPB) gene to chromosome lp36
JOURNAL Genomics 26 (2), 385-389 (1995)
PUBMED 7601467
REFERENCE 7 (bases 1 to 708)
AUTHORS Suga S., Nakao K., Hosoda K., Mukoyama M., Ogawa Y., Shirakami G., Arai H., Saito Y., Kambayashi Y., Inouye K. et al.
TITLE Receptor selectivity of natriuretic peptide family, atrial natriuretic peptide, brain natriuretic peptide, and C-type natriuretic peptide
JOURNAL Endocrinology 130 (1), 229-239 (1992)
PUBMED 1309330

REFERENCE 8 (bases 1 to 708)
AUTHORS Bennett B. D., Bennett G. L., Vitangcol R. V., Jewett J. R., Burnier J., Henzel W. and Lowe D. G..
TITLE Extracellular domain-IgG fusion proteins for three human natriuretic peptide receptors. Hormone pharmacology and application to solid phase screening of synthetic peptide antisera
JOURNAL J. Biol. Chern. 266 (34), 23060-23067 (1991)
PUBMED 1660465

REFERENCE 9 (bases 1 to 708)
AUTHORS Koller K. J., Lowe D. G., Bennett G. L., Minamino N., Kangawa K., Matsuo H. and Goeddel D. V..
TITLE Selective activation of the B natriuretic peptide receptor by C-type natriuretic peptide (CNP)
JOURNAL Science 252 (5002), 120-123 (1991)
PUBMED 1672777

REFERENCE 10 (bases 1 to 708)
AUTHORS Sudoh T., Maekawa K., Kojima M., Minamino N., Kangawa K. and Matsuo H.
TITLE Cloning and sequence analysis of cDNA encoding a precursor for human brain natriuretic peptide
JOURNAL Biochem. Biophys. Res. Commun. 159 (3), 1427-1434 (1989)
PUBMED 2522777

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from AJ708502.1, M25296.1 and BC025785.1.

On Dec. 16, 2005 this sequence version replaced NM_002521.1.

Summary: This gene is a member of the natriuretic peptide family and encodes a secreted protein which functions as a cardiac hormone. The protein undergoes two cleavage events, one within the cell and a second after secretion into the blood. The protein's biological actions include natriuresis, diuresis, vasorelaxation, inhibition of renin and aldosterone secretion, and a key role in cardiovascular homeostasis. A high concentration of this protein in the bloodstream is indicative of heart failure. The protein also acts as an antimicrobial peptide with antibacterial and antifungal activity. Mutations in this gene have been associated with postmenopausal osteoporosis, [provided by RefSeq, November 2014].

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

##Evidence-Data-START##
Transcript exon combination :: BC025785.1, ERR279856.3578.1
[ECO: 0000332]
RNAseq introns :: single sample supports all introns
SAMEA2148093, SAMEA2151741
[ECO: 0000348]
##Evidence-Data-END##
##RefSeq-Attributes-START##
Protein has antimicrobial activity :: PMID: 11410403
##RefSeq-Attributes-END##
COMPLETENESS: complete on the 3'end.

PRIMARY COMP	REFSEQ_SPAN	PRIMARY_IDENTIFIER	PRIMARY_SPAN
1-4	AJ708502.1		19-22
5-695	M25296.1		2-692
696-708	BC025785.1		683-695

FEATURES Location/Qualifiers

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               /db_xref = "taxon: 9606"
               /chromosome = "1"
               /map = "1p36.22"

gene            1 . . . 708
               /gene = "NPPB"
               /gene_synonym = "BNP"
               /note = "natriuretic peptide B"
               /db_xref = "GeneID: 4879"
               /db_xref = "HGNC: HGNC: 7940"
               /db_xref = "MIM: 600295"

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               /gene_synonym = "BNP"
               /inference = "alignment: Splign: 2.1.0"

CDS            103 . . . 507
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               /gene_sy nony m = "BNP"
               /note = "natriuretic peptide precursor B; brain type
               natriuretic peptide; natriuretic peptides B; natriuretic
               protein; gamma-brain natriuretic peptide"
               /codon_start = 1
               /product = "natriuretic peptides B preproprotein"
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               /db_xref = "GeneID: 4879"
               /db_xref = "HGNC HGNC: 7940"
               /db_xref = "MIM: 600295"

/translation = "MDPQTAPSRALLLLLFLHLAFLGGRSHPLGSPGSASDLETSGLQ
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SPKMVQGSGCFGRKMDRISSSSGLGCKVLRRH"(SEQ ID NO: 160)

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            /gene_synonym = "BNP"
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mat_peptide 409 . . . 504
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            /product = "natriuretic peptides B"
            /experiment = "DESCRIPTION: antimicrobial
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            /note = "brain natriuretic peptide 32"

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            /inference = "alignment: Splign: 2.1.0"

exon        491 . . . 698
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            /gene_synonym = "BNP"
            /inference = "alignment: Splign: 2.1.0"

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            /gene = "NPPB"
            /gene_synonym = "BNP"

polyA_site  698
            /gene = "NPPB"
            /gene_synonym = "BNP"
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    121     ccttcccggg cgctcctgct cctgctcttc ttgcatctgg ctttcctggg aggtcgttcc
    181     cacccgctgg gcagccccgg ttcagcctcg gacttggaaa cgtccgggtt acaggagcag
    241     cgcaaccatt tgcagggcaa actgtcggag ctgcaggtgg agcagacatc cctggagccc
    301     ctccaggaga gcccccgtcc cacaggtgtc tggaagtccc gggaggtagc caccgagggc
    361     atccgtgggc accgcaaaat ggtcctctac accctgcggg caccacgaag ccccaagatg
    421     gtgcaagggt ctggctgctt tgggaggaag atggaccgga tcagctcctc cagtggcctg
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    541     ttccacaagg ggctttttcc tcaaccctgt ggccgccttt gaagtgactc atttttttaa
    601     tgtatttatg tatttatttg attgttttat ataagatggt ttcttacctt tgagcacaaa
    661     atttccacgg tgaaataaag tcaacattat aagctttaaa aaaaaaaa (SEQ ID NO: 161)
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45

APPENDIX F

```
Rattus norvegicus myosin heavy chain 7 (Myh7), mRNA
NCBI Reference Sequence: NM_017240.2
FASTA Graphics
Go to:
LOCUS NM_0172405923 bp mRNA linear ROD 31-MAY.-2018
DEFINITION Rattus norvegicus myosin heavy chain 7 (Myh7), mRNA.
ACCESSION NM_017240
VERSION NM_017240.2
KEYWORDS RefSeq.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 5923)
AUTHORS Tomita-Mitchell A., Stamm K. D., Mahnke D. K., Kim M. S., Hidestrand P. M.,
Liang H. L., Goetsch M. A., Hidestrand M., Simpson P., Pelech A. N., Tweddell
J. S., Benson D. W., Lough J. W. and Mitchell M.E.
TITLE Impact of MYH6 variants in hypoplastic left heart syndrome
JOURNAL Physiol. Genomics 48 (12), 912-921 (2016)
PUBMED 27789736
```

REFERENCE 2 (bases 1 to 5923)
AUTHORS Chandra V., Gollapudi S. K. and Chandra M.
TITLE Rat cardiac troponin T mutation (F72L)-mediated impact on thin filament cooperativity is divergently modulated by alpha- and beta-myosin heavy chain isoforms
JOURNAL Am. J. Physiol. Heart Circ. Physiol. 309 (8), H1260-H1270 (2015)
PUBMED 26342069
REMARK GeneRIF: TnT mutation F72L leads to contractile changes that are linked to dilated cardiomyopathy in the presence of MYH6 and hypertrophic cardiomyopathy in the presence of MYH7.

REFERENCE 3 (bases 1 to 5923)
AUTHORS Kralova E., Doka G., Pivackova L., Srankova J., Kuracinova K., Janega P., Babal P., Klimas J. and Krenek P.
TITLE 1-Arginine Attenuates Cardiac Dysfunction, But Further Down-Regulates alpha-Myosin Heavy Chain Expression in Isoproterenol-Induced Cardiomyopathy
JOURNAL Basic Clin. Pharmacol. Toxicol. 117 (4), 251-260 (2015)
PUBMED 25865156

REFERENCE 4 (bases 1 to 5923)
AUTHORS Taylor K. C., Buvoli M., Korkmaz E. N., Buvoli A., Zheng Y., Heinze N. T., Cui Q., Leinwand L. A. and Rayment I.
TITLE Skip residues modulate the structural properties of the myosin rod and guide thick filament assembly
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 112 (29), E3806-E3815 (2015)
PUBMED 26150528

REFERENCE 5 (bases 1 to 5923)
AUTHORS Zhang P., Shan T., Liang X., Deng C. and Kuang S.
TITLE Mammalian target of rapamycin is essential for cardiomyocyte survival and heart development in mice
JOURNAL Biochem. Biophys. Res. Commun. 452 (1), 53-59 (2014)
PUBMED 25139234

REFERENCE 6 (bases 1 to 5923)
AUTHORS O'Neill L., Holbrook N. J., Fargnoli J. and Lakatta E. G.
TITLE Progressive changes from young adult age to senescence in mRNA for rat cardiac myosin heavy chain genes
JOURNAL Cardioscience 2 (1), 1-5 (1991)
PUBMED 1888877

REFERENCE 7 (bases 1 to 5923)
AUTHORS Schuyler G. T. and Yarbrough L. R.
TITLE Changes in myosin and creatine kinase mRNA levels with cardiac hypertrophy and hypothyroidism
JOURNAL Basic Res. Cardiol. 85 (5), 481-494 (1990)
PUBMED 1703406

REFERENCE 8 (bases 1 to 5923)
AUTHORS McNally E. M., Kraft R., Bravo-Zehnder M., Taylor D. A. and Leinwand L. A.
TITLE Full-length rat alpha and beta cardiac myosin heavy chain sequences. Comparisons suggest a molecular basis for functional differences
JOURNAL J. Mol. Biol. 210 (3), 665-671 (1989)
PUBMED 2614840

REFERENCE 9 (bases 1 to 5923)
AUTHORS Kraft R., Bravo-Zehnder M., Taylor D. A. and Leinwand L. A.
TITLE Complete nucleotide sequence of full length cDNA for rat beta cardiac myosin heavy chain
JOURNAL Nucleic Acids Res. 17 (18), 7529-7530 (1989)
PUBMED 2798112

REFERENCE 10 (bases 1 to 5923)
AUTHORS Izumo, S., Lompre, A. M., Matsuoka, R., Koren, G., Schwartz, K., Nadal-Ginard, B. and Mahdavi, V.
TITLE Myosin heavy chain messenger RNA and protein isoform transitions during cardiac hypertrophy. Interaction between hemodynamic and thyroid hormone-induced signals
JOURNAL J. Clin. Invest. 79 (3), 970-977 (1987)
PUBMED 2950137

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from X15939.1.
On Feb. 21, 2013 this sequence version replaced NM_017240.1.

Summary: heavy chain of myosin; involved in muscle contraction

[RGD, February 2006].

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

##Evidence-Data-START##
Transcript exon combination :: X15939.1 [ECO: 0000332]
RNAseq introns :: mixed/partial sample support
SAMD00052296, SAMD00052297
[ECO: 0000350]
##Evidence-Data-END##

PRIMARY COMP	REFSEQ_SPAN	PRIMARY_IDENTIFIER	PRIMARY_ SPAN
1-5923	X15939.1		3-5925

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               /db xref = "taxon: 10116"
               /chromosome = "15"
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               myosin heavy chain, cardiac muscle beta isoform; myosin,
               heavy polypeptide 7, cardiac muscle, beta; myosin heavy
               chain, polypeptide 7; myosin heavy chain polypeptide 7
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               muscle, beta"
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exon         1008 . . . 1146
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exon         1416 . . . 1586
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exon         2432 . . . 2687
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exon         2688 . . . 2930
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exon         2931 . . . 3107
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APPENDIX G

Rattus norvegicus natriuretic peptide A (Nppa), mRNA
NCBI Reference Sequence: NM_012612.2

FASTA Graphics
Go to:

LOCUS	NM_012612831 bp mRNA linear ROD 10-JUN-2018
DEFINITION	*Rattus norvegicus* natriuretic peptide A (Nppa), mRNA.
ACCESSION	NM_012612
VERSION	NM_012612.2
KEYWORDS	RefSeq.
SOURCE	*Rattus norvegicus* (Norway rat)
ORGANISM	*Rattus norvegicus* Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 831) AUTHORS Barallobre-Barreiro J, Gupta SK, Zoccarato A, Kitazume-Taneike R, Fava M, Yin X, Werner T, Hirt MN, Zampetaki A, Viviano A, Chong M, Bern M, Kourliouros A, Domenech N, Willeit P, Shah AM, Jahangiri M, Schaefer L, Fischer JW, lozzo RV, Viner R, Thum T, Heineke J, Ki chi er A, Otsu K and Mayr M.
TITLE	Glycoproteomics Reveals Decorin Peptides With Anti-Myostatin Activity in Human Atrial Fibrillation
JOURNAL	Circulation 134 (11), 817-832 (2016)

PUBMED 27559042

REFERENCE 2 (bases 1 to 831)

AUTHORS Yuan K, Park BM, Choi YT, Kim JH, Cho KW and Kim SH.

TITLE Effects of endothelin family on ANP secretion

JOURNAL Peptides 82, 12-19 (2016)

PUBMED 27208702

REMARK GeneRIF: we suggest that the order of secretagogue effect of ET family on ANP secretion was ET-1>/ = ET-2>>ET-3>s6C and ET-1-induced atrial natriuretic peptide secretion negatively regulates the pressor effect of ET-1.

REFERENCE 3 (bases 1 to 831)

AUTHORS Lee CH, Ha GW, Kim JH and Kim SH.

TITLE Modulation in Natriuretic Peptides System in Experimental Colitis in Rats

JOURNAL Dig. Dis. Sci. 61 (4), 1060-1068 (2016)

PUBMED 26660905

REMARK GeneRIF: augmentation of inhibitory effect on basal motility by ANP in experimental colitis may be due an increased expression of colonic natriuretic peptide receptor-A mRNA

REFERENCE 4 (bases 1 to 831)

AUTHORS Bugrova, M.L.

TITLE [ATRIAL AND BRAIN NATRIURETIC PEPTIDES OF CARDIAC MUSCLE CELLS IN POSTREPERFUSION PERIOD IN RATS]

JOURNAL Tsitologiia 58 (2), 129-134 (2016)

PUBMED 27228659

REMARK GeneRIF: This is due to the fact that ANP is the main hormone of the natriuretic peptide system involved in the regulation of blood pressure in normal conditions, while BNP is the principal regulator of pressure in cardiovascular pathology

REFERENCE 5 (bases 1 to 831)

AUTHORS Pang A, Hu Y, Zhou P, Long G, Tian X, Men L, Shen Y, Liu Y and Cui Y.

TITLE Corin is down-regulated and exerts cardioprotective action via activating pro-atrial natriuretic peptide pathway in diabetic cardiomyopathy

JOURNAL Cardiovasc Diabetol 14, 134 (2015)

PUBMED 26446774

REMARK GeneRIF: ANP mRNA and protein are decreased in diabetic cardiomyopathy.
Publication Status: Online-Only

REFERENCE 6 (bases 1 to 831)

AUTHORS Bennett BD, Bennett GL, Vitangcol RV, Jewett JR, Burnier J, Henzel W and Lowe DG.

TITLE Extracellular domain-IgG fusion proteins for three human natriuretic peptide receptors. Hormone pharmacology and application to solid phase screening of synthetic peptide antisera

JOURNAL J. Biol. Chern. 266 (34), 23060-23067 (1991)

PUBMED 1660465

REFERENCE 7 (bases 1 to 831)

AUTHORS Levin ER and Frank HJ.

TITLE Natriuretic peptides inhibit rat astroglial proliferation: mediation by C receptor

JOURNAL Am. J. Physiol. 261 (2 Pt 2), R453-R457 (1991)

PUBMED 1652217

REFERENCE 8 (bases 1 to 831)

AUTHORS Koller KJ, Lowe DG, Bennett GL, Minamino N, Kangawa K, Matsuo H and Goeddel DV.

TITLE Selective activation of the B natriuretic peptide receptor by C-type natriuretic peptide (CNP)

JOURNAL Science 252 (5002), 120-123 (1991)

PUBMED 1672777

REFERENCE 9 (bases 1 to 831)

AUTHORS Mukoyama,M., Nakao,K., Saito,Y., Ogawa,Y., Hosoda,K., Suga,S., Shirakami,G., Jougasaki,M. and Imura,H.

TITLE Increased human brain natriuretic peptide in congestive heart failure

JOURNAL N. Engl. J. Med. 323 (11), 757-758 (1990)

PUBMED 2143809

REFERENCE 10 (bases 1 to 831)

AUTHORS Jin H, Yang RH, Chen YF, Jackson RM and Oparil S.

TITLE Atrial natriuretic peptide attenuates the development of pulmonary hypertension in rats adapted to chronic hypoxia

JOURNAL J. Clin. Invest. 85 (1), 115-120 (1990)

PUBMED 2136863

COMMENT This record has undergone validation or preliminary review. The reference sequence was derived from CB724799.1, X00665.1 and AI602287.1.
On Oct 17, 2007 this sequence version replaced NM_012612.1.
Summary: peptide involved in the control of fluid volume and vascular function [RGD, Feb 2006].
Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.
##Evidence-Data-START##
Transcript exon combination:: EV765126.1, BC158590.1 [ECO:0000332]
RNAseq introns:: single sample supports all introns SAMD00052296, SAMD00052297 [ECO:0000348]
##Evidence-Data-END##

VALIDATED REFSEQ:

PRIMARY COMP	REFSEQ_SPAN	PRIMARY IDENTIFIER	PRIMARY SPAN
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9-576	X00665.1	1-568	
577-831	AI602287.1	1-255 c	

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APPENDIX H

Rattus norvegicus natriuretic peptide B (Nppb), mRNA
NCBI Reference Sequence: NM_031545.1

FASTA Graphics
Go to:

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LOCUS           NM_031545628 bp mRNA linear ROD 21-JUL-2018

DEFINITION      Rattus norvegicus natriuretic peptide B (Nppb), mRNA.

ACCESSION       NM_031545

VERSION         NM_031545.1

KEYWORDS        RefSeq.
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SOURCE	*Rattus norvegicus* (Norway rat)
ORGANISM	*Rattus norvegicus* Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 628)
AUTHORS	Saklani R, Gupta SK, Mohanty IR, Kumar B, Srivastava S and Mathur R.
TITLE	Cardioprotective effects of rutin via alteration in TNF-alpha, CRP, and BNP levels coupled with antioxidant effect in STZ-induced diabetic rats
JOURNAL	Mol. Cell. Biochem. 420 (1-2), 65-72 (2016)
PUBMED	27443845
REMARK	GeneRIF: Cardioprotective effects of rutin via alteration in TNF-alpha, CRP, and BNP levels coupled with antioxidant effect in STZ-induced diabetic rats.
REFERENCE	2 (bases 1 to 628)
AUTHORS	Holditch SJ, Schreiber CA, Burnett JC and Ikeda Y.
TITLE	Arterial Remodeling in B-Type Natriuretic Peptide Knock-Out Females
JOURNAL	Sci Rep 6, 25623 (2016)
PUBMED	27162120
REMARK	GeneRIF: Data show that approximately 60% of natriuretic peptide precursor type B (Nppb)-/- females developed mesenteric polyarteritis-nodosa (PAN)-like vasculitis in their life span, some as early as 4 months of age. Publication Status: Online-Only
REFERENCE	3 (bases 1 to 628)
AUTHORS	Terse PS, Joshi PS, Bordelon NR, Brys AM, Patton KM, Arndt TP and Sutula TP.
TITLE	2-Deoxy-d-Glucose (2-DG)-Induced Cardiac Toxicity in Rat: NT-proBNP and BNP as Potential Early Cardiac Safety Biomarkers
JOURNAL	Int. J. Toxicol. 35 (3), 284-293 (2016)
PUBMED	26838190
REMARK	GeneRIF: NT-proBNP and BNP are potential early biomarkers for 2-DG-induced cardiac toxicity that can be useful to monitor 2-DG therapy in clinical trials.
REFERENCE	4 (bases 1 to 628)
AUTHORS	Bugrova,ML.
TITLE	[ATRIAL AND BRAIN NATRIURETIC PEPTIDES OF CARDIAC MUSCLE CELLS IN POSTREPERFUSION PERIOD IN RATS]
JOURNAL	Tsitologiia 58 (2), 129-134 (2016)
PUBMED	27228659
REMARK	GeneRIF: This is due to the fact that ANP is the main hormone of the natriuretic peptide system involved in the regulation of blood pressure in normal conditions, while BNP is the principal regulator of pressure in cardiovascular pathology
REFERENCE	5 (bases 1 to 628)
AUTHORS	Dogan H, Sarikaya S, Neijmann ST, Uysal E, Yucel N, Ozucelik DN, Okuturlar Y, Solak S, Sever N and Ayan C.
TITLE	N-terminal pro-B-type natriuretic peptide as a marker of blunt cardiac contusion in trauma

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JOURNAL         Int J Clin Exp Pathol 8 (6), 6786-6792 (2015)

PUBMED          26261563

REMARK          GeneRIF: Serum NT-proBNP levels significantly increased after 5
                hours of the blunt chest trauma.
                Publication Status: Online-Only

REFERENCE       6 (bases 1 to 628)
                AUTHORS Bennett BD, Bennett GL, Vitangcol RV, Jewett JR, Burnier J,
                Henzel W and Lowe DG.

TITLE           Extracellular domain-IgG fusion proteins for three human
                natriuretic peptide receptors. Hormone pharmacology and application
                to solid phase screening of synthetic peptide antisera

JOURNAL         J. Biol. Chern. 266 (34), 23060-23067 (1991)

PUBMED          1660465

REFERENCE       7 (bases 1 to 628)

AUTHORS         Dagnino L, Drouin J and Nemer M.

TITLE           Differential expression of natriuretic peptide genes in cardiac and
                extracardiac tissues

JOURNAL         Mol. Endocrinol. 5 (9), 1292-1300 (1991)

PUBMED          1837590

REFERENCE       8 (bases 1 to 628)

AUTHORS         Levin ER and Frank HJ.

TITLE           Natriuretic peptides inhibit rat astroglial proliferation:
                mediation by C receptor

JOURNAL         Am. J. Physiol. 261 (2 Pt 2), R453-R457 (1991)

PUBMED          1652217

REFERENCE       9 (bases 1 to 628)

AUTHORS         Hoffman A, Grossman E and Keiser HR.

TITLE           Increased plasma levels and blunted effects of brain natriuretic
                peptide in rats with congestive heart failure

JOURNAL         Am. J. Hypertens. 4 (7 Pt 1), 597-601 (1991)

PUBMED          1831369

REFERENCE       10 (bases 1 to 628)

AUTHORS         Koller KJ, Lowe DG, Bennett GL, Minamino N, Kangawa K, Matsuo H and
                Goeddel DV.

TITLE           Selective activation of the B natriuretic peptide receptor by
                C-type natriuretic peptide (CNP)

JOURNAL         Science 252 (5002), 120-123 (1991)

PUBMED          1672777

COMMENT         This record has not yet been subject to final
PROVISIONAL     NCBI review. The reference sequence was derived from M25297.1.
REFSEQ:         Summary: hormone produced primarily by the atrium and ventricle of
                the heart [RGD, Feb 2006].
                Publication Note: This RefSeq record includes a subset of the
                publications that are available for this gene. Please see the Gene
                record to access additional publications.
                ##Evidence-Data-START##
                Transcript exon combination:: M25297.1, FQ228997.1 [ECO:0000332]
                RNAseq introns:: single sample supports all introns
                SAMEA2689596, SAMEA2689600
                [ECO:0000348]
                ##Evidence-Data-END##
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301     ttccggatcc aggagagact tcgaaattcc aagatggcac atagttcaag ctgctttggg
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421     taggaagacc tcctggctgc agactccggc ttctgactct gcctgcggct cttctttccc
481     cagctctggg accacctctc aagtgatcct gtttatttat ttgtttattt atttattttt
541     atgttgctga ttttctacaa gactgtttct tatcttccag cacaaacttg ccacagtgta
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ttcatctatc acgatcgatg ttaagtgtag atgagtggtt tagtgaggcc ttacctctcc 180

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gatgttaagt gtagatgagt ggtttagtga ggccttacct ctcccactct gcatattaag 180

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<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: LNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: phosphorothioate backbone connection
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: LNA

<400> SEQUENCE: 42

ccngaguguu guuuggcuuu uccuguu 27

<210> SEQ ID NO 43
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Mir-23a-3p sensor
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (31)..(31)
<223> OTHER INFORMATION: primary amine modification

<400> SEQUENCE: 43

cgaagaacgg aaaucccugg caaugtgatn 30

<210> SEQ ID NO 44
<211> LENGTH: 48
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: core strand
<220> FEATURE:
<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: phosphorothioate backbone connection
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(15)
<223> OTHER INFORMATION: LNA
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(16)
<223> OTHER INFORMATION: phosphorothioate backbone connection
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (17)..(17)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (36)..(36)
<223> OTHER INFORMATION: n is a, c, g, or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (37)..(37)
<223> OTHER INFORMATION: phosphorothioate backbone connection
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (38)..(38)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (48)..(48)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (50)..(50)
<223> OTHER INFORMATION: 2'-O-methyl

<400> SEQUENCE: 44

uccguucuuc gcnanggaaa agccaaacaa cacucngugc cagggauu 48

<210> SEQ ID NO 45
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: cond-siRNA guide

<400> SEQUENCE: 45

ccacuuuacc agcaucucag ucauu 25

<210> SEQ ID NO 46
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cond-siRNA Sensor

<400> SEQUENCE: 46

ggagaggcga ggaagucacc aucaaaccac u 31

<210> SEQ ID NO 47
<211> LENGTH: 46
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: core strand

<400> SEQUENCE: 47

cucgccucuc cugacugaga ugcugguaaa gugggauggu gacuuc 46

<210> SEQ ID NO 48
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: cond-siRNA sensor

<400> SEQUENCE: 48

ggaaucagaa gcaggugucu gcagccagga c 31

<210> SEQ ID NO 49
<211> LENGTH: 46
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: core strand

<400> SEQUENCE: 49

cuucugauuc cugacugaga ugcugguaaa guggugcaga caccug 46

<210> SEQ ID NO 50
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: cond-siRNA sensor

<400> SEQUENCE: 50

ccaaggagcu guuacacagg cuccagcaug g 31

<210> SEQ ID NO 51
<211> LENGTH: 46
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: core strand

<400> SEQUENCE: 51

cagcuccuug gugacugaga ugcugguaaa gugggagccu guguaa 46

<210> SEQ ID NO 52
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: cond-siRNA guide

<400> SEQUENCE: 52

ccacuucauc acaagcuauc cgcuu 25

<210> SEQ ID NO 53
<211> LENGTH: 46
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: core strand

<400> SEQUENCE: 53

cucgccucuc cgcggauagc uugugaugaa gugggauggu gacuuc 46

<210> SEQ ID NO 54
<211> LENGTH: 46

<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: core strand

<400> SEQUENCE: 54

cuucugauuc cgcggauagc uugugaugaa guggugcaga caccug 46

<210> SEQ ID NO 55
<211> LENGTH: 46
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: core strand

<400> SEQUENCE: 55

cagcuccuug ggcggauagc uugugaugaa gugggagccu guguaa 46

<210> SEQ ID NO 56
<211> LENGTH: 45
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: core strand

<400> SEQUENCE: 56

uccguucuuc gugacugaga ugcugguaaa guggugccag ggauu 45

<210> SEQ ID NO 57
<211> LENGTH: 29
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cond-siRNA sensor

<400> SEQUENCE: 57

cgacaguuca caaguuaggg ucucaggga 29

<210> SEQ ID NO 58
<211> LENGTH: 45
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: core strand

<400> SEQUENCE: 58

gugaacuguc gugacugaga ugcugguaaa gugggacccu aacuu 45

<210> SEQ ID NO 59
<211> LENGTH: 29
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cond-siRNA sensor

<400> SEQUENCE: 59

ccugaagaac agauagucua aacacuggg 29

<210> SEQ ID NO 60
<211> LENGTH: 45
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: core strand

<400> SEQUENCE: 60

uguucuucag gugacugaga ugcugguaaa gugguuuaga cuauc 45

<210> SEQ ID NO 61
<211> LENGTH: 47
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: core strand

<400> SEQUENCE: 61

aacagcuccu ugggcggaua gcuugugaug aagugggag ccugugu 47

<210> SEQ ID NO 62
<211> LENGTH: 45
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: core strand

<400> SEQUENCE: 62

uccguucuuc ggcggauagc uugugaugaa guggugccag ggauu 45

<210> SEQ ID NO 63
<211> LENGTH: 45
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: core strand

<400> SEQUENCE: 63

uguucuucag ggcggauagc uugugaugaa gugguuuaga cuauc 45

<210> SEQ ID NO 64
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA target site

<400> SEQUENCE: 64

gaacaagauc cgagcaauau u 21

<210> SEQ ID NO 65
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA guide strand

<400> SEQUENCE: 65

uauugcucgg aucuuguucu u 21

<210> SEQ ID NO 66
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cond-siRNA guide

<400> SEQUENCE: 66

cgacuauugc ucggaucuug uucuu 25

<210> SEQ ID NO 67
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: siRNA target site

<400> SEQUENCE: 67

ugacugagau gcugguaaau u 21

<210> SEQ ID NO 68
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA guide strand

<400> SEQUENCE: 68

uuuaccagca ucucagucau u 21

<210> SEQ ID NO 69
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cond-siRNA guide

<400> SEQUENCE: 69

cgacuuuacc agcaucucag ucauu 25

<210> SEQ ID NO 70
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA target site

<400> SEQUENCE: 70

ggucagaaga agauggauuu u 21

<210> SEQ ID NO 71
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA guide strand

<400> SEQUENCE: 71

aauccaucuu cuucugaccu u 21

<210> SEQ ID NO 72
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cond-siRNA guide

<400> SEQUENCE: 72

ccacaaucca ucuucuucug accuu 25

<210> SEQ ID NO 73
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA target site

<400> SEQUENCE: 73

gcuauagaau guacagaaau u 21

<210> SEQ ID NO 74
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA guide strand

<400> SEQUENCE: 74

uuucuguaca uucuauagcu u 21

<210> SEQ ID NO 75
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cond-siRNA guide

<400> SEQUENCE: 75

cgacuuucug uacauucuau agcuu 25

<210> SEQ ID NO 76
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA target site

<400> SEQUENCE: 76

ccuuuaagca ggaauguaau u 21

<210> SEQ ID NO 77
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA guide strand

<400> SEQUENCE: 77

uuacauuccu gcuuaaaggu u 21

<210> SEQ ID NO 78
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cond-siRNA guide

<400> SEQUENCE: 78

ggacuuacau uccugcuuaa agguu 25

<210> SEQ ID NO 79
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA target site

<400> SEQUENCE: 79

gcaauuggca agauggcaau u 21

<210> SEQ ID NO 80
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA guide strand

<400> SEQUENCE: 80

uugccaucuu gccaauugcu u 21

<210> SEQ ID NO 81
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cond-siRNA guide

<400> SEQUENCE: 81

ccacuugcca ucuugccaau ugcuu 25

<210> SEQ ID NO 82
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA target site

<400> SEQUENCE: 82

guauagagug ugugcuguau u 21

<210> SEQ ID NO 83
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA guide strand

<400> SEQUENCE: 83

uacagcacac acucuauacu u 21

<210> SEQ ID NO 84
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cond-siRNA guide

<400> SEQUENCE: 84

ccacuacagc acacacucua uacuu 25

<210> SEQ ID NO 85
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA target site

<400> SEQUENCE: 85

aguauuugag aaugggaaau u 21

<210> SEQ ID NO 86
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA guide strand

<400> SEQUENCE: 86

uuucccauuc ucaaauacuu u 21

<210> SEQ ID NO 87

<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cond-siRNA guide

<400> SEQUENCE: 87

ccacuuuccc auucucaaau acuuu 25

<210> SEQ ID NO 88
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA target site

<400> SEQUENCE: 88

cuauguggac agaggcuauu u 21

<210> SEQ ID NO 89
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA guide strand

<400> SEQUENCE: 89

auagccucug uccacauagu u 21

<210> SEQ ID NO 90
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cond-siRNA guide

<400> SEQUENCE: 90

ccacauagcc ucuguccaca uaguu 25

<210> SEQ ID NO 91
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA target site

<400> SEQUENCE: 91

gcggauagcu ugugaugaau u 21

<210> SEQ ID NO 92
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA guide strand

<400> SEQUENCE: 92

uucaucacaa gcuauccgcu u 21

<210> SEQ ID NO 93
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA target site

<400> SEQUENCE: 93

ggauauuggu gcuggaaaau u 21

<210> SEQ ID NO 94
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA guide strand

<400> SEQUENCE: 94

uuuuccagca ccaauauccu u 21

<210> SEQ ID NO 95
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cond-siRNA guide

<400> SEQUENCE: 95

ccacuuuucc agcaccaaua uccuu 25

<210> SEQ ID NO 96
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA target site

<400> SEQUENCE: 96

aagcagaugc agagauuuau u 21

<210> SEQ ID NO 97
<211> LENGTH: 21
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: siRNA guide strand

<400> SEQUENCE: 97

uaaaucucug caucugcuuu u 21

<210> SEQ ID NO 98
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Cond-siRNA guide

<400> SEQUENCE: 98

ccacuaaauc ucugcaucug cuuuu 25

<210> SEQ ID NO 99
<211> LENGTH: 22
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: hsa-miR-125b-5p MIMAT0000423

<400> SEQUENCE: 99

ucccugagac ccuaacuugu ga 22

<210> SEQ ID NO 100
<211> LENGTH: 22
<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: reverse complement hsa-miR-125b-5p MIMAT0000423

<400> SEQUENCE: 100

ucacaaguua gggucucagg ga 22

<210> SEQ ID NO 101
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: hsa-miR-199b-5p MIMAT0000263

<400> SEQUENCE: 101

cccaguguuu agacuaucug uuc 23

<210> SEQ ID NO 102
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: reverse complement hsa-miR-199b-5p MIMAT0000263

<400> SEQUENCE: 102

gaacagauag ucuaaacacu ggg 23

<210> SEQ ID NO 103
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: mmu-miR-199b-5p MIMAT0000672

<400> SEQUENCE: 103

cccaguguuu agacuaccug uuc 23

<210> SEQ ID NO 104
<211> LENGTH: 73
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 104

ggccggcugg gguuccuggg gaugggauuu gcuuccuguc acaaaucaca uugccaggga 60

uuuccaaccg acc 73

<210> SEQ ID NO 105
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 105

ggaaatccct ggcaatgtga t 21

<210> SEQ ID NO 106
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 106

ggtaatccct ggcaatgtga t 21

<210> SEQ ID NO 107
<211> LENGTH: 20

<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 107

tgttgtttgg cttttcctgt 20

<210> SEQ ID NO 108
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 108

ttagattgaa acaacccagt 20

<210> SEQ ID NO 109
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: miR-23a-3p sensor strand with LNA modifications

<400> SEQUENCE: 109

ggagaagaac ggaaatccct ggcaatgtga t 31

<210> SEQ ID NO 110
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic

<400> SEQUENCE: 110

tccctggcat ccctggca 18

<210> SEQ ID NO 111
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: HDAC2 target guide

<400> SEQUENCE: 111

acggtcaata agaccagata aca 23

<210> SEQ ID NO 112
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: HDAC2 target guide

<400> SEQUENCE: 112

acggucaaua acaccagaua aca 23

<210> SEQ ID NO 113
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 113

atctggtgtt attgacc 17

<210> SEQ ID NO 114
<211> LENGTH: 17
<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 114

atctggtgta attgacc 17

<210> SEQ ID NO 115
<211> LENGTH: 13
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 115

atctggtgtt att 13

<210> SEQ ID NO 116
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 116

gagatctggt gttattg 17

<210> SEQ ID NO 117
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 117

gagatctggt cttattg 17

<210> SEQ ID NO 118
<211> LENGTH: 14
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 118

gagatctggt gtta 14

<210> SEQ ID NO 119
<211> LENGTH: 13
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 119

ctggtgttat tga 13

<210> SEQ ID NO 120
<211> LENGTH: 14
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 120

gatctggtgt tatt 14

<210> SEQ ID NO 121
<211> LENGTH: 201
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: BNP mRNA

<400> SEQUENCE: 121

aaaaaaaaaa auuucgaaua uuacaacuga aauaaagugg caccuuuaaa acacgaguuu 60

ccauucuuug guagaauaua uuuuguuagu uuauuuaugu auuuauguaa uuuuuuuacu 120

cagugaaguu uccgccggug ucccaacucc uuuuucgggg aacaccuuag ucuucgucca 180

cagacgucgg uccugaagga g 201

<210> SEQ ID NO 122
<211> LENGTH: 46
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: core guide strand

<400> SEQUENCE: 122

ccugcuucug auacggucaa uaacaccaga ucucgggcug cagaca 46

<210> SEQ ID NO 123
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 123

cttgatctgc tcagcc 16

<210> SEQ ID NO 124
<211> LENGTH: 11
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: sensor strand

<400> SEQUENCE: 124

ggcugcagac a 11

<210> SEQ ID NO 125
<211> LENGTH: 12
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: sensor strand

<400> SEQUENCE: 125

ccugcuucug au 12

<210> SEQ ID NO 126
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 126

aggtgtctgc agccaggact 20

<210> SEQ ID NO 127
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 127

aggtgtctgc aggcaggact 20

<210> SEQ ID NO 128
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 128

agcaggtgtc tgcagccagg 20

<210> SEQ ID NO 129
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 129

agcaggtctc tgcagccagg 20

<210> SEQ ID NO 130
<211> LENGTH: 12
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: BNP sensor

<400> SEQUENCE: 130

acaccugcuu cu 12

<210> SEQ ID NO 131
<211> LENGTH: 11
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: BNP sensor

<400> SEQUENCE: 131

gauuccacaa g 11

<210> SEQ ID NO 132
<211> LENGTH: 25
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: MFE structure

<400> SEQUENCE: 132

cgagaucugg uguuauugac cguuu 25

<210> SEQ ID NO 133
<211> LENGTH: 46
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: MFE structure

<400> SEQUENCE: 133

gauuccacaa gacggucaau aacaccagau cucgacaccu gcuucu 46

<210> SEQ ID NO 134
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 134

agaagcaggt gtctgc 16

<210> SEQ ID NO 135
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 135

gaatcagaag caggtg 16

<210> SEQ ID NO 136
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 136

aagcaggtgt ctgcag 16

<210> SEQ ID NO 137
<211> LENGTH: 15
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 137

atcagaagca ggtgt 15

<210> SEQ ID NO 138
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 138

gaagcaggtg tctgcagcc 19

<210> SEQ ID NO 139
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 139

gaagcaggtg cctgcagcc 19

<210> SEQ ID NO 140
<211> LENGTH: 15
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 140

tgtggaatca gaagc 15

<210> SEQ ID NO 141
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 141

ggccacaggg ttgagg 16

<210> SEQ ID NO 142
<211> LENGTH: 15
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 142

agggttgagg aaaaa 15

<210> SEQ ID NO 143
<211> LENGTH: 130
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: UTR of MYH7 mRNA

<400> SEQUENCE: 143

gaaacggugu agaacuagac gagucgggac cuccacgguc guuucggggu acgaccucgg 60

acacauuguc gaggaacccu ccuucgucuu auuucguuaa aaggaacuuc ggcucuuuuu 120

uuuuuuuuuu 130

<210> SEQ ID NO 144
<211> LENGTH: 11
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: MFE structure

<400> SEQUENCE: 144

uccagggcug a 11

<210> SEQ ID NO 145
<211> LENGTH: 12
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: MFE structure

<400> SEQUENCE: 145

gcagaucaag au 12

<210> SEQ ID NO 146
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 146

atcttgatct gctcag 16

<210> SEQ ID NO 147
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: sensor strand

<400> SEQUENCE: 147

caacaagatg acacaaatgc agcagagacc c 31

<210> SEQ ID NO 148
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: sensor strand

<400> SEQUENCE: 148

atgacacaaa tgcagcagag accccagggg a 31

<210> SEQ ID NO 149
<211> LENGTH: 46
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: core strand

<400> SEQUENCE: 149

gucaucuugu ugcaggaaaa gccaaacaac acucggcugc auuugu 46

<210> SEQ ID NO 150
<211> LENGTH: 116
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 150

gctttgccac atcttgatct gctcagccct ggaggtgcca gcaaagcccc atgctggagc 60

ctgtgtaaca gctccttggg aggaagcaga ataaagcaat tttccttgaa gccgag 116

<210> SEQ ID NO 151
<211> LENGTH: 297
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 151

agataacagc cagggaggac aagcagggct gggcctaggg acagactgca agaggctcct 60

gtcccctggg gtctctgctg catttgtgtc atcttgttgc catggagttg tgatcatccc 120

atctaagctg cagcttcctg tcaacacttc tcacatctta tgctaactgt agataaagtg 180

gtttgatggt gacttcctcg cctctcccac cccatgcatt aaattttaag gtagaacctc 240

acctgttact gaaagtggtt tgaaagtgaa taaacttcag caccatggac agaagac 297

<210> SEQ ID NO 152
<211> LENGTH: 190
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 152

gaggaagtcc tggctgcaga cacctgcttc tgattccaca aggggctttt tcctcaaccc 60

tgtggccgcc tttgaagtga ctcatttttt taatgtattt atgtatttat ttgattgttt 120

tatataagat ggtttcttac ctttgagcac aaaatttcca cggtgaaata aagtcaacat 180

tataagcttt 190

<210> SEQ ID NO 153
<211> LENGTH: 105
<212> TYPE: DNA
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 153

atcttgtgct acccaaccct aaggatgcct gtgaagccct gagacctgga gcctttgaaa 60

cagcacctta ggcagaaaca caataaagca attttccttc aagcc 105

<210> SEQ ID NO 154
<211> LENGTH: 279
<212> TYPE: DNA
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 154

cagccaaatc tgctcgagca gatcgcaaaa gatcccaagc ccttgcggtg tgtcacacag 60

cttggtcgca ttgccactga gaggtggtga ataccctcct ggagctgcag cttcctgtct 120

tcatctatca cgatcgatgt taagtgtaga tgagtggttt agtgaggcct tacctctccc 180

actctgcata ttaaggtaga tcctcacccc tttcagaaag cagttggaaa aaaataaatc 240

cgaataaact tcagcaccac ggacagacgc tgaggcctg 279

<210> SEQ ID NO 155
<211> LENGTH: 205
<212> TYPE: DNA

<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 155

gaagacctcc tggctgcaga ctccggcttc tgactctgcc tgcggctctt ctttccccag 60

ctctgggacc acctctcaag tgatcctgtt tatttatttg tttatttatt tatttttatg 120

ttgctgattt tctacaagac tgtttcttat cttccagcac aaacttgcca cagtgtaata 180

aacatagcct atttcttgct tttgg 205

<210> SEQ ID NO 156
<211> LENGTH: 1935
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 156

Met Gly Asp Ser Glu Met Ala Val Phe Gly Ala Ala Ala Pro Tyr Leu
1 5 10 15

Arg Lys Ser Glu Lys Glu Arg Leu Glu Ala Gln Thr Arg Pro Phe Asp
20 25 30

Leu Lys Lys Asp Val Phe Val Pro Asp Asp Lys Gln Glu Phe Val Lys
35 40 45

Ala Lys Ile Val Ser Arg Glu Gly Gly Lys Val Thr Ala Glu Thr Glu
50 55 60

Tyr Gly Lys Thr Val Thr Val Lys Glu Asp Gln Val Met Gln Gln Asn
65 70 75 80

Pro Pro Lys Phe Asp Lys Ile Glu Asp Met Ala Met Leu Thr Phe Leu
85 90 95

His Glu Pro Ala Val Leu Tyr Asn Leu Lys Asp Arg Tyr Gly Ser Trp
100 105 110

Met Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Thr Val Asn Pro Tyr
115 120 125

Lys Trp Leu Pro Val Tyr Thr Pro Glu Val Val Ala Ala Tyr Arg Gly
130 135 140

Lys Lys Arg Ser Glu Ala Pro Pro His Ile Phe Ser Ile Ser Asp Asn
145 150 155 160

Ala Tyr Gln Tyr Met Leu Thr Asp Arg Glu Asn Gln Ser Ile Leu Ile
165 170 175

Thr Gly Glu Ser Gly Ala Gly Lys Thr Val Asn Thr Lys Arg Val Ile
180 185 190

Gln Tyr Phe Ala Val Ile Ala Ala Ile Gly Asp Arg Ser Lys Lys Asp
195 200 205

Gln Ser Pro Gly Lys Gly Thr Leu Glu Asp Gln Ile Ile Gln Ala Asn
210 215 220

Pro Ala Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg Asn Asp Asn
225 230 235 240

Ser Ser Arg Phe Gly Lys Phe Ile Arg Ile His Phe Gly Ala Thr Gly
245 250 255

Lys Leu Ala Ser Ala Asp Ile Glu Thr Tyr Leu Leu Glu Lys Ser Arg
260 265 270

Val Ile Phe Gln Leu Lys Ala Glu Arg Asp Tyr His Ile Phe Tyr Gln
275 280 285

Ile Leu Ser Asn Lys Lys Pro Glu Leu Leu Asp Met Leu Leu Ile Thr
290 295 300

Asn Asn Pro Tyr Asp Tyr Ala Phe Ile Ser Gln Gly Glu Thr Thr Val
305 310 315 320

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Ala Ser Ile Asp Asp Ala Glu Glu Leu Met Ala Thr Asp Asn Ala Phe
                325                 330                 335

Asp Val Leu Gly Phe Thr Ser Glu Glu Lys Asn Ser Met Tyr Lys Leu
            340                 345                 350

Thr Gly Ala Ile Met His Phe Gly Asn Met Lys Phe Lys Leu Lys Gln
        355                 360                 365

Arg Glu Glu Gln Ala Glu Pro Asp Gly Thr Glu Glu Ala Asp Lys Ser
    370                 375                 380

Ala Tyr Leu Met Gly Leu Asn Ser Ala Asp Leu Leu Lys Gly Leu Cys
385                 390                 395                 400

His Pro Arg Val Lys Val Gly Asn Glu Tyr Val Thr Lys Gly Gln Asn
                405                 410                 415

Val Gln Gln Val Ile Tyr Ala Thr Gly Ala Leu Ala Lys Ala Val Tyr
            420                 425                 430

Glu Arg Met Phe Asn Trp Met Val Thr Arg Ile Asn Ala Thr Leu Glu
        435                 440                 445

Thr Lys Gln Pro Arg Gln Tyr Phe Ile Gly Val Leu Asp Ile Ala Gly
    450                 455                 460

Phe Glu Ile Phe Asp Phe Asn Ser Phe Glu Gln Leu Cys Ile Asn Phe
465                 470                 475                 480

Thr Asn Glu Lys Leu Gln Gln Phe Phe Asn His His Met Phe Val Leu
                485                 490                 495

Glu Gln Glu Glu Tyr Lys Lys Glu Gly Ile Glu Trp Thr Phe Ile Asp
            500                 505                 510

Phe Gly Met Asp Leu Gln Ala Cys Ile Asp Leu Ile Glu Lys Pro Met
        515                 520                 525

Gly Ile Met Ser Ile Leu Glu Glu Glu Cys Met Phe Pro Lys Ala Thr
    530                 535                 540

Asp Met Thr Phe Lys Ala Lys Leu Phe Asp Asn His Leu Gly Lys Ser
545                 550                 555                 560

Ala Asn Phe Gln Lys Pro Arg Asn Ile Lys Gly Lys Pro Glu Ala His
                565                 570                 575

Phe Ser Leu Ile His Tyr Ala Gly Ile Val Asp Tyr Asn Ile Ile Gly
            580                 585                 590

Trp Leu Gln Lys Asn Lys Asp Pro Leu Asn Glu Thr Val Val Gly Leu
        595                 600                 605

Tyr Gln Lys Ser Ser Leu Lys Leu Leu Ser Thr Leu Phe Ala Asn Tyr
    610                 615                 620

Ala Gly Ala Asp Ala Pro Ile Glu Lys Gly Lys Gly Lys Ala Lys Lys
625                 630                 635                 640

Gly Ser Ser Phe Gln Thr Val Ser Ala Leu His Arg Glu Asn Leu Asn
                645                 650                 655

Lys Leu Met Thr Asn Leu Arg Ser Thr His Pro His Phe Val Arg Cys
            660                 665                 670

Ile Ile Pro Asn Glu Thr Lys Ser Pro Gly Val Met Asp Asn Pro Leu
        675                 680                 685

Val Met His Gln Leu Arg Cys Asn Gly Val Leu Glu Gly Ile Arg Ile
    690                 695                 700

Cys Arg Lys Gly Phe Pro Asn Arg Ile Leu Tyr Gly Asp Phe Arg Gln
705                 710                 715                 720

Arg Tyr Arg Ile Leu Asn Pro Ala Ala Ile Pro Glu Gly Gln Phe Ile
                725                 730                 735
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Asp Ser Arg Lys Gly Ala Glu Lys Leu Leu Ser Ser Leu Asp Ile Asp
            740                 745                 750

His Asn Gln Tyr Lys Phe Gly His Thr Lys Val Phe Phe Lys Ala Gly
        755                 760                 765

Leu Leu Gly Leu Leu Glu Glu Met Arg Asp Glu Arg Leu Ser Arg Ile
    770                 775                 780

Ile Thr Arg Ile Gln Ala Gln Ser Arg Gly Val Leu Ala Arg Met Glu
785                 790                 795                 800

Tyr Lys Lys Leu Leu Glu Arg Arg Asp Ser Leu Leu Val Ile Gln Trp
                805                 810                 815

Asn Ile Arg Ala Phe Met Gly Val Lys Asn Trp Pro Trp Met Lys Leu
            820                 825                 830

Tyr Phe Lys Ile Lys Pro Leu Leu Lys Ser Ala Glu Arg Glu Lys Glu
        835                 840                 845

Met Ala Ser Met Lys Glu Glu Phe Thr Arg Leu Lys Glu Ala Leu Glu
    850                 855                 860

Lys Ser Glu Ala Arg Arg Lys Glu Leu Glu Glu Lys Met Val Ser Leu
865                 870                 875                 880

Leu Gln Glu Lys Asn Asp Leu Gln Leu Gln Val Gln Ala Glu Gln Asp
                885                 890                 895

Asn Leu Ala Asp Ala Glu Glu Arg Cys Asp Gln Leu Ile Lys Asn Lys
            900                 905                 910

Ile Gln Leu Glu Ala Lys Val Lys Glu Met Asn Glu Arg Leu Glu Asp
        915                 920                 925

Glu Glu Glu Met Asn Ala Glu Leu Thr Ala Lys Lys Arg Lys Leu Glu
    930                 935                 940

Asp Glu Cys Ser Glu Leu Lys Arg Asp Ile Asp Asp Leu Glu Leu Thr
945                 950                 955                 960

Leu Ala Lys Val Glu Lys Glu Lys His Ala Thr Glu Asn Lys Val Lys
                965                 970                 975

Asn Leu Thr Glu Glu Met Ala Gly Leu Asp Glu Ile Ile Ala Lys Leu
            980                 985                 990

Thr Lys Glu Lys Lys Ala Leu Gln  Glu Ala His Gln Gln  Ala Leu Asp
        995                 1000                1005

Asp Leu  Gln Ala Glu Glu Asp  Lys Val Asn Thr Leu  Thr Lys Ala
    1010                1015                1020

Lys Val  Lys Leu Glu Gln Gln  Val Asp Asp Leu Glu  Gly Ser Leu
    1025                1030                1035

Glu Gln  Glu Lys Lys Val Arg  Met Asp Leu Glu Arg  Ala Lys Arg
    1040                1045                1050

Lys Leu  Glu Gly Asp Leu Lys  Leu Thr Gln Glu Ser  Ile Met Asp
    1055                1060                1065

Leu Glu  Asn Asp Lys Gln Gln  Leu Asp Glu Arg Leu  Lys Lys Lys
    1070                1075                1080

Asp Phe  Glu Leu Asn Ala Leu  Asn Ala Arg Ile Glu  Asp Glu Gln
    1085                1090                1095

Ala Leu  Gly Ser Gln Leu Gln  Lys Lys Leu Lys Glu  Leu Gln Ala
    1100                1105                1110

Arg Ile  Glu Glu Leu Glu Glu  Glu Leu Glu Ala Glu  Arg Thr Ala
    1115                1120                1125

Arg Ala  Lys Val Glu Lys Leu  Arg Ser Asp Leu Ser  Arg Glu Leu
    1130                1135                1140

Glu Glu  Ile Ser Glu Arg Leu  Glu Glu Ala Gly Gly  Ala Thr Ser
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    1145                1150                1155

Val Gln  Ile Glu Met Asn Lys  Lys Arg Glu Ala Glu  Phe Gln Lys
    1160                1165                1170

Met Arg  Arg Asp Leu Glu Glu  Ala Thr Leu Gln His  Glu Ala Thr
    1175                1180                1185

Ala Ala  Ala Leu Arg Lys Lys  His Ala Asp Ser Val  Ala Glu Leu
    1190                1195                1200

Gly Glu  Gln Ile Asp Asn Leu  Gln Arg Val Lys Gln  Lys Leu Glu
    1205                1210                1215

Lys Glu  Lys Ser Glu Phe Lys  Leu Glu Leu Asp Asp  Val Thr Ser
    1220                1225                1230

Asn Met  Glu Gln Ile Ile Lys  Ala Lys Ala Asn Leu  Glu Lys Met
    1235                1240                1245

Cys Arg  Thr Leu Glu Asp Gln  Met Asn Glu His Arg  Ser Lys Ala
    1250                1255                1260

Glu Glu  Thr Gln Arg Ser Val  Asn Asp Leu Thr Ser  Gln Arg Ala
    1265                1270                1275

Lys Leu  Gln Thr Glu Asn Gly  Glu Leu Ser Arg Gln  Leu Asp Glu
    1280                1285                1290

Lys Glu  Ala Leu Ile Ser Gln  Leu Thr Arg Gly Lys  Leu Thr Tyr
    1295                1300                1305

Thr Gln  Gln Leu Glu Asp Leu  Lys Arg Gln Leu Glu  Glu Glu Val
    1310                1315                1320

Lys Ala  Lys Asn Ala Leu Ala  His Ala Leu Gln Ser  Ala Arg His
    1325                1330                1335

Asp Cys  Asp Leu Leu Arg Glu  Gln Tyr Glu Glu Glu  Thr Glu Ala
    1340                1345                1350

Lys Ala  Glu Leu Gln Arg Val  Leu Ser Lys Ala Asn  Ser Glu Val
    1355                1360                1365

Ala Gln  Trp Arg Thr Lys Tyr  Glu Thr Asp Ala Ile  Gln Arg Thr
    1370                1375                1380

Glu Glu  Leu Glu Glu Ala Lys  Lys Lys Leu Ala Gln  Arg Leu Gln
    1385                1390                1395

Glu Ala  Glu Glu Ala Val Glu  Ala Val Asn Ala Lys  Cys Ser Ser
    1400                1405                1410

Leu Glu  Lys Thr Lys His Arg  Leu Gln Asn Glu Ile  Glu Asp Leu
    1415                1420                1425

Met Val  Asp Val Glu Arg Ser  Asn Ala Ala Ala Ala  Ala Leu Asp
    1430                1435                1440

Lys Lys  Gln Arg Asn Phe Asp  Lys Ile Leu Ala Glu  Trp Lys Gln
    1445                1450                1455

Lys Tyr  Glu Glu Ser Gln Ser  Glu Leu Glu Ser Ser  Gln Lys Glu
    1460                1465                1470

Ala Arg  Ser Leu Ser Thr Glu  Leu Phe Lys Leu Lys  Asn Ala Tyr
    1475                1480                1485

Glu Glu  Ser Leu Glu His Leu  Glu Thr Phe Lys Arg  Glu Asn Lys
    1490                1495                1500

Asn Leu  Gln Glu Glu Ile Ser  Asp Leu Thr Glu Gln  Leu Gly Ser
    1505                1510                1515

Ser Gly  Lys Thr Ile His Glu  Leu Glu Lys Val Arg  Lys Gln Leu
    1520                1525                1530

Glu Ala  Glu Lys Met Glu Leu  Gln Ser Ala Leu Glu  Glu Ala Glu
    1535                1540                1545
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Ala Ser  Leu Glu His Glu Glu  Gly Lys Ile Leu Arg  Ala Gln Leu
    1550                 1555                 1560

Glu Phe  Asn Gln Ile Lys Ala  Glu Ile Glu Arg Lys  Leu Ala Glu
    1565                 1570                 1575

Lys Asp  Glu Glu Met Glu Gln  Ala Lys Arg Asn His  Leu Arg Val
    1580                 1585                 1590

Val Asp  Ser Leu Gln Thr Ser  Leu Asp Ala Glu Thr  Arg Ser Arg
    1595                 1600                 1605

Asn Glu  Ala Leu Arg Val Lys  Lys Lys Met Glu Gly  Asp Leu Asn
    1610                 1615                 1620

Glu Met  Glu Ile Gln Leu Ser  His Ala Asn Arg Met  Ala Ala Glu
    1625                 1630                 1635

Ala Gln  Lys Gln Val Lys Ser  Leu Gln Ser Leu Leu  Lys Asp Thr
    1640                 1645                 1650

Gln Ile  Gln Leu Asp Asp Ala  Val Arg Ala Asn Asp  Asp Leu Lys
    1655                 1660                 1665

Glu Asn  Ile Ala Ile Val Glu  Arg Arg Asn Asn Leu  Leu Gln Ala
    1670                 1675                 1680

Glu Leu  Glu Glu Leu Arg Ala  Val Val Glu Gln Thr  Glu Arg Ser
    1685                 1690                 1695

Arg Lys  Leu Ala Glu Gln Glu  Leu Ile Glu Thr Ser  Glu Arg Val
    1700                 1705                 1710

Gln Leu  Leu His Ser Gln Asn  Thr Ser Leu Ile Asn  Gln Lys Lys
    1715                 1720                 1725

Lys Met  Asp Ala Asp Leu Ser  Gln Leu Gln Thr Glu  Val Glu Glu
    1730                 1735                 1740

Ala Val  Gln Glu Cys Arg Asn  Ala Glu Glu Lys Ala  Lys Lys Ala
    1745                 1750                 1755

Ile Thr  Asp Ala Ala Met Met  Ala Glu Glu Leu Lys  Lys Glu Gln
    1760                 1765                 1770

Asp Thr  Ser Ala His Leu Glu  Arg Met Lys Lys Asn  Met Glu Gln
    1775                 1780                 1785

Thr Ile  Lys Asp Leu Gln His  Arg Leu Asp Glu Ala  Glu Gln Ile
    1790                 1795                 1800

Ala Leu  Lys Gly Gly Lys Lys  Gln Leu Gln Lys Leu  Glu Ala Arg
    1805                 1810                 1815

Val Arg  Glu Leu Glu Asn Glu  Leu Glu Ala Glu Gln  Lys Arg Asn
    1820                 1825                 1830

Ala Glu  Ser Val Lys Gly Met  Arg Lys Ser Glu Arg  Arg Ile Lys
    1835                 1840                 1845

Glu Leu  Thr Tyr Gln Thr Glu  Glu Asp Arg Lys Asn  Leu Leu Arg
    1850                 1855                 1860

Leu Gln  Asp Leu Val Asp Lys  Leu Gln Leu Lys Val  Lys Ala Tyr
    1865                 1870                 1875

Lys Arg  Gln Ala Glu Glu Ala  Glu Glu Gln Ala Asn  Thr Asn Leu
    1880                 1885                 1890

Ser Lys  Phe Arg Lys Val Gln  His Glu Leu Asp Glu  Ala Glu Glu
    1895                 1900                 1905

Arg Ala  Asp Ile Ala Glu Ser  Gln Val Asn Lys Leu  Arg Ala Lys
    1910                 1915                 1920

Ser Arg  Asp Ile Gly Thr Lys  Gly Leu Asn Glu Glu
    1925                 1930                 1935
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<210> SEQ ID NO 157
<211> LENGTH: 6069
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 157

cagcccctga gaccaggtct ggctccacag ctctgtcctg ctctgtgtct ttccctgctg 60

ctctcaggtc ccctgcaggc cttggcccct ttcctcatct gtagacacac ttgagtagcc 120

caggcacagc catgggagat tcggagatgg cagtctttgg ggctgccgcc ccctacctgc 180

gcaagtcaga gaaggagcgg ctagaagcgc agaccaggcc ttttgacctc aagaaggatg 240

tcttcgtgcc tgatgacaaa caggagtttg tcaaggccaa gatcgtgtct cgagagggtg 300

gcaaagtcac tgccgagacc gagtatggca agacagtgac cgtgaaggag gaccaggtga 360

tgcagcagaa cccacccaag ttcgacaaaa tcgaggacat ggccatgctg accttcctgc 420

atgagcccgc ggtgctctac aacctcaagg atcgctacgg ctcctggatg atctacacct 480

actcgggcct cttctgtgtc accgtcaacc cttacaagtg gctgccggtg tacactcctg 540

aggtggtggc tgcctaccgg ggcaagaaga ggagcgaggc cccgccccac atcttctcca 600

tctccgacaa cgcctatcag tacatgctga cagacagaga aaaccagtcc atcctgatca 660

ccggagaatc cggagcaggg aagacagtca acaccaagag ggtcatccag tactttgctg 720

ttattgcagc cattggggac cgcagcaaga aggaccagag cccgggcaag ggcaccctgg 780

aggaccagat catccaggcc aaccctgctc tggaggcctt tggcaatgcc aagaccgtcc 840

ggaacgacaa ctcctcccgc ttcgggaaat tcattcgaat tcattttggg gcaacaggaa 900

agttggcatc tgcagacata gagacctatc ttctggaaaa atccagagtt attttccagc 960

tgaaagcaga gagagattat cacattttct accaaatcct gtctaacaaa aagcctgagc 1020

tgctggacat gctgctgatc accaacaacc cctacgatta tgcattcatc tcccaaggag 1080

agaccaccgt ggcctccatt gatgacgctg aggagctcat ggccactgat aacgcttttg 1140

atgtgctggg cttcacttca gaggagaaaa actccatgta taagctgaca ggcgccatca 1200

tgcactttgg aaacatgaag ttcaagctga agcagcggga ggagcaggcg gagccagacg 1260

gcactgaaga ggctgacaag tctgcctacc tcatggggct gaactcagcc gacctgctca 1320

aggggctgtg ccaccctcgg gtgaaagtgg gcaatgagta cgtcaccaag gggcagaatg 1380

tccagcaggt gatatatgcc actggggcac tggccaaggc agtgtatgag aggatgttca 1440

actggatggt gacgcgcatc aatgccaccc tggagaccaa gcagccacgc cagtacttca 1500

taggagtcct ggacatcgct ggcttcgaga tcttcgattt caacagcttt gagcagctct 1560

gcatcaactt caccaacgag aagctgcagc agttcttcaa ccaccacatg tttgtgctgg 1620

agcaggagga gtacaagaag gagggcatcg agtggacatt cattgacttt ggcatggacc 1680

tgcaggcctg cattgacctc atcgagaagc ccatgggcat catgtccatc ctggaagagg 1740

agtgcatgtt ccccaaggcc accgacatga ccttcaaggc caagctgttt gacaaccacc 1800

tgggcaaatc cgccaacttc cagaagccac gcaatatcaa ggggaagcct gaagcccact 1860

tctccctgat ccactatgcc ggcatcgtgg actacaacat cattggctgg ctgcagaaga 1920

acaaggatcc tctcaatgag actgtcgtgg gcttgtatca gaagtcttcc ctcaagctgc 1980

tcagcaccct gtttgccaac tatgctgggg ctgatgcgcc tattgagaag ggcaaaggca 2040

aggccaagaa aggctcgtcc tttcagactg tgtcagctct gcacagggaa aatctgaaca 2100

agctgatgac caacttgcgc tccacccatc cccactttgt acgttgtatc atccctaatg 2160

```
agacaaagtc tccaggggtg atggacaacc ccctggtcat gcaccagctg cgctgcaatg   2220
gtgtgctgga gggcatccgc atctgcagga aaggcttccc caaccgcatc ctctacgggg   2280
acttccggca gaggtatcgc atcctgaacc cagcggccat ccctgaggga cagttcattg   2340
atagcaggaa gggggcagag aagctgctca gctccctgga cattgatcac aaccagtaca   2400
agtttggcca caccaaggtg ttcttcaagg ccgggctgct ggggctgctg gaggaaatga   2460
gggacgagag gctgagccgc atcatcacgc gtatccaggc ccagtcccga ggtgtgctcg   2520
ccagaatgga gtacaaaaag ctgctggaac gtagagactc cctgctggta atccagtgga   2580
acattcgggc cttcatgggg gtcaagaatt ggccctggat gaagctctac ttcaagatca   2640
agccgctgct gaagagtgca gaaagagaga aggagatggc ctccatgaag gaggagttca   2700
cacgcctcaa agaggcgcta gagaagtccg aggctcgccg caaggagctg gaggagaaga   2760
tggtgtccct gctgcaggag aagaatgacc tgcagctcca agtgcaggcg gaacaagaca   2820
acctggcaga tgctgaggag cgctgtgatc agctgatcaa aaacaagatt cagctggagg   2880
ccaaggtgaa ggagatgaac gagaggctgg aggatgagga ggagatgaat gctgagctca   2940
ctgccaagaa gcgcaagctg gaagatgagt gctcagagct caaaagggac atcgatgatc   3000
tggagctgac actggccaaa gtggagaagg agaaacacgc aacagagaac aaggtgaaaa   3060
acctgacaga ggagatggct gggctggatg agatcattgc caagctgacc aaggagaaga   3120
aagctctgca agaggcccac caacaggctc tggatgacct tcaggccgag gaggacaagg   3180
tcaacaccct gactaaggcc aaagtcaagc tggagcagca agtggatgat ctggaaggat   3240
ccctggagca agagaagaag gtgcgcatgg acctggagcg agcgaagcgg aagctggagg   3300
gcgacctgaa gctgacccag gagagcatca tggacctgga gaatgacaag cagcagctgg   3360
atgagcggct gaaaaaaaaa gactttgagc tgaatgctct caacgcaagg attgaggatg   3420
aacaggccct cggcagccag ctgcagaaga agctcaagga gcttcaggca cgcatcgagg   3480
agctggagga ggagctggag gccgagcgca ccgccagggc taaggtggag aagctgcgct   3540
cagacctgtc tcgggagctg gaggagatca gcgagcggct ggaagaggcc ggcggggcca   3600
cgtccgtgca gatcgagatg aacaagaagc gcgaggccga gttccagaag atgcggcggg   3660
acctggagga ggccacgctg cagcacgagg ccactgccgc ggccctgcgc aagaagcacg   3720
ccgacagcgt ggccgagctg ggcgagcaga tcgacaacct gcagcgggtg aagcagaagc   3780
tggagaagga gaagagcgag ttcaagctgg agctggatga cgtcacctcc aacatggagc   3840
agatcatcaa ggccaaggct aacctggaga agatgtgccg gaccttggaa gaccagatga   3900
atgagcaccg gagcaaggcg gaggagaccc agcgttctgt caacgacctc accagccagc   3960
gggccaagtt gcaaaccgag aatggtgagc tgtcccggca gctggatgag aaggaggcac   4020
tgatctccca gctgacccga ggcaagctca cctacaccca gcagctggag gacctcaaga   4080
ggcagctgga ggaggaggtt aaggcgaaga acgccctggc ccacgcactg cagtcggccc   4140
ggcatgactg cgacctgctg cgggagcagt acgaggagga gacggaggcc aaggccgagc   4200
tgcagcgcgt cctttccaag gccaactcgg aggtggccca gtggaggacc aagtatgaga   4260
cggacgccat tcagcggact gaggagctcg aggaggccaa gaagaagctg gcccagcggc   4320
tgcaggaagc tgaggaggcc gtggaggctg ttaatgccaa gtgctcctcg ctggagaaga   4380
ccaagcaccg gctacagaat gagatcgagg acttgatggt ggacgtagag cgctccaatg   4440
ctgctgctgc agccctggac aagaagcaga ggaacttcga caagatcctg gccgagtgga   4500
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agcagaagta tgaggagtcg cagtcggagc tggagtcctc gcagaaggag gctcgctccc   4560
tcagcacaga gctcttcaaa ctcaagaacg cctatgagga gtccctggaa catctggaga   4620
ccttcaagcg ggagaacaaa aacctgcagg aggagatctc cgacttgact gagcagttgg   4680
gttccagcgg aaagactatc catgagctgg agaaggtccg aaagcagctg gaggccgaga   4740
agatggagct gcagtcagcc ctggaggagg ccgaggcctc cctggagcac gaggagggca   4800
agatcctccg ggcccagctg gagttcaacc agatcaaggc agagatcgag cggaagctgg   4860
cagagaagga cgaggagatg gaacaggcca agcgcaacca cctgcgggtg gtggactcgc   4920
tgcagacctc cctggacgca gagacacgca gccgcaacga ggccctgagg gtgaagaaga   4980
agatggaagg agacctcaat gagatggaga tccagctcag ccacgccaac cgcatggccg   5040
ccgaggccca gaagcaagtc aagagcctcc agagcttgtt gaaggacacc cagattcagc   5100
tggacgatgc agtccgtgcc aacgacgacc tgaaggagaa catcgccatc gtggagcggc   5160
gcaacaacct gctgcaggct gagctggagg agttgcgtgc cgtggtggag cagacagagc   5220
ggtcccggaa gctggcggag caggagctga ttgagactag tgagcgggtg cagctgctgc   5280
attcccagaa caccagcctc atcaaccaga agaagaagat ggatgctgac ctgtcccagc   5340
tccagactga agtggaggag gcagtgcagg agtgcaggaa tgctgaggag aaggccaaga   5400
aggccatcac ggatgccgcc atgatggcag aggagctgaa gaaggagcag gacaccagcg   5460
cccacctgga gcgcatgaag aagaacatgg aacagaccat taaggacctg cagcaccggc   5520
tggacgaagc cgagcagatc gccctcaagg gcggcaagaa gcagctgcag aagctggaag   5580
cgcgggtgcg ggagctggag aatgagctgg aggccgagca gaagcgcaac gcagagtcgg   5640
tgaagggcat gaggaagagc gagcggcgca tcaaggagct cacctaccag acggaggagg   5700
acaggaaaaa cctgctgcgg ctgcaggacc tggtagacaa gctgcagcta aaggtcaagg   5760
cctacaagcg ccaggccgag gaggcggagg agcaagccaa caccaacctg tccaagttcc   5820
gcaaggtgca gcacgagctg gatgaggcag aggagcgggc ggacatcgcc gagtcccagg   5880
tcaacaagct gcgggccaag agccgtgaca ttggcacgaa gggcttgaat gaggagtagc   5940
tttgccacat cttgatctgc tcagccctgg aggtgccagc aaagccccat gctggagcct   6000
gtgtaacagc tccttgggag gaagcagaat aaagcaattt tccttgaagc cgagaaaaaa   6060
aaaaaaaaa                                                           6069
```

<210> SEQ ID NO 158
<211> LENGTH: 151
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 158

```
Met Ser Ser Phe Ser Thr Thr Thr Val Ser Phe Leu Leu Leu Leu Ala
1               5                   10                  15

Phe Gln Leu Leu Gly Gln Thr Arg Ala Asn Pro Met Tyr Asn Ala Val
            20                  25                  30

Ser Asn Ala Asp Leu Met Asp Phe Lys Asn Leu Leu Asp His Leu Glu
        35                  40                  45

Glu Lys Met Pro Leu Glu Asp Glu Val Val Pro Pro Gln Val Leu Ser
    50                  55                  60

Glu Pro Asn Glu Glu Ala Gly Ala Ala Leu Ser Pro Leu Pro Glu Val
65                  70                  75                  80

Pro Pro Trp Thr Gly Glu Val Ser Pro Ala Gln Arg Asp Gly Gly Ala
                85                  90                  95
```

```
Leu Gly Arg Gly Pro Trp Asp Ser Ser Asp Arg Ser Ala Leu Leu Lys
            100                 105                 110

Ser Lys Leu Arg Ala Leu Leu Thr Ala Pro Arg Ser Leu Arg Arg Ser
        115                 120                 125

Ser Cys Phe Gly Gly Arg Met Asp Arg Ile Gly Ala Gln Ser Gly Leu
    130                 135                 140

Gly Cys Asn Ser Phe Arg Tyr
145                 150


<210> SEQ ID NO 159
<211> LENGTH: 858
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 159

gagacaggga cagacgtagg ccaagagagg ggaaccagag aggaaccaga ggggagagac     60

agagcagcaa gcagtggatt gctccttgac gacgccagca tgagctcctt ctccaccacc    120

accgtgagct tcctcctttt actggcattc cagctcctag gtcagaccag agctaatccc    180

atgtacaatg ccgtgtccaa cgcagacctg atggatttca agaatttgct ggaccatttg    240

gaagaaaaga tgcctttaga agatgaggtc gtgcccccac aagtgctcag tgagccgaat    300

gaagaagcgg gggctgctct cagccccctc cctgaggtgc ctccctggac cggggaagtc    360

agcccagccc agagagatgg aggtgccctc gggcggggcc cctgggactc ctctgatcga    420

tctgccctcc taaaaagcaa gctgagggcg ctgctcactg cccctcggag cctgcggaga    480

tccagctgct tcgggggcag gatggacagg attggagccc agagcggact gggctgtaac    540

agcttccggt actgaagata acagccaggg aggacaagca gggctgggcc tagggacaga    600

ctgcaagagg ctcctgtccc ctggggtctc tgctgcattt gtgtcatctt gttgccatgg    660

agttgtgatc atcccatcta agctgcagct tcctgtcaac acttctcaca tcttatgcta    720

actgtagata aagtggtttg atggtgactt cctcgcctct cccaccccat gcattaaatt    780

ttaaggtaga acctcacctg ttactgaaag tggtttgaaa gtgaataaac ttcagcacca    840

tggacagaag acaaaaaa                                                  858


<210> SEQ ID NO 160
<211> LENGTH: 134
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 160

Met Asp Pro Gln Thr Ala Pro Ser Arg Ala Leu Leu Leu Leu Leu Phe
1               5                   10                  15

Leu His Leu Ala Phe Leu Gly Gly Arg Ser His Pro Leu Gly Ser Pro
            20                  25                  30

Gly Ser Ala Ser Asp Leu Glu Thr Ser Gly Leu Gln Glu Gln Arg Asn
        35                  40                  45

His Leu Gln Gly Lys Leu Ser Glu Leu Gln Val Glu Gln Thr Ser Leu
    50                  55                  60

Glu Pro Leu Gln Glu Ser Pro Arg Pro Thr Gly Val Trp Lys Ser Arg
65                  70                  75                  80

Glu Val Ala Thr Glu Gly Ile Arg Gly His Arg Lys Met Val Leu Tyr
                85                  90                  95

Thr Leu Arg Ala Pro Arg Ser Pro Lys Met Val Gln Gly Ser Gly Cys
            100                 105                 110
```

```
Phe Gly Arg Lys Met Asp Arg Ile Ser Ser Ser Ser Gly Leu Gly Cys
        115                 120                 125

Lys Val Leu Arg Arg His
    130


<210> SEQ ID NO 161
<211> LENGTH: 708
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 161

ccccgcaggc tgagggcagg tgggaagcaa acccggacgc atcgcagcag cagcagcagc     60

agcagaagca gcagcagcag cctccgcagt ccctccagag acatggatcc ccagacagca    120

ccttcccggg cgctcctgct cctgctcttc ttgcatctgg ctttcctggg aggtcgttcc    180

cacccgctgg gcagccccgg ttcagcctcg gacttggaaa cgtccgggtt acaggagcag    240

cgcaaccatt tgcagggcaa actgtcggag ctgcaggtgg agcagacatc cctggagccc    300

ctccaggaga gcccccgtcc cacaggtgtc tggaagtccc gggaggtagc caccgagggc    360

atccgtgggc accgcaaaat ggtcctctac accctgcggg caccacgaag ccccaagatg    420

gtgcaagggt ctggctgctt tgggaggaag atggaccgga tcagctcctc cagtggcctg    480

ggctgcaaag tgctgaggcg gcattaagag gaagtcctgg ctgcagacac ctgcttctga    540

ttccacaagg ggctttttcc tcaaccctgt ggccgccttt gaagtgactc atttttttaa    600

tgtatttatg tatttatttg attgttttat ataagatggt ttcttacctt tgagcacaaa    660

atttccacgg tgaaataaag tcaacattat aagctttaaa aaaaaaaa                 708


<210> SEQ ID NO 162
<211> LENGTH: 1935
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 162

Met Ala Asp Arg Glu Met Ala Ala Phe Gly Ala Gly Ala Pro Phe Leu
1               5                   10                  15

Arg Lys Ser Glu Lys Glu Arg Leu Glu Ala Gln Thr Arg Pro Phe Asp
            20                  25                  30

Leu Lys Lys Asp Val Phe Val Pro Asp Asp Lys Glu Glu Phe Val Lys
        35                  40                  45

Ala Lys Ile Val Ser Arg Glu Gly Gly Lys Val Thr Ala Glu Thr Glu
    50                  55                  60

Asn Gly Lys Thr Val Thr Val Lys Glu Asp Gln Val Met Gln Gln Asn
65                  70                  75                  80

Pro Pro Lys Phe Asp Lys Ile Glu Asp Met Ala Met Leu Thr Phe Leu
                85                  90                  95

His Glu Pro Ala Val Leu Tyr Asn Leu Lys Glu Arg Tyr Ala Ser Trp
            100                 105                 110

Met Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Thr Val Asn Pro Tyr
        115                 120                 125

Lys Trp Leu Pro Val Tyr Asn Ala Gln Val Val Ala Ala Tyr Arg Gly
    130                 135                 140

Lys Lys Arg Ser Glu Ala Pro Pro His Ile Phe Ser Ile Ser Asp Asn
145                 150                 155                 160

Ala Tyr Gln Tyr Met Leu Thr Asp Arg Glu Asn Gln Ser Ile Leu Ile
                165                 170                 175
```

```
Thr Gly Glu Ser Gly Ala Gly Lys Thr Val Asn Thr Lys Arg Val Ile
            180                 185                 190

Gln Tyr Phe Ala Val Ile Ala Ala Ile Gly Asp Arg Ser Lys Lys Asp
        195                 200                 205

Gln Thr Pro Gly Lys Gly Thr Leu Glu Asp Gln Ile Ile Gln Ala Asn
    210                 215                 220

Pro Ala Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Arg Asn Asp Asn
225                 230                 235                 240

Ser Ser Arg Phe Gly Lys Phe Ile Arg Ile His Phe Gly Ala Thr Gly
                245                 250                 255

Lys Leu Ala Ser Ala Asp Ile Glu Thr Tyr Leu Leu Glu Lys Ser Arg
            260                 265                 270

Val Ile Phe Gln Leu Lys Ala Glu Arg Asp Tyr His Ile Phe Tyr Gln
        275                 280                 285

Ile Leu Ser Asn Lys Lys Pro Glu Leu Leu Asp Met Leu Leu Ile Thr
    290                 295                 300

Asn Asn Pro Tyr Asp Tyr Ala Phe Phe Ser Gln Gly Glu Thr Thr Val
305                 310                 315                 320

Ala Ser Ile Asp Asp Ser Glu Glu His Met Ala Thr Asp Ser Ala Phe
                325                 330                 335

Asp Val Leu Gly Phe Thr Pro Glu Glu Lys Asn Ser Ile Tyr Lys Leu
            340                 345                 350

Thr Gly Ala Ile Met His Phe Gly Asn Met Lys Phe Lys Gln Lys Gln
        355                 360                 365

Arg Glu Glu Gln Ala Glu Pro Asp Gly Thr Glu Glu Ala Asp Lys Ser
    370                 375                 380

Ala Tyr Leu Met Gly Leu Asn Ser Ala Asp Leu Leu Lys Gly Leu Cys
385                 390                 395                 400

His Pro Arg Val Lys Val Gly Asn Glu Tyr Val Thr Lys Gly Gln Asn
                405                 410                 415

Val Gln Gln Val Ala Tyr Ala Ile Gly Ala Leu Ala Lys Ser Val Tyr
            420                 425                 430

Glu Lys Met Phe Asn Trp Met Val Thr Arg Ile Asn Ala Thr Leu Glu
        435                 440                 445

Thr Lys Gln Pro Arg Gln Tyr Phe Ile Gly Val Leu Asp Ile Ala Gly
    450                 455                 460

Phe Glu Ile Phe Asp Phe Asn Ser Phe Glu Gln Leu Cys Ile Asn Phe
465                 470                 475                 480

Thr Asn Glu Lys Leu Gln Gln Phe Phe Asn His His Met Phe Val Leu
                485                 490                 495

Glu Gln Glu Glu Tyr Lys Lys Glu Gly Ile Glu Trp Thr Phe Ile Asp
            500                 505                 510

Phe Gly Met Asp Leu Gln Ala Cys Ile Asp Leu Ile Glu Lys Pro Met
        515                 520                 525

Gly Ile Met Ser Ile Leu Glu Glu Glu Cys Met Phe Pro Lys Ala Thr
    530                 535                 540

Asp Met Thr Phe Lys Ala Lys Leu Tyr Asp Asn His Leu Gly Lys Ser
545                 550                 555                 560

Asn Asn Phe Gln Lys Pro Arg Asn Ile Lys Gly Lys Gln Glu Ala His
                565                 570                 575

Phe Ser Leu Ile His Tyr Ala Gly Thr Val Asp Tyr Asn Ile Leu Gly
            580                 585                 590
```

```
Trp Leu Gln Lys Asn Lys Asp Pro Leu Asn Glu Thr Val Val Gly Leu
        595                 600                 605

Tyr Gln Lys Ser Ser Leu Lys Leu Leu Ser Asn Leu Phe Ala Asn Tyr
    610                 615                 620

Ala Gly Ala Asp Ala Pro Val Asp Lys Gly Lys Gly Lys Ala Lys Lys
625                 630                 635                 640

Gly Ser Ser Phe Gln Thr Val Ser Ala Leu His Arg Glu Asn Leu Asn
                645                 650                 655

Lys Leu Met Thr Asn Leu Arg Ser Thr His Pro His Phe Val Arg Cys
            660                 665                 670

Ile Ile Pro Asn Glu Thr Lys Ser Pro Gly Val Met Asp Asn Pro Leu
        675                 680                 685

Val Met His Gln Leu Arg Cys Asn Gly Val Leu Glu Gly Ile Arg Ile
    690                 695                 700

Cys Arg Lys Gly Phe Pro Asn Arg Ile Leu Tyr Gly Asp Phe Arg Gln
705                 710                 715                 720

Arg Tyr Arg Ile Leu Asn Pro Ala Ala Ile Pro Glu Gly Gln Phe Ile
                725                 730                 735

Asp Ser Arg Lys Gly Ala Glu Lys Leu Leu Gly Ser Leu Asp Ile Asp
            740                 745                 750

His Asn Gln Tyr Lys Phe Gly His Thr Lys Val Phe Phe Lys Ala Gly
        755                 760                 765

Leu Leu Gly Leu Leu Glu Glu Met Arg Asp Glu Arg Leu Ser Arg Ile
    770                 775                 780

Ile Thr Arg Ile Gln Ala Gln Ser Arg Gly Val Leu Ser Arg Met Glu
785                 790                 795                 800

Phe Lys Lys Leu Leu Glu Arg Arg Asp Ser Leu Leu Ile Ile Gln Trp
                805                 810                 815

Asn Ile Arg Ala Phe Met Gly Val Lys Asn Trp Pro Trp Met Lys Leu
            820                 825                 830

Tyr Phe Lys Ile Lys Pro Leu Leu Lys Ser Ala Glu Thr Glu Lys Glu
        835                 840                 845

Met Ala Asn Met Lys Glu Glu Phe Gly Arg Val Lys Asp Ala Leu Glu
    850                 855                 860

Lys Ser Glu Ala Arg Arg Lys Glu Leu Glu Glu Lys Met Val Ser Leu
865                 870                 875                 880

Leu Gln Glu Lys Asn Asp Leu Gln Leu Gln Val Gln Ala Glu Gln Asp
                885                 890                 895

Asn Leu Ala Asp Ala Glu Glu Arg Cys Asp Gln Leu Ile Lys Asn Lys
            900                 905                 910

Ile Gln Leu Glu Ala Lys Val Lys Glu Met Thr Glu Arg Leu Glu Asp
        915                 920                 925

Glu Glu Glu Met Asn Ala Glu Leu Thr Ala Lys Lys Arg Lys Leu Glu
    930                 935                 940

Asp Glu Cys Ser Glu Leu Lys Arg Asp Ile Asp Asp Leu Glu Leu Thr
945                 950                 955                 960

Leu Ala Lys Val Glu Lys Glu Lys His Ala Thr Glu Asn Lys Val Lys
                965                 970                 975

Asn Leu Thr Glu Glu Met Ala Gly Leu Asp Glu Ile Ile Val Lys Leu
            980                 985                 990

Thr Lys Glu Lys Lys Ala Leu Gln  Glu Ala His Gln Gln  Ala Leu Asp
        995                 1000                1005

Asp Leu  Gln Ala Glu Glu Asp  Lys Val Asn Thr Leu  Thr Lys Ala
```

```
    1010                1015                1020

Lys Val  Lys Leu Glu Gln Gln  Val Asp Asp Leu Glu  Gly Ser Leu
    1025                1030                1035

Asp Gln  Asp Lys Lys Val Arg  Met Asp Leu Glu Arg  Ala Lys Arg
    1040                1045                1050

Lys Leu  Glu Gly Asp Leu Lys  Leu Thr Gln Glu Ser  Ile Met Asp
    1055                1060                1065

Leu Glu  Asn Asp Lys Gln Gln  Leu Asp Glu Arg Leu  Lys Lys Lys
    1070                1075                1080

Asp Phe  Glu Leu Asn Ala Leu  Asn Ala Arg Ile Glu  Asp Glu Gln
    1085                1090                1095

Ala Leu  Gly Ser Gln Leu Gln  Lys Lys Leu Lys Glu  Leu Gln Ala
    1100                1105                1110

Arg Ile  Glu Glu Leu Glu Glu  Glu Leu Glu Ala Glu  Arg Thr Ala
    1115                1120                1125

Arg Ala  Lys Val Glu Lys Leu  Arg Ser Asp Leu Ser  Arg Glu Leu
    1130                1135                1140

Glu Glu  Ile Ser Glu Arg Leu  Glu Glu Ala Gly Gly  Ala Thr Ser
    1145                1150                1155

Val Gln  Ile Glu Met Asn Lys  Lys Arg Glu Ala Glu  Phe Gln Lys
    1160                1165                1170

Met Arg  Arg Asp Leu Glu Glu  Ala Thr Leu Gln His  Glu Ala Thr
    1175                1180                1185

Ala Ala  Ala Leu Arg Lys Lys  His Ala Asp Ser Val  Ala Glu Leu
    1190                1195                1200

Gly Glu  Gln Ile Asp Asn Leu  Gln Arg Val Lys Gln  Lys Leu Glu
    1205                1210                1215

Lys Glu  Lys Ser Glu Phe Lys  Leu Glu Leu Asp Asp  Val Thr Ser
    1220                1225                1230

Asn Met  Glu Gln Ile Ile Lys  Ala Lys Ala Asn Leu  Glu Lys Met
    1235                1240                1245

Cys Arg  Thr Leu Glu Asp Gln  Met Asn Glu His Arg  Ser Lys Ala
    1250                1255                1260

Glu Glu  Thr Gln Arg Ser Val  Asn Asp Leu Thr Arg  Gln Arg Ala
    1265                1270                1275

Lys Leu  Gln Thr Glu Asn Gly  Glu Leu Ser Arg Gln  Leu Asp Glu
    1280                1285                1290

Lys Glu  Ala Leu Ile Ser Gln  Leu Thr Arg Gly Lys  Leu Thr Tyr
    1295                1300                1305

Thr Gln  Gln Leu Glu Asp Leu  Lys Arg Gln Leu Glu  Glu Glu Val
    1310                1315                1320

Lys Ala  Lys Asn Ala Leu Ala  His Ala Leu Gln Ser  Ala Arg His
    1325                1330                1335

Asp Cys  Asp Leu Leu Arg Glu  Gln Tyr Glu Glu Glu  Thr Glu Ala
    1340                1345                1350

Lys Ala  Glu Leu Gln Arg Val  Leu Ser Lys Ala Asn  Ser Glu Val
    1355                1360                1365

Ala Gln  Trp Arg Thr Lys Tyr  Glu Thr Asp Ala Ile  Gln Arg Thr
    1370                1375                1380

Glu Glu  Leu Glu Glu Ala Lys  Lys Lys Leu Ala Gln  Arg Leu Gln
    1385                1390                1395

Asp Ala  Glu Glu Ala Val Glu  Ala Val Asn Ala Lys  Cys Ser Ser
    1400                1405                1410
```

```
Leu Glu  Lys Thr Lys His Arg  Leu Gln Asn Glu Ile  Glu Asp Leu
    1415                 1420                 1425

Met Val  Asp Val Glu Arg Ser  Asn Ala Ala Ala Ala  Ala Leu Asp
    1430                 1435                 1440

Lys Lys  Gln Arg Asn Phe Asp  Lys Ile Leu Val Glu  Trp Lys Gln
    1445                 1450                 1455

Lys Tyr  Glu Glu Ser Gln Ser  Glu Leu Glu Ser Ser  Gln Lys Glu
    1460                 1465                 1470

Ala Arg  Ser Leu Ser Thr Glu  Leu Phe Lys Leu Lys  Asn Ala Tyr
    1475                 1480                 1485

Glu Glu  Ser Leu Glu His Leu  Glu Thr Phe Lys Arg  Glu Asn Lys
    1490                 1495                 1500

Asn Leu  Gln Glu Glu Ile Ser  Asp Leu Thr Glu Gln  Leu Gly Ser
    1505                 1510                 1515

Thr Gly  Lys Ser Ile His Glu  Leu Glu Lys Ile Arg  Lys Gln Leu
    1520                 1525                 1530

Glu Ala  Glu Lys Leu Glu Leu  Gln Ser Ala Leu Glu  Glu Ala Glu
    1535                 1540                 1545

Ala Ser  Leu Glu His Glu Glu  Gly Lys Ile Leu Arg  Ala Gln Leu
    1550                 1555                 1560

Glu Phe  Asn Gln Ile Lys Ala  Glu Ile Glu Arg Lys  Leu Ala Glu
    1565                 1570                 1575

Lys Asp  Glu Glu Met Glu Gln  Ala Lys Arg Asn His  Leu Arg Val
    1580                 1585                 1590

Val Asp  Ser Leu Gln Thr Ser  Leu Asp Ala Glu Thr  Arg Ser Arg
    1595                 1600                 1605

Asn Glu  Ala Leu Arg Val Lys  Lys Lys Met Glu Gly  Asp Leu Asn
    1610                 1615                 1620

Glu Met  Glu Ile Gln Leu Ser  His Ala Asn Arg Met  Ala Ala Glu
    1625                 1630                 1635

Ala Gln  Lys Gln Val Lys Ser  Leu Gln Ser Leu Leu  Lys Asp Thr
    1640                 1645                 1650

Gln Ile  Gln Leu Asp Asp Ala  Val Arg Ala Asn Asp  Asp Leu Lys
    1655                 1660                 1665

Glu Asn  Ile Ala Ile Val Glu  Arg Arg Asn Asn Leu  Leu Gln Ala
    1670                 1675                 1680

Glu Leu  Glu Glu Leu Arg Ala  Val Val Glu Gln Thr  Glu Arg Ser
    1685                 1690                 1695

Arg Lys  Leu Ala Glu Gln Glu  Leu Ile Glu Thr Ser  Glu Arg Val
    1700                 1705                 1710

Gln Leu  Leu His Ser Gln Asn  Thr Ser Leu Ile Asn  Gln Lys Lys
    1715                 1720                 1725

Lys Met  Asp Ala Asp Leu Ser  Gln Leu Gln Thr Glu  Val Glu Glu
    1730                 1735                 1740

Ala Val  Gln Glu Cys Arg Asn  Ala Glu Glu Lys Ala  Lys Lys Ala
    1745                 1750                 1755

Ile Thr  Asp Ala Ala Met Met  Ala Glu Glu Leu Lys  Lys Glu Gln
    1760                 1765                 1770

Asp Thr  Ser Ala His Leu Glu  Arg Met Lys Asn Asn  Met Glu Gln
    1775                 1780                 1785

Thr Ile  Lys Asp Leu Gln His  Arg Leu Asp Glu Ala  Glu Gln Ile
    1790                 1795                 1800
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Ala Leu  Lys Gly Gly Lys Lys  Gln Leu Gln Lys Leu  Glu Ala Arg
    1805                 1810                 1815

Val Arg  Glu Leu Glu Asn Glu  Leu Glu Ala Glu Gln  Lys Arg Asn
    1820                 1825                 1830

Ala Glu  Ser Val Lys Gly Met  Arg Lys Ser Glu Arg  Arg Ile Lys
    1835                 1840                 1845

Glu Leu  Thr Tyr Gln Thr Glu  Glu Asp Arg Lys Asn  Leu Leu Arg
    1850                 1855                 1860

Leu Gln  Asp Leu Val Asp Lys  Leu Gln Leu Lys Val  Lys Ala Tyr
    1865                 1870                 1875

Lys Arg  Gln Ala Glu Glu Ala  Glu Glu Gln Ala Asn  Thr Asn Leu
    1880                 1885                 1890

Ser Lys  Phe Arg Lys Val Gln  His Glu Leu Asp Glu  Ala Glu Glu
    1895                 1900                 1905

Arg Ala  Asp Ile Ala Glu Ser  Gln Val Asn Lys Leu  Arg Ala Lys
    1910                 1915                 1920

Ser Arg  Asp Ile Gly Ala Lys  Gly Leu Asn Glu Glu
    1925                 1930                 1935


<210> SEQ ID NO 163
<211> LENGTH: 5923
<212> TYPE: DNA
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 163

gctcagtcat ggcggatcga gagatggctg catttggggc cggagccccc ttcctgcgaa     60

aatctgagaa ggagcggctg gaggcgcaga ccaggccctt tgacctcaag aaagatgttt    120

ttgtgcctga tgacaaagaa gagtttgtca aggccaagat cgtgtctcga gagggtggca    180

aagtcaccgc tgagacagag aatggcaaga cggtgactgt gaaggaggac caggtgatgc    240

agcagaaccc tcccaagttc gacaagatcg aggacatggc catgctgacc ttcctgcacg    300

agccggctgt gctctacaat ctcaaggaga ggtacgcttc ctggatgatc tacacctact    360

caggcctctt ctgtgtcacc gtcaacccct ataagtggct gccagtgtac aatgcgcaag    420

tggtagctgc ctaccggggc aagaagagga gcgaggctcc accccacatc ttctccatct    480

ctgacaacgc ctatcagtac atgctgacag atcgggagaa ccagtccatc ctcatcaccg    540

gagaatccgg agctggtaag accgtcaaca ccaagagggt catccaatat tttgctgtta    600

ttgctgccat tggggaccgc agcaagaagg accagacccc aggcaagggc accttggaag    660

atcaaatcat ccaagccaac cccgctctgg aggcctttgg caatgccaag acagttcgga    720

atgataactc ctcccgattt gggaaattca ttcgaatcca ttttggggca acaggaaagt    780

tggcatctgc agatatagag acctaccttc tggaaaaatc cagagttatt ttccagctga    840

aagcagaaag agattatcac attttctacc aaatcctgtc taataaaaag cctgagcttc    900

tagacatgct gctgatcacc aacaacccct acgattatgc gttcttctcc cagggagaga    960

cgactgtggc ctcaatagat gactctgaag agcacatggc caccgatagc gcctttgatg   1020

tgctgggctt cactccagaa gagaagaact ccatttacaa gctgacaggc gccatcatgc   1080

actttggaaa catgaagttc aaacagaagc agagggagga gcaggcagag ccagacggca   1140

cggaagaagc tgacaagtca gcctacctca tgggactgaa ctcggctgac ctgctcaagg   1200

ggttgtgcca ccctcgagtc aaagtgggca acgagtatgt caccaaaggg cagaatgtcc   1260

agcaggtggc atatgccatc ggggcactgg ccaagtcagt gtacgagaag atgttcaact   1320
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ggatggtgac acgcatcaac gcaaccctgg agaccaagca gccacgccag tacttcatag   1380
gtgtcctgga catcgccggc tttgagatct ttgatttcaa cagctttgag cagctgtgca   1440
tcaacttcac caatgagaag ctgcagcagt tcttcaacca ccacatgttc gtgctggagc   1500
aggaggagta caagaaggaa ggcatcgagt ggacgtttat tgacttcggc atggacctgc   1560
aggcctgcat cgacctcatc gagaagccca tgggcatcat gtccatcctg gaggaggagt   1620
gcatgttccc caaggccacg gacatgacct tcaaggccaa gctgtacgac aaccacctgg   1680
gcaagtccaa caacttccag aagcctcgca atatcaaggg aaagcaggaa gcccacttct   1740
ctctgatcca ctatgctggc accgtggact acaatatcct gggctggcta cagaagaaca   1800
aggaccctct caatgagacg gtggtggggc tgtaccagaa gtcctccctc aagctcctaa   1860
gtaatctgtt tgccaactat gctggagctg atgcacctgt agacaagggc aaaggcaaag   1920
caaagaaagg ctcatccttt cagaccgtgt ccgcactgca cagggaaaat ctgaacaaac   1980
ttatgacaaa cctgcgctcc acgcaccctc actttgtacg ctgcatcatc cccaatgaga   2040
cgaagtctcc aggggtgatg gacaaccccc tggtcatgca ccagctgcga tgcaacggag   2100
tgctggaggg tatccgcatc tgtaggaagg gcttccccaa ccgcattctt tatggggact   2160
tccggcagag gtatcgaatc ctgaacccag cagccatccc tgagggccaa ttcattgata   2220
gccggaaagg ggctgagaag ctgctgggct ccctggacat tgaccacaac cagtacaagt   2280
ttggccacac caaggtgttc ttcaaggcgg ggctgctggg gctgctggag gagatgcgag   2340
atgagaggct gagccgcatc atcaccagaa tccaggccca gtcccgaggt gtactttcca   2400
gaatggagtt taagaagctg ctggagcgca gagactccct gctgattatc cagtggaaca   2460
tccgcgcctt catgggggtc aagaattggc cgtggatgaa gctctacttc aagatcaagc   2520
cgctgctgaa gagcgcagag acagagaagg agatggccaa catgaaggag gagttcgggc   2580
gagtcaaaga tgcactagag aagtctgagg ctcgccgcaa ggagctggag gagaagatgg   2640
tgtccctgct gcaggagaag aatgacctgc agctccaagt gcaggcggaa caagacaacc   2700
tggcagatgc cgaggagcgc tgcgaccagc tgatcaagaa caagatccag ctggaggcca   2760
aggtgaagga gatgaccgag aggctggagg acgaggagga gatgaacgcc gagctcacgg   2820
ccaagaagcg caaactggaa gacgagtgct cagagctcaa gagagatatc gatgacctgg   2880
agctgaccct ggccaaggtg gagaaggaaa agcacgcaac agagaacaag gtgaaaaacc   2940
tgacagagga gatggctggg ctggacgaga tcattgtcaa gctgaccaag gagaagaaag   3000
ctctacaaga ggcccaccag caagccctag atgaccttca ggctgaggag gacaaggtca   3060
acactctgac caaggccaag gtcaagctgg agcagcaagt ggatgatctg gagggatccc   3120
tggatcagga caagaaggtg cgcatggacc tggagcgagc aaagcggaag ctggagggtg   3180
acctgaagct gacccaggag agcatcatgg acctggagaa cgacaagcag cagttggatg   3240
agcgactcaa aaagaaggac tttgagttaa atgcactcaa cgccaggatt gaggatgagc   3300
aggccctggg cagccagctg cagaagaagc tcaaagagct tcaggcacgc atcgaggagc   3360
tggaggagga gctggaggct gagcgcacag cccgggccaa ggtggagaag ctgcgctcag   3420
acctgtcccg ggagctggag gagatcagtg agaggctaga ggaagccggt ggggccacat   3480
ctgtgcagat agagatgaac aagaagcgcg aggccgagtt ccagaagatg cggcgggacc   3540
tagaggaggc cacgctgcag catgaggcca cagctgcggc cctgcgcaag aaacacgcgg   3600
acagcgtggc cgagctgggc gagcagatag acaatctaca gcgggtgaag cagaagctgg   3660
agaaagagaa gagcgagttc aagctggagc tggatgacgt tacctccaac atggagcaga   3720
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tcatcaaggc caaggctaac ctggagaaga tgtgccggac cctggaggac cagatgaatg   3780
aacaccggag caaggctgag gagacacagc gttctgtcaa tgacctcacc cgccagcggg   3840
ccaagctgca gacagagaat ggggagctgt ccagacagct ggatgagaag gaggctctta   3900
tctctcagct gacccgaggc aagctcacgt atacccagca gctggaggac ctcaagaggc   3960
agctggagga ggaggtcaag gccaagaatg ccctggccca cgcactgcag tcagcccggc   4020
atgattgcga cctgctgcgg gaacagtacg aggaggaaac agaagccaag gctgagctgc   4080
agcgtgtcct gtccaaggcc aactcagagg tggcccagtg gaggaccaag tatgagacgg   4140
acgccataca gaggacggag gagctggagg aagccaagaa gaagctggct cagaggcttc   4200
aggatgctga ggaggcagtg gaggccgtca acgccaagtg ctcctcgctg gagaagacca   4260
agcacaggct gcagaacgag atcgaggacc tgatggtgga tgtggagcgc tccaatgcgg   4320
ccgccgcagc cctggacaag aagcagagga acttcgacaa gatcctggtt gagtggaagc   4380
agaagtatga ggagtcccag tcagagctgg agtcttccca gaaggaggcg cgctccctga   4440
gcacagagct cttcaagctg aagaatgcct atgaggagtc tctggagcac ctggagacct   4500
tcaagcggga gaacaagaac ctccaggagg agatctcaga cctgactgaa cagctgggct   4560
caactgggaa gagcatccac gagctggaga agatccgaaa gcaactggag gctgagaagc   4620
tggagctgca gtcagccctg gaagaggctg aggcctccct ggagcatgag gagggcaaga   4680
tcctccgagc ccagctggag ttcaaccaga tcaaggcaga gatcgaaagg aagctggcag   4740
agaaggacga ggagatggag caggccaagc gcaaccacct gcgggtggtg gactccctgc   4800
agacctccct ggatgccgag acgcgcagcc gcaacgaggc cctgcgggtg aagaagaaga   4860
tggagggcga cctcaacgag atggagatcc agctcagtca tgccaaccgc atggctgctg   4920
aggcccagaa acaagtgaag agcctccaga gtttgctgaa ggacactcaa atccagctgg   4980
atgacgcagt ccgtgccaat gacgacctga aggagaacat cgccatcgtg gagcggcgca   5040
acaacctgct gcaggcggag ctggaggagc tgcgggccgt ggtggagcag acggagcggt   5100
ctcggaagct ggcagagcag gagctgatcg agaccagcga gcgggtgcag ctgctgcact   5160
cccagaacac cagcctcatc aaccagaaga agaagatgga tgcagacctc tcccagctcc   5220
agacagaggt ggaggaggcg gtgcaggagt gtaggaacgc agaggagaag gccaagaagg   5280
ccatcacaga tgccgccatg atggccgagg agctgaagaa ggagcaggac accagcgccc   5340
acctggagcg catgaagaat aacatggagc agaccatcaa ggacctgcag caccggctgg   5400
acgaggcaga gcagatcgcc ctcaagggtg gcaagaagca gctgcagaag ctggaggccc   5460
gggtccggga gctggagaat gagctggagg ctgagcagaa gcgcaatgcg gagtcggtga   5520
agggcatgag gaagagcgag cggcgcatca aggagctcac ctaccagaca gaggaagaca   5580
ggaagaacct actgcgactg caggacctgg tggacaagct gcagttaaag gtgaaggcct   5640
acaagcgcca ggctgaggag gcggaggaac aggccaacac caacctgtcc aagttccgca   5700
aggtgcagca cgagctggat gaggcagagg agagggcgga cattgccgag tcccaggtca   5760
acaagctgcg ggccaagagc cgtgacattg gcgccaaggg cctgaatgaa gagtagatct   5820
tgtgctaccc aaccctaagg atgcctgtga agccctgaga cctggagcct ttgaaacagc   5880
accttaggca gaaacacaat aaagcaattt tccttcaagc caa                     5923
```

<210> SEQ ID NO 164
<211> LENGTH: 152
<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 164

Met Gly Ser Phe Ser Ile Thr Lys Gly Phe Phe Leu Phe Leu Ala Phe
1 5 10 15

Trp Leu Pro Gly His Ile Gly Ala Asn Pro Val Tyr Ser Ala Val Ser
20 25 30

Asn Thr Asp Leu Met Asp Phe Lys Asn Leu Leu Asp His Leu Glu Glu
35 40 45

Lys Met Pro Val Glu Asp Glu Val Met Pro Pro Gln Ala Leu Ser Glu
50 55 60

Gln Thr Asp Glu Ala Gly Ala Ala Leu Ser Ser Leu Ser Glu Val Pro
65 70 75 80

Pro Trp Thr Gly Glu Val Asn Pro Ser Gln Arg Asp Gly Gly Ala Leu
85 90 95

Gly Arg Gly Pro Trp Asp Pro Ser Asp Arg Ser Ala Leu Leu Lys Ser
100 105 110

Lys Leu Arg Ala Leu Leu Ala Gly Pro Arg Ser Leu Arg Arg Ser Ser
115 120 125

Cys Phe Gly Gly Arg Ile Asp Arg Ile Gly Ala Gln Ser Gly Leu Gly
130 135 140

Cys Asn Ser Phe Arg Tyr Arg Arg
145 150

<210> SEQ ID NO 165
<211> LENGTH: 831
<212> TYPE: DNA
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 165

cggacaaagg ctgagagaga aaccagagag tgagccgaga cagcaaacat cagatcgtgc 60

cccgacccac gccagcatgg gctccttctc catcaccaag ggcttcttcc tcttcctggc 120

cttttggctc ccaggccata ttggagcaaa tcccgtatac agtgcggtgt ccaacacaga 180

tctgatggat ttcaagaacc tgctagacca cctggaggag aagatgccgg tagaagatga 240

ggtcatgcct ccgcaggccc tgagcgagca gaccgatgaa gcgggggcgg cacttagctc 300

cctctctgag gtgcctccct ggactgggga agtcaacccg tctcagagag atggaggtgc 360

tctcgggcgc ggcccctggg acccctccga tagatctgcc ctcttgaaaa gcaaactgag 420

ggctctgctc gctggccctc ggagcctgcg aaggtcaagc tgcttcgggg gtaggattga 480

caggattgga gcccagagcg gactaggctg caacagcttc cggtaccgaa gataacagcc 540

aaatctgctc gagcagatcg caaaagatcc caagcccttg cggtgtgtca cacagcttgg 600

tcgcattgcc actgagaggt ggtgaatacc ctcctggagc tgcagcttcc tgtcttcatc 660

tatcacgatc gatgttaagt gtagatgagt ggtttagtga ggccttacct ctcccactct 720

gcatattaag gtagatcctc acccctttca gaaagcagtt ggaaaaaaat aaatccgaat 780

aaacttcagc accacggaca gacgctgagg cctgaaaaaa aaaaaaaaaa a 831

<210> SEQ ID NO 166
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 166

Met Asp Leu Gln Lys Val Leu Pro Gln Met Ile Leu Leu Leu Leu Phe

```
1               5                   10                  15

Leu Asn Leu Ser Pro Leu Gly Gly His Ser His Pro Leu Gly Ser Pro
            20                  25                  30

Ser Gln Ser Pro Glu Gln Ser Thr Met Gln Lys Leu Leu Glu Leu Ile
        35                  40                  45

Arg Glu Lys Ser Glu Glu Met Ala Gln Arg Gln Leu Ser Lys Asp Gln
    50                  55                  60

Gly Pro Thr Lys Glu Leu Leu Lys Arg Val Leu Arg Ser Gln Asp Ser
65                  70                  75                  80

Ala Phe Arg Ile Gln Glu Arg Leu Arg Asn Ser Lys Met Ala His Ser
                85                  90                  95

Ser Ser Cys Phe Gly Gln Lys Ile Asp Arg Ile Gly Ala Val Ser Arg
            100                 105                 110

Leu Gly Cys Asp Gly Leu Arg Leu Phe
        115                 120


<210> SEQ ID NO 167
<211> LENGTH: 628
<212> TYPE: DNA
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 167

gcgagacaag agagagcagg acaccatcgc agctgcctgg cccatcactt ctgcagcatg     60

gatctccaga aggtgctgcc ccagatgatt ctgctcctgc ttttccttaa tctgtcgccg    120

ctgggaggtc actcccatcc cctgggaagt cctagccagt ctccagaaca atccacgatg    180

cagaagctgc tggagctgat aagagaaaag tcagaggaaa tggctcagag acagctctca    240

aaggaccaag gccctacaaa agaacttcta aaaagagtcc ttaggtctca agacagcgcc    300

ttccggatcc aggagagact tcgaaattcc aagatggcac atagttcaag ctgctttggg    360

cagaagatag accggatcgg cgcagtcagt cgcttgggct gtgacgggct gaggttgttt    420

taggaagacc tcctggctgc agactccggc ttctgactct gcctgcggct cttctttccc    480

cagctctggg accacctctc aagtgatcct gtttatttat ttgtttattt atttattttt    540

atgttgctga ttttctacaa gactgtttct tatcttccag cacaaacttg ccacagtgta    600

ataaacatag cctatttctt gcttttgg                                       628


<210> SEQ ID NO 168
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 168

ggcuccagca uggggcuuug cuggcaccuc c                                    31


<210> SEQ ID NO 169
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 169

ccagggcuga gcagaucaag auguggcaaa g                                    31


<210> SEQ ID NO 170
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens
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<400> SEQUENCE: 170

cagggcugag cagaucaaga uguggcaaag c 31

<210> SEQ ID NO 171
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 171

gcuggcaccu ccagggcuga gcagaucaag a 31

<210> SEQ ID NO 172
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 172

caggcuccag caugggggcuu ugcuggcacc u 31

<210> SEQ ID NO 173
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 173

aggcuccagc augggggcuuu gcuggcaccu c 31

<210> SEQ ID NO 174
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 174

gcuccagcau ggggcuuugc uggcaccucc a 31

<210> SEQ ID NO 175
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 175

cuccagcaug gggcuuugcu ggcaccucca g 31

<210> SEQ ID NO 176
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 176

uccagcaugg ggcuuugcug gcaccuccag g 31

<210> SEQ ID NO 177
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 177

auucugcuuc cucccaagga gcuguuacac a 31

<210> SEQ ID NO 178
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 178

uccagggcug agcagaucaa gauguggcaa a 31

<210> SEQ ID NO 179
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 179

uguuacacag gcuccagcau ggggcuuugc u 31

<210> SEQ ID NO 180
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 180

cuccagggcu gagcagauca agauguggca a 31

<210> SEQ ID NO 181
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 181

cucccaagga gcuguuacac aggcuccagc a 31

<210> SEQ ID NO 182
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 182

cccaaggagc uguuacacag gcuccagcau g 31

<210> SEQ ID NO 183
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 183

caaggagcug uuacacaggc uccagcaugg g 31

<210> SEQ ID NO 184
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 184

aaggagcugu uacacaggcu ccagcauggg g 31

<210> SEQ ID NO 185
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 185

gcuguuacac aggcuccagc augggcuuu g 31

<210> SEQ ID NO 186
<211> LENGTH: 31
<212> TYPE: RNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 186

cuguuacaca ggcuccagca uggggcuuug c 31

<210> SEQ ID NO 187
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 187

guuacacagg cuccagcaug gggcuuugcu g 31

<210> SEQ ID NO 188
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 188

uuacacaggc uccagcaugg ggcuuugcug g 31

<210> SEQ ID NO 189
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 189

cuggcaccuc cagggcugag cagaucaaga u 31

<210> SEQ ID NO 190
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 190

uggcaccucc agggcugagc agaucaagau g 31

<210> SEQ ID NO 191
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 191

ggcaccucca gggcugagca gaucaagaug u 31

<210> SEQ ID NO 192
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 192

gcaccuccag ggcugagcag aucaagaugu g 31

<210> SEQ ID NO 193
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 193

caccuccagg gcugagcaga ucaagaugug g 31

<210> SEQ ID NO 194
<211> LENGTH: 31

<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 194

accuccaggg cugagcagau caagaugugg c 31

<210> SEQ ID NO 195
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 195

ccuccagggc ugagcagauc aagauguggc a 31

<210> SEQ ID NO 196
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 196

ccucccaagg agcuguuaca caggcuccag c 31

<210> SEQ ID NO 197
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 197

aggagcuguu acacaggcuc cagcaugggg c 31

<210> SEQ ID NO 198
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 198

uacacaggcu ccagcauggg gcuuugcugg c 31

<210> SEQ ID NO 199
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 199

gcuuugcugg caccuccagg gcugagcaga u 31

<210> SEQ ID NO 200
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 200

cuuugcuggc accuccaggg cugagcagau c 31

<210> SEQ ID NO 201
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 201

ugcuggcacc uccagggcug agcagaucaa g 31

<210> SEQ ID NO 202

<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 202

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<400> SEQUENCE: 236

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<400> SEQUENCE: 237

cuuuauucug cuuccuccca aggagcuguu a 31

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<400> SEQUENCE: 240

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<400> SEQUENCE: 241

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<400> SEQUENCE: 242

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<400> SEQUENCE: 243

ggcuucaagg aaaauugcuu uauucugcuu c 31

<210> SEQ ID NO 244
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<400> SEQUENCE: 244

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<400> SEQUENCE: 245

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aggaaaauug cuuuauucug cuuccuccca a 31

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caaggaaaau ugcuuuauuc ugcuuccucc c 31

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<400> SEQUENCE: 249

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<210> SEQ ID NO 250
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<400> SEQUENCE: 250

gaaaauugcu uuauucugcu uccucccaag g 31

<210> SEQ ID NO 251
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<400> SEQUENCE: 251

aaauugcuuu auucugcuuc cucccaagga g 31

<210> SEQ ID NO 252
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<400> SEQUENCE: 252

aauugcuuua uucugcuucc ucccaaggag c 31

<210> SEQ ID NO 253
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<400> SEQUENCE: 253

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<210> SEQ ID NO 254
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<400> SEQUENCE: 254

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<210> SEQ ID NO 255
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 255

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<210> SEQ ID NO 256
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 256

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<210> SEQ ID NO 257
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 257

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<210> SEQ ID NO 258
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 258

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<210> SEQ ID NO 259
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<400> SEQUENCE: 259

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<400> SEQUENCE: 260

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<210> SEQ ID NO 261
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<400> SEQUENCE: 261

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<210> SEQ ID NO 262
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 262

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<210> SEQ ID NO 263
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<400> SEQUENCE: 263

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<400> SEQUENCE: 264

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<210> SEQ ID NO 265
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 265

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<210> SEQ ID NO 266
<211> LENGTH: 31
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<400> SEQUENCE: 266

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<210> SEQ ID NO 267
<211> LENGTH: 31
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<400> SEQUENCE: 267

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<400> SEQUENCE: 268

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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 269

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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 270

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<400> SEQUENCE: 271

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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 272

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<210> SEQ ID NO 273
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<212> TYPE: RNA
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<400> SEQUENCE: 273

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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 274

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<210> SEQ ID NO 275
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<400> SEQUENCE: 275

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<400> SEQUENCE: 276

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<400> SEQUENCE: 277

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<400> SEQUENCE: 278

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<400> SEQUENCE: 279

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<400> SEQUENCE: 280

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<400> SEQUENCE: 281

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<400> SEQUENCE: 282

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<400> SEQUENCE: 283

cuccaggucu cagggcuuca caggcauccu u 31

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<400> SEQUENCE: 284

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<400> SEQUENCE: 285

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<400> SEQUENCE: 287

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<400> SEQUENCE: 288

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<400> SEQUENCE: 289

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<400> SEQUENCE: 290

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<210> SEQ ID NO 291
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<400> SEQUENCE: 291

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<400> SEQUENCE: 292

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<400> SEQUENCE: 294

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<400> SEQUENCE: 295

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<400> SEQUENCE: 296

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<210> SEQ ID NO 297
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<400> SEQUENCE: 297

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<210> SEQ ID NO 298
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<212> TYPE: RNA
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<400> SEQUENCE: 298

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<210> SEQ ID NO 299
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<400> SEQUENCE: 299

gcuugaagga aaauugcuuu auuguguuuc u 31

<210> SEQ ID NO 300
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 300

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<211> LENGTH: 31
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<400> SEQUENCE: 301

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<210> SEQ ID NO 302
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<400> SEQUENCE: 302

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<210> SEQ ID NO 303
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<400> SEQUENCE: 303

gaaggaaaau ugcuuuauug uguuucugcc u 31

<210> SEQ ID NO 304
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<400> SEQUENCE: 304

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<210> SEQ ID NO 305
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<400> SEQUENCE: 305

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<210> SEQ ID NO 306
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<400> SEQUENCE: 306

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<400> SEQUENCE: 307

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<400> SEQUENCE: 308

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<400> SEQUENCE: 309

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<400> SEQUENCE: 310

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<210> SEQ ID NO 311
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<400> SEQUENCE: 311

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<400> SEQUENCE: 312

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<210> SEQ ID NO 313
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<400> SEQUENCE: 313

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<210> SEQ ID NO 314
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 314

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<210> SEQ ID NO 315
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 315

aauugcuuua uuguguuucu gccuaaggug c 31

<210> SEQ ID NO 316
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<400> SEQUENCE: 316

aggucucagg gcuucacagg cauccuuagg g 31

<210> SEQ ID NO 317
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<400> SEQUENCE: 317

gcuucacagg cauccuuagg guuggguagc a 31

<210> SEQ ID NO 318
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<212> TYPE: RNA
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<400> SEQUENCE: 318

cuucacaggc auccuuaggg uuggguagca c 31

<210> SEQ ID NO 319
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 319

cacaggcauc cuuaggguug gguagcacaa g 31

<210> SEQ ID NO 320
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 320

acaggcaucc uuaggguugg guagcacaag a 31

<210> SEQ ID NO 321
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 321

caggcauccu uaggguuggg uagcacaaga u 31

<210> SEQ ID NO 322
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 322

uucacaggca uccuuagggu uggguagcac a 31

<210> SEQ ID NO 323
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 323

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<400> SEQUENCE: 324

ucagggcuuc acaggcaucc uuaggguugg g 31

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<400> SEQUENCE: 325

cagggcuuca caggcauccu uaggguuggg u 31

<210> SEQ ID NO 326
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<400> SEQUENCE: 326

gggcuucaca ggcauccuua gggugggua g 31

<210> SEQ ID NO 327
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<400> SEQUENCE: 327

agggcuucac aggcauccuu aggguugggu a 31

<210> SEQ ID NO 328
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 328

ggagaggcga ggaagucacc aucaaaccac u 31

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agaugugaga aguguugaca ggaagcugca g 31

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<400> SEQUENCE: 330

uaagauguga gaaguguuga caggaagcug c 31

<210> SEQ ID NO 331
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 331

aagaugugag aaguguugac aggaagcugc a 31

<210> SEQ ID NO 332
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 332

auucacuuuc aaaccacuuu caguaacagg u 31

<210> SEQ ID NO 333
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<400> SEQUENCE: 333

gagaggcgag gaagucacca ucaaaccacu u 31

<210> SEQ ID NO 334
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<400> SEQUENCE: 334

gaugugagaa guguugacag gaagcugcag c 31

<210> SEQ ID NO 335
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 335

augugagaag uguugacagg aagcugcagc u 31

<210> SEQ ID NO 336
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<400> SEQUENCE: 336

ugugagaagu guugacagga agcugcagcu u 31

<210> SEQ ID NO 337
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<400> SEQUENCE: 337

gugagaagug uugacaggaa gcugcagcuu a 31

<210> SEQ ID NO 338
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<213> ORGANISM: Homo sapiens

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ugagaagugu ugacaggaag cugcagcuua g 31

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<400> SEQUENCE: 339

gagaaguguu gacaggaagc ugcagcuuag a 31

<210> SEQ ID NO 340
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 340

gaaguguuga caggaagcug cagcuuagau g 31

<210> SEQ ID NO 341
<211> LENGTH: 31
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<400> SEQUENCE: 341

aaguguugac aggaagcugc agcuuagaug g 31

<210> SEQ ID NO 342
<211> LENGTH: 31
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<400> SEQUENCE: 342

agaaguguug acaggaagcu gcagcuuaga u 31

<210> SEQ ID NO 343
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 343

gaucacaacu ccauggcaac aagaugacac a 31

<210> SEQ ID NO 344
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 344

aucacaacuc cauggcaaca agaugacaca a 31

<210> SEQ ID NO 345
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 345

ucacaacucc auggcaacaa gaugacacaa a 31

<210> SEQ ID NO 346
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 346

uucacuuuca aaccacuuuc aguaacaggu g 31

<210> SEQ ID NO 347
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 347

ucacuuucaa accacuuuca guaacaggug a 31

<210> SEQ ID NO 348
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 348

agaggcgagg aagucaccau caaaccacuu u 31

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<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 349

ggaugaucac aacuccaugg caacaagaug a 31

<210> SEQ ID NO 350
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 350

gaugaucaca acuccauggc aacaagauga c 31

<210> SEQ ID NO 351
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 351

ugaucacaac uccauggcaa caagaugaca c 31

<210> SEQ ID NO 352
<211> LENGTH: 31

<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 352

cacuuucaaa ccacuuucag uaacagguga g 31

<210> SEQ ID NO 353
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 353

augaucacaa cuccauggca acaagaugac a 31

<210> SEQ ID NO 354
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 354

aaccacuuuc aguaacaggu gagguucuac c 31

<210> SEQ ID NO 355
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 355

accacuuuca guaacaggug agguucuacc u 31

<210> SEQ ID NO 356
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 356

ccacuuucag uaacagguga gguucuaccu u 31

<210> SEQ ID NO 357
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 357

acuuucaaac cacuuucagu aacaggugag g 31

<210> SEQ ID NO 358
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 358

cuuucaaacc acuuucagua acaggugagg u 31

<210> SEQ ID NO 359
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 359

uucaaaccac uuucaguaac aggugagguu c 31

<210> SEQ ID NO 360

<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 360

ucaaaccacu uucaguaaca ggugagguuc u 31

<210> SEQ ID NO 361
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 361

caaaccacuu ucaguaacag gugagguucu a 31

<210> SEQ ID NO 362
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 362

aaaccacuuu caguaacagg ugagguucua c 31

<210> SEQ ID NO 363
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 363

cacuuucagu aacaggugag guucuaccuu a 31

<210> SEQ ID NO 364
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 364

uuucaaacca cuuucaguaa caggugaggu u 31

<210> SEQ ID NO 365
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 365

uuuauucacu uucaaaccac uuucaguaac a 31

<210> SEQ ID NO 366
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 366

gggagaggcg aggaagucac caucaaacca c 31

<210> SEQ ID NO 367
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 367

ggcaacaaga ugacacaaau gcagcagaga c 31

<210> SEQ ID NO 368
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 368

gcaacaagau gacacaaaug cagcagagac c 31

<210> SEQ ID NO 369
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 369

guuagcauaa gaugugagaa guguugacag g 31

<210> SEQ ID NO 370
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 370

agcauaagau gugagaagug uugacaggaa g 31

<210> SEQ ID NO 371
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 371

auaagaugug agaaguguug acaggaagcu g 31

<210> SEQ ID NO 372
<211> LENGTH: 31
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<400> SEQUENCE: 372

ucaccaucaa accacuuuau cuacaguuag c 31

<210> SEQ ID NO 373
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 373

caccaucaaa ccacuuuauc uacaguuagc a 31

<210> SEQ ID NO 374
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 374

aguuagcaua agaugugaga aguguugaca g 31

<210> SEQ ID NO 375
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 375

uuagcauaag augugagaag uguugacagg a 31

<210> SEQ ID NO 376
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 376

uagcauaaga ugugagaagu guugacagga a 31

<210> SEQ ID NO 377
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 377

aagucaccau caaaccacuu uaucuacagu u 31

<210> SEQ ID NO 378
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 378

agucaccauc aaaccacuuu aucuacaguu a 31

<210> SEQ ID NO 379
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 379

accaucaaac cacuuuaucu acaguuagca u 31

<210> SEQ ID NO 380
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 380

ccaucaaacc acuuuaucua caguuagcau a 31

<210> SEQ ID NO 381
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 381

uacaguuagc auaagaugug agaaguguug a 31

<210> SEQ ID NO 382
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 382

cugaaguuua uucacuuuca aaccacuuuc a 31

<210> SEQ ID NO 383
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 383

guuuauucac uuucaaacca cuuucaguaa c 31

<210> SEQ ID NO 384
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 384

uuauucacuu ucaaaccacu uucaguaaca g 31

<210> SEQ ID NO 385
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 385

aaguuuauuc acuuucaaac cacuuucagu a 31

<210> SEQ ID NO 386
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 386

aguuuauuca cuuucaaacc acuuucagua a 31

<210> SEQ ID NO 387
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 387

gguggagag gcgaggaagu caccaucaaa c 31

<210> SEQ ID NO 388
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 388

gugggagagg cgaggaaguc accaucaaac c 31

<210> SEQ ID NO 389
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 389

ugggagaggc gaggaaguca ccaucaaacc a 31

<210> SEQ ID NO 390
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 390

ccauggcaac aagaugacac aaaugcagca g 31

<210> SEQ ID NO 391
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 391

gcauaagaug ugagaagugu ugacaggaag c 31

<210> SEQ ID NO 392
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 392

cauggcaaca agaugacaca aaugcagcag a 31

<210> SEQ ID NO 393
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 393

auggcaacaa gaugacacaa augcagcaga g 31

<210> SEQ ID NO 394
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 394

uggcaacaag augacacaaa ugcagcagag a 31

<210> SEQ ID NO 395
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 395

cauaagaugu gagaaguguu gacaggaagc u 31

<210> SEQ ID NO 396
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 396

aggaagucac caucaaacca cuuuaucuac a 31

<210> SEQ ID NO 397
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 397

gaagucacca ucaaaccacu uuaucuacag u 31

<210> SEQ ID NO 398
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 398

gucaccauca aaccacuuua ucuacaguua g 31

<210> SEQ ID NO 399
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 399

cuacaguuag cauaagaugu gagaaguguu g 31

<210> SEQ ID NO 400
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<400> SEQUENCE: 400

acaguuagca uaagauguga gaaguguuga c 31

<210> SEQ ID NO 401
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 401

caguuagcau aagaugugag aaguguugac a 31

<210> SEQ ID NO 402
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 402

gcugaaguuu auucacuuuc aaaccacuuu c 31

<210> SEQ ID NO 403
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 403

uauucacuuu caaaccacuu ucaguaacag g 31

<210> SEQ ID NO 404
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 404

uaucuacagu uagcauaaga ugugagaagu g 31

<210> SEQ ID NO 405
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 405

aucuacaguu agcauaagau gugagaagug u 31

<210> SEQ ID NO 406
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 406

ucuacaguua gcauaagaug ugagaagugu u 31

<210> SEQ ID NO 407
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 407

ugcugaaguu uauucacuuu caaaccacuu u 31

<210> SEQ ID NO 408
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 408

ugaaguuuau ucacuuucaa accacuuuca g 31

<210> SEQ ID NO 409
<211> LENGTH: 31
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<400> SEQUENCE: 409

gaaguuuauu cacuuucaaa ccacuuucag u 31

<210> SEQ ID NO 410
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 410

aguguugaca ggaagcugca gcuuagaugg g 31

<210> SEQ ID NO 411
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 411

guguugacag gaagcugcag cuuagauggg a 31

<210> SEQ ID NO 412
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 412

guugacagga agcugcagcu uagaugggau g 31

<210> SEQ ID NO 413
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 413

uguugacagg aagcugcagc uuagauggga u 31

<210> SEQ ID NO 414
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 414

uugacaggaa gcugcagcuu agaugggaug a 31

<210> SEQ ID NO 415
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 415

ugacaggaag cugcagcuua gaugggauga u 31

<210> SEQ ID NO 416
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 416

cuccauggca acaagaugac acaaaugcag c 31

<210> SEQ ID NO 417
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 417

caacuccaug gcaacaagau gacacaaaug c 31

<210> SEQ ID NO 418
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 418

acuccauggc aacaagauga cacaaaugca g 31

<210> SEQ ID NO 419
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 419

uccauggcaa caagaugaca caaaugcagc a 31

<210> SEQ ID NO 420
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 420

cgaggaaguc accaucaaac cacuuuaucu a 31

<210> SEQ ID NO 421
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 421

gaggaaguca ccaucaaacc acuuuaucua c 31

<210> SEQ ID NO 422
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 422

ggaagucacc aucaaaccac uuuaucuaca g 31

<210> SEQ ID NO 423
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 423

cacaacucca uggcaacaag augacacaaa u 31

<210> SEQ ID NO 424
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 424

acaacuccau ggcaacaaga ugacacaaau g 31

<210> SEQ ID NO 425
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 425

aacuccaugg caacaagaug acacaaaugc a 31

<210> SEQ ID NO 426
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 426

gugcugaagu uuauucacuu ucaaaccacu u 31

<210> SEQ ID NO 427
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 427

ccaggggaca ggagccucuu gcagucuguc c 31

<210> SEQ ID NO 428
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 428

ggacaggagc cucuugcagu cugucccuag g 31

<210> SEQ ID NO 429
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 429

gacaggagcc ucuugcaguc ugucccuagg c 31

<210> SEQ ID NO 430
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 430

acaggagccu cuugcagucu gucccuaggc c 31

<210> SEQ ID NO 431
<211> LENGTH: 31

<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 431

gacaggaagc ugcagcuuag augggaugau c 31

<210> SEQ ID NO 432
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 432

gaggcgagga agucaccauc aaaccacuuu a 31

<210> SEQ ID NO 433
<211> LENGTH: 31
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<400> SEQUENCE: 433

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<400> SEQUENCE: 434

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<400> SEQUENCE: 435

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gaugggauga ucacaacucc auggcaacaa g 31

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gggaugauca caacuccaug gcaacaagau g 31

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uggugcugaa guuuauucac uuucaaacca c 31

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ggugcugaag uuuauucacu uucaaaccac u 31

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aggcgaggaa gucaccauca aaccacuuua u 31

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aagcugcagc uuagauggga ugaucacaac u 31

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<400> SEQUENCE: 461

ugggaugauc acaacuccau ggcaacaaga u 31

<210> SEQ ID NO 462
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uguccauggu gcugaaguuu auucacuuuc a 31

<210> SEQ ID NO 463
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<400> SEQUENCE: 463

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<400> SEQUENCE: 465

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<210> SEQ ID NO 466
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 466

gcugcagcuu agaugggaug aucacaacuc c 31

<210> SEQ ID NO 467
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<400> SEQUENCE: 467

agcugcagcu uagaugggau gaucacaacu c 31

<210> SEQ ID NO 468
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 468

cugcagcuua gaugggauga ucacaacucc a 31

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<400> SEQUENCE: 469

gcagcuuaga ugggaugauc acaacuccau g 31

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<400> SEQUENCE: 470

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<210> SEQ ID NO 471
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<400> SEQUENCE: 471

agcuuagaug ggaugaucac aacuccaugg c 31

<210> SEQ ID NO 472
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<400> SEQUENCE: 472

gcuuagaugg gaugaucaca acuccauggc a 31

<210> SEQ ID NO 473
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 473

ugcagcuuag augggaugau cacaacucca u 31

<210> SEQ ID NO 474
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<400> SEQUENCE: 474

cuuagauggg augaucacaa cuccauggca a 31

<210> SEQ ID NO 475
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 475

uuagauggga ugaucacaac uccauggcaa c 31

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<400> SEQUENCE: 476

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<210> SEQ ID NO 477
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 477

ugcagcagag accccagggg acaggagccu c 31

<210> SEQ ID NO 478
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<400> SEQUENCE: 478

gcagcagaga ccccagggga caggagccuc u 31

<210> SEQ ID NO 479
<211> LENGTH: 31
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<400> SEQUENCE: 479

augcagcaga gaccccaggg gacaggagcc u 31

<210> SEQ ID NO 480
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<400> SEQUENCE: 480

caagaugaca caaaugcagc agagacccca g 31

<210> SEQ ID NO 481
<211> LENGTH: 31
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<400> SEQUENCE: 481

aagaugacac aaaugcagca gagaccccag g 31

<210> SEQ ID NO 482
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<400> SEQUENCE: 482

caacaagaug acacaaaugc agcagagacc c 31

<210> SEQ ID NO 483
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<400> SEQUENCE: 483

aacaagauga cacaaaugca gcagagaccc c 31

<210> SEQ ID NO 484
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<400> SEQUENCE: 484

acaagaugac acaaaugcag cagagacccc a 31

<210> SEQ ID NO 485
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<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 485

caucaaacca cuuuaucuac aguuagcaua a 31

<210> SEQ ID NO 486
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<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 486

gcagagaccc caggggacag gagccucuug c 31

<210> SEQ ID NO 487
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 487

gcaugggugg ggagaggcga ggaagucacc a 31

<210> SEQ ID NO 488
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<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 488

cagcagagac cccaggggac aggagccucu u 31

<210> SEQ ID NO 489
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 489

agcagagacc ccaggggaca ggagccucuu g 31

<210> SEQ ID NO 490
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 490

cagagacccc aggggacagg agccucuugc a 31

<210> SEQ ID NO 491
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 491

agagacccca ggggacagga gccucuugca g 31

<210> SEQ ID NO 492
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 492

gggguggggag aggcgaggaa gucaccauca a 31

<210> SEQ ID NO 493
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 493

aaugcauggg gugggagagg cgaggaaguc a 31

<210> SEQ ID NO 494
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<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 494

ggguggggaga ggcgaggaag ucaccaucaa a 31

<210> SEQ ID NO 495
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<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 495

aucaaaccac uuuaucuaca guuagcauaa g 31

<210> SEQ ID NO 496
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<400> SEQUENCE: 496

ucaaaccacu uuaucuacag uuagcauaag a 31

<210> SEQ ID NO 497
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<400> SEQUENCE: 497

caaaccacuu uaucuacagu uagcauaaga u 31

<210> SEQ ID NO 498
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<400> SEQUENCE: 498

uuuaucuaca guuagcauaa gaugugagaa g 31

<210> SEQ ID NO 499
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<400> SEQUENCE: 499

uuaucuacag uuagcauaag augugagaag u 31

<210> SEQ ID NO 500
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<400> SEQUENCE: 500

ugcauggggu gggagaggcg aggaagucac c 31

<210> SEQ ID NO 501
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 501

gagaccccag gggacaggag ccucuugcag u 31

<210> SEQ ID NO 502
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 502

agaccccagg ggacaggagc cucuugcagu c 31

<210> SEQ ID NO 503
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 503

caggagccuc uugcagucug ucccuaggcc c 31

<210> SEQ ID NO 504
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 504

ggagccucuu gcagucuguc ccuaggccca g 31

<210> SEQ ID NO 505
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<400> SEQUENCE: 505

gagccucuug cagucugucc cuaggcccag c 31

<210> SEQ ID NO 506
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 506

agccucuugc agucuguccc uaggcccagc c 31

<210> SEQ ID NO 507
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<400> SEQUENCE: 507

augcaugggg ugggagaggc gaggaaguca c 31

<210> SEQ ID NO 508
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<400> SEQUENCE: 508

caugggugg gagaggcgag gaagucacca u 31

<210> SEQ ID NO 509
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<400> SEQUENCE: 509

augggguggg agaggcgagg aagucaccau c 31

<210> SEQ ID NO 510
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<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 510

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 511

aguaacaggu gagguucuac cuuaaaauuu a 31

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<400> SEQUENCE: 512

guaacaggug agguucuacc uuaaaauuua a 31

<210> SEQ ID NO 513
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 513

aaaccacuuu aucuacaguu agcauaagau g 31

<210> SEQ ID NO 514
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<400> SEQUENCE: 514

aaccacuuua ucuacaguua gcauaagaug u 31

<210> SEQ ID NO 515
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<400> SEQUENCE: 515

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<210> SEQ ID NO 516
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<400> SEQUENCE: 516

cuuuaucuac aguuagcaua agaugugaga a 31

<210> SEQ ID NO 517
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<400> SEQUENCE: 517

gaccccaggg gacaggagcc ucuugcaguc u 31

<210> SEQ ID NO 518

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<400> SEQUENCE: 518

accccagggg acaggagccu cuugcagucu g 31

<210> SEQ ID NO 519
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<400> SEQUENCE: 519

ccccagggga caggagccuc uugcagucug u 31

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<400> SEQUENCE: 520

cccaggggac aggagccucu ugcagucugu c 31

<210> SEQ ID NO 521
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<400> SEQUENCE: 521

caggggacag gagccucuug cagucugucc c 31

<210> SEQ ID NO 522
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<400> SEQUENCE: 522

aggggacagg agccucuugc agucuguccc u 31

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<400> SEQUENCE: 523

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<400> SEQUENCE: 524

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<210> SEQ ID NO 525
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<400> SEQUENCE: 525

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<210> SEQ ID NO 526
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 526

ucaguaacag gugagguucu accuuaaaau u 31

<210> SEQ ID NO 527
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 527

caguaacagg ugagguucua ccuuaaaauu u 31

<210> SEQ ID NO 528
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<400> SEQUENCE: 528

accacuuuau cuacaguuag cauaagaugu g 31

<210> SEQ ID NO 529
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 529

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<210> SEQ ID NO 530
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 530

cacuuuaucu acaguuagca uaagauguga g 31

<210> SEQ ID NO 531
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 531

ggcccagccc ugcuuguccu cccuggcugu u 31

<210> SEQ ID NO 532
<211> LENGTH: 31
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<400> SEQUENCE: 532

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<210> SEQ ID NO 533
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 533

caaaugcagc agagacccca ggggacagga g 31

<210> SEQ ID NO 534
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<400> SEQUENCE: 534

aaaugcagca gagaccccag gggacaggag c 31

<210> SEQ ID NO 535
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 535

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<210> SEQ ID NO 536
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<400> SEQUENCE: 536

acacaaaugc agcagagacc ccaggggaca g 31

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<400> SEQUENCE: 537

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<400> SEQUENCE: 538

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<400> SEQUENCE: 542

aggcccagcc cugcuugucc ucccuggcug u 31

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 543

gucuguccccu aggcccagcc cugcuugucc u 31

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<400> SEQUENCE: 544

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<400> SEQUENCE: 545

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<400> SEQUENCE: 546

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<210> SEQ ID NO 547
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 547

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cagcccugcu uguccucccu ggcuguuauc u 31

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uuuaaugcau gggugggag aggcgaggaa g 31

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uuaaugcaug gggugggaga ggcgaggaag u 31

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agaugacaca aaugcagcag agaccccagg g 31

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gccucuugca gucuguccu aggcccagcc c 31

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ccucuugcag ucuguccua ggcccagccc u 31

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cccagcccug cuuguccucc cuggcuguua u 31

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 581

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<210> SEQ ID NO 582
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<400> SEQUENCE: 582

gagguucuac cuuaaaauuu aaugcauggg g 31

<210> SEQ ID NO 583
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<400> SEQUENCE: 583

gguucuaccu uaaaauuuaa ugcauggggu g 31

<210> SEQ ID NO 584
<211> LENGTH: 31
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<400> SEQUENCE: 584

guucuaccuu aaaauuuaau gcauggggug g 31

<210> SEQ ID NO 585
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 585

ugagguucua ccuuaaaauu uaaugcaugg g 31

<210> SEQ ID NO 586
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 586

agguucuacc uuaaaauuua augcaugggg u 31

<210> SEQ ID NO 587
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 587

uuaaaauuua augcaugggg ugggagaggc g 31

<210> SEQ ID NO 588
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 588

ccuuaaaauu uaaugcaugg gguggggagag g 31

<210> SEQ ID NO 589
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<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 589

cuuaaaauuu aaugcauggg gugggagagg c 31

<210> SEQ ID NO 590
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<400> SEQUENCE: 590

accuuaaaau uuaaugcaug gggugggaga g 31

<210> SEQ ID NO 591
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<400> SEQUENCE: 591

uaccuuaaaa uuuaaugcau gggugggag a 31

<210> SEQ ID NO 592
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 592

cuaccuuaaa auuuaaugca ugggguggga g 31

<210> SEQ ID NO 593
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<400> SEQUENCE: 593

uucuaccuua aaauuuaaug caugggugg g 31

<210> SEQ ID NO 594
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 594

ucuaccuuaa aauuuaaugc augggugg a 31

<210> SEQ ID NO 595
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 595

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<210> SEQ ID NO 596
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<400> SEQUENCE: 596

gccucagcgu cuguccgugg ugcugaaguu u 31

<210> SEQ ID NO 597

<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 597

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<210> SEQ ID NO 598
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 598

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<210> SEQ ID NO 599
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 599

caggccucag cgucuguccg uggugcugaa g 31

<210> SEQ ID NO 600
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 600

aggccucagc gucuguccgu ggugcugaag u 31

<210> SEQ ID NO 601
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 601

ggcaaugcga ccaagcugug ugacacaccg c 31

<210> SEQ ID NO 602
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 602

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<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 603

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<210> SEQ ID NO 604
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 604

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<210> SEQ ID NO 605
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 605

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<210> SEQ ID NO 606
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 606

gauagaugaa gacaggaagc ugcagcucca g 31

<210> SEQ ID NO 607
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 607

auagaugaag acaggaagcu gcagcuccag g 31

<210> SEQ ID NO 608
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 608

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<210> SEQ ID NO 609
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 609

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<210> SEQ ID NO 610
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 610

aucgaucgug auagaugaag acaggaagcu g 31

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<400> SEQUENCE: 611

aacaucgauc gugauagaug aagacaggaa g 31

<210> SEQ ID NO 612
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 612

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<400> SEQUENCE: 613

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<210> SEQ ID NO 614
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<400> SEQUENCE: 614

caccaccucu caguggcaau gcgaccaagc u 31

<210> SEQ ID NO 615
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 615

accaccucuc aguggcaaug cgaccaagcu g 31

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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 616

guggcaaugc gaccaagcug ugugacacac c 31

<210> SEQ ID NO 617
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 617

uggcaaugcg accaagcugu gugacacacc g 31

<210> SEQ ID NO 618
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 618

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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 619

aguggcaaug cgaccaagcu gugugacaca c 31

<210> SEQ ID NO 620
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 620

cgugauagau gaagacagga agcugcagcu c 31

<210> SEQ ID NO 621
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 621

gugauagaug aagacaggaa gcugcagcuc c 31

<210> SEQ ID NO 622
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 622

auucaccacc ucucaguggc aaugcgacca a 31

<210> SEQ ID NO 623
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 623

ucgaucguga uagaugaaga caggaagcug c 31

<210> SEQ ID NO 624
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 624

cgaucgugau agaugaagac aggaagcugc a 31

<210> SEQ ID NO 625
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 625

aucgugauag augaagacag gaagcugcag c 31

<210> SEQ ID NO 626
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<400> SEQUENCE: 626

ucgugauaga ugaagacagg aagcugcagc u 31

<210> SEQ ID NO 627
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 627

ugauagauga agacaggaag cugcagcucc a 31

<210> SEQ ID NO 628
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 628

acaucgaucg ugauagauga agacaggaag c 31

<210> SEQ ID NO 629
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<400> SEQUENCE: 629

caucgaucgu gauagaugaa gacaggaagc u 31

<210> SEQ ID NO 630
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<400> SEQUENCE: 630

ccaccucuca guggcaaugc gaccaagcug u 31

<210> SEQ ID NO 631
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 631

caccucucag uggcaaugcg accaagcugu g 31

<210> SEQ ID NO 632
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<400> SEQUENCE: 632

ccucucagug gcaaugcgac caagcugugu g 31

<210> SEQ ID NO 633
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<400> SEQUENCE: 633

uucaccaccu cucaguggca augcgaccaa g 31

<210> SEQ ID NO 634
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 634

cucaguggca augcgaccaa gcugugugac a 31

<210> SEQ ID NO 635
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<400> SEQUENCE: 635

ucaguggcaa ugcgaccaag cugugugaca c 31

<210> SEQ ID NO 636
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<400> SEQUENCE: 636

accucucagu ggcaaugcga ccaagcugug u 31

<210> SEQ ID NO 637
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 637

cucucagugg caaugcgacc aagcugugug a 31

<210> SEQ ID NO 638
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 638

ucucaguggc aaugcgacca agcuguguga c 31

<210> SEQ ID NO 639
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<400> SEQUENCE: 639

uaaggccuca cuaaaccacu caucuacacu u 31

<210> SEQ ID NO 640
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 640

aaggccucac uaaaccacuc aucuacacuu a 31

<210> SEQ ID NO 641
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 641

aaaccacuca ucuacacuua acaucgaucg u 31

<210> SEQ ID NO 642
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 642

gcgaccaagc ugugugacac accgcaaggg c 31

<210> SEQ ID NO 643
<211> LENGTH: 31
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<400> SEQUENCE: 643

augaagacag gaagcugcag cuccaggagg g 31

<210> SEQ ID NO 644
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 644

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<210> SEQ ID NO 645
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 645

gcgucugucc guggugcuga aguuuauucg g 31

<210> SEQ ID NO 646
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 646

guaaggccuc acuaaaccac ucaucuacac u 31

<210> SEQ ID NO 647
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 647

aaccacucau cuacacuuaa caucgaucgu g 31

<210> SEQ ID NO 648
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 648

accacucauc uacacuuaac aucgaucgug a 31

<210> SEQ ID NO 649
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 649

ccacucaucu acacuuaaca ucgaucguga u 31

<210> SEQ ID NO 650
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 650

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<210> SEQ ID NO 651
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 651

ugcgaccaag cugugugaca caccgcaagg g 31

<210> SEQ ID NO 652
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 652

cgaccaagcu gugugacaca ccgcaagggc u 31

<210> SEQ ID NO 653
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 653

ugaagacagg aagcugcagc uccaggaggg u 31

<210> SEQ ID NO 654
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 654

ccucagcguc uguccguggu gcugaaguuu a 31

<210> SEQ ID NO 655
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 655

aagacaggaa gcugcagcuc caggagggua u 31

<210> SEQ ID NO 656
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 656

cucagcgucu guccguggug cugaaguuua u 31

<210> SEQ ID NO 657
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<400> SEQUENCE: 657

cagcgucugu ccguggugcu gaaguuuauu c 31

<210> SEQ ID NO 658
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 658

agcgucuguc cguggugcug aaguuuauuc g 31

<210> SEQ ID NO 659
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 659

cgucuguccg uggugcugaa guuuauucgg a 31

<210> SEQ ID NO 660
<211> LENGTH: 31
<212> TYPE: RNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 660

ucagcgucug uccguggugc ugaaguuuau u 31

<210> SEQ ID NO 661
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 661

gucuguccgu ggugcugaag uuuauucgga u 31

<210> SEQ ID NO 662
<211> LENGTH: 31
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<400> SEQUENCE: 662

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<210> SEQ ID NO 759
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<400> SEQUENCE: 762

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<210> SEQ ID NO 763
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<400> SEQUENCE: 763

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<210> SEQ ID NO 766
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<400> SEQUENCE: 766

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<210> SEQ ID NO 769
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<400> SEQUENCE: 772

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<210> SEQ ID NO 773
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<400> SEQUENCE: 773

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<210> SEQ ID NO 774
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<213> ORGANISM: Mus musculus

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cuuucugaaa ggggugagga ucuaccuuaa u 31

<210> SEQ ID NO 776
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<400> SEQUENCE: 776

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<400> SEQUENCE: 823

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<400> SEQUENCE: 824

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gugacacacc gcaagggcuu gggaucuuuu g 31

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<213> ORGANISM: Mus musculus

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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 831

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<210> SEQ ID NO 832
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 832

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<210> SEQ ID NO 833
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<213> ORGANISM: Mus musculus

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<210> SEQ ID NO 834

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<210> SEQ ID NO 835
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<210> SEQ ID NO 836
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<213> ORGANISM: Mus musculus

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<210> SEQ ID NO 837
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<210> SEQ ID NO 838
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<400> SEQUENCE: 838

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<210> SEQ ID NO 839
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 839

guuuauucgg auuuauuuuu uuccaacugc u 31

<210> SEQ ID NO 840
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<400> SEQUENCE: 840

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<210> SEQ ID NO 841
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<400> SEQUENCE: 842

gaaguuuauu cggauuuauu uuuuuccaac u 31

<210> SEQ ID NO 843
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 843

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<210> SEQ ID NO 844
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<210> SEQ ID NO 845
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 845

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<210> SEQ ID NO 846
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 846

uggaaucaga agcaggugug cugccaggag a 31

<210> SEQ ID NO 847
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 847

gaaucagaag caggugucug cagccaggac u 31

<210> SEQ ID NO 848
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<400> SEQUENCE: 848

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 854

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<210> SEQ ID NO 856
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 856

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<210> SEQ ID NO 857
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<400> SEQUENCE: 857

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<400> SEQUENCE: 858

aaaaaugagu cacuucaaag gcggccacag g 31

<210> SEQ ID NO 859
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<400> SEQUENCE: 859

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<210> SEQ ID NO 860
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<400> SEQUENCE: 860

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<210> SEQ ID NO 861
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<400> SEQUENCE: 861

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<210> SEQ ID NO 862
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<210> SEQ ID NO 863
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<210> SEQ ID NO 864
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<210> SEQ ID NO 866
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<400> SEQUENCE: 866

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<210> SEQ ID NO 867
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<400> SEQUENCE: 867

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<210> SEQ ID NO 868
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 868

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<210> SEQ ID NO 869
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 869

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<210> SEQ ID NO 870
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<400> SEQUENCE: 870

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<210> SEQ ID NO 871
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 871

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<210> SEQ ID NO 872
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<400> SEQUENCE: 872

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<210> SEQ ID NO 873
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<400> SEQUENCE: 873

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<210> SEQ ID NO 875
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 875

aaauuuugug cucaaaggua agaaaccauc u 31

<210> SEQ ID NO 876
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 876

aauuuugugc ucaaagguaa gaaaccaucu u 31

<210> SEQ ID NO 877
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 877

auuuugugcu caaagguaag aaaccaucuu a 31

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<400> SEQUENCE: 878

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<210> SEQ ID NO 879
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<400> SEQUENCE: 879

uugugcucaa agguaagaaa ccaucuuaua u 31

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 880

ugugcucaaa gguaagaaac caucuuauau a 31

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 881

gccccuugug gaaucagaag caggugucug c 31

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<400> SEQUENCE: 882

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<210> SEQ ID NO 883
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<400> SEQUENCE: 883

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 884

aaugagucac uucaaaggcg gccacagggu u 31

<210> SEQ ID NO 885
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 885

aaagccccuu guggaaucag aagcaggugu c 31

<210> SEQ ID NO 886
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 886

agccccuugu ggaaucagaa gcaggugucu g 31

<210> SEQ ID NO 887
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<400> SEQUENCE: 887

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cccuugugga aucagaagca ggugucugca g 31

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guaagaaacc aucuuauaua aaacaaucaa a 31

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ucaaaggcgg ccacaggguu gaggaaaaag c 31

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cucaaaggua agaaaccauc uuauauaaaa c 31

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<210> SEQ ID NO 895
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uguugacuuu auuucaccgu ggaaauuuug u 31

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gaaaaagccc cuuguggaau cagaagcagg u 31

<210> SEQ ID NO 921
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aaaaagcccc uuguggaauc agaagcaggu g 31

<210> SEQ ID NO 922
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uugaggaaaa agccccuugu ggaaucagaa g 31

<210> SEQ ID NO 924
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uaaaaaaaug agucacuuca aaggcggcca c 31

<210> SEQ ID NO 925
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uauuucaccg uggaaauuuu gugcucaaag g 31

<210> SEQ ID NO 926
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<400> SEQUENCE: 926

auuucaccgu ggaaauuuug ugcucaaagg u 31

<210> SEQ ID NO 927
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agcuuauaau guugacuuua uuucaccgug g 31

<210> SEQ ID NO 928
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gcuuauaaug uugacuuuau uucaccgugg a 31

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<400> SEQUENCE: 929

uugacuuuau uucaccgugg aaauuuugug c 31

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ugacuuuauu ucaccgugga aauuuugugc u 31

<210> SEQ ID NO 931
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acuuuauuuc accguggaaa uuuugugcuc a 31

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<400> SEQUENCE: 932

cuuuauuuca ccguggaaau uuugugcuca a 31

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<400> SEQUENCE: 933

uuauuucacc guggaaauuu ugugcucaaa g 31

<210> SEQ ID NO 934
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<400> SEQUENCE: 934

acauuaaaaa aaugagucac uucaaaggcg g 31

<210> SEQ ID NO 935
<211> LENGTH: 31
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<400> SEQUENCE: 935

aagcuuauaa uguugacuuu auuucaccgu g 31

<210> SEQ ID NO 936
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<400> SEQUENCE: 936

cuuauaaugu ugacuuuauu ucaccgugga a 31

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<213> ORGANISM: Homo sapiens

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uuuauuucac cguggaaauu uugugcucaa a 31

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<400> SEQUENCE: 938

uuuugugcuc aaagguaaga aaccaucuua u 31

<210> SEQ ID NO 939
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<400> SEQUENCE: 939

gugcucaaag guaagaaacc aucuuauaua a 31

<210> SEQ ID NO 940
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uacauuaaaa aaaugaguca cuucaaaggc g 31

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<400> SEQUENCE: 941

aaaagccccu uguggaauca gaagcaggug u 31

<210> SEQ ID NO 942
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<400> SEQUENCE: 942

gacuuuauuu caccguggaa auuuugugcu c 31

<210> SEQ ID NO 943
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<400> SEQUENCE: 943

cauuaaaaaa augagucacu ucaaaggcgg c 31

<210> SEQ ID NO 944
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<400> SEQUENCE: 944

auuaaaaaaa ugagucacuu caaaggcggc c 31

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<400> SEQUENCE: 945

uuaaaaaaau gagucacuuc aaaggcggcc a 31

<210> SEQ ID NO 946
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<400> SEQUENCE: 946

uaagaaacca ucuuauauaa aacaaucaaa u 31

<210> SEQ ID NO 947
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<400> SEQUENCE: 947

aagaaaccau cuuauauaaa acaaucaaau a 31

<210> SEQ ID NO 948
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<400> SEQUENCE: 948

agaaaccauc uuauauaaaa caaucaaaua a 31

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<400> SEQUENCE: 949

gaaaccaucu uauauaaaac aaucaaauaa a 31

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aaggcggcca caggguugag gaaaaagccc c 31

<210> SEQ ID NO 951
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<400> SEQUENCE: 951

aaaggcggcc acaggguuga ggaaaaagcc c 31

<210> SEQ ID NO 952
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 952

acauaaauac auuaaaaaaa ugagucacuu c 31

<210> SEQ ID NO 953
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 953

cauaaauaca uuaaaaaaau gagucacuuc a 31

<210> SEQ ID NO 954
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<400> SEQUENCE: 954

auacauaaau acauuaaaaa aaugagucac u 31

<210> SEQ ID NO 955
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<400> SEQUENCE: 955

uacauaaaua cauuaaaaaa augagucacu u 31

<210> SEQ ID NO 956
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 956

auaaauacau uaaaaaaaug agucacuuca a 31

<210> SEQ ID NO 957
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 957

uaaauacauu aaaaaaauga gucacuucaa a 31

<210> SEQ ID NO 958
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<400> SEQUENCE: 958

aggcggccac aggguugagg aaaaagcccc u 31

<210> SEQ ID NO 959
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 959

aaauacauua aaaaaaugag ucacuucaaa g 31

<210> SEQ ID NO 960
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<400> SEQUENCE: 960

ggcggccaca ggguugagga aaaagccccu u 31

<210> SEQ ID NO 961
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 961

gcggccacag gguugaggaa aaagccccuu g 31

<210> SEQ ID NO 962
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<400> SEQUENCE: 962

uauaauguug acuuuauuuc accguggaaa u 31

<210> SEQ ID NO 963
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<400> SEQUENCE: 963

auaauguuga cuuuauuuca ccguggaaau u 31

<210> SEQ ID NO 964
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<400> SEQUENCE: 964

uaauguugac uuuauuucac cguggaaauu u 31

<210> SEQ ID NO 965
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<400> SEQUENCE: 965

aauacauuaa aaaaaugagu cacuucaaag g 31

<210> SEQ ID NO 966
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 966

cggccacagg guugaggaaa aagccccuug u 31

<210> SEQ ID NO 967
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<213> ORGANISM: Homo sapiens

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ggccacaggg uugaggaaaa agccccuugu g 31

<210> SEQ ID NO 968
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<400> SEQUENCE: 968

gccacagggu ugaggaaaaa gccccuugug g 31

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ccacaggguu gaggaaaaag ccccuugugg a 31

<210> SEQ ID NO 970
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cacaggguug aggaaaaagc cccuugugga a 31

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<400> SEQUENCE: 971

ggguugagga aaaagccccu uguggaauca g 31

<210> SEQ ID NO 972
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acaggguuga ggaaaaagcc ccuuguggaa u 31

<210> SEQ ID NO 973
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aggguugagg aaaaagcccc uuguggaauc a 31

<210> SEQ ID NO 974
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<400> SEQUENCE: 974

caggguugag gaaaaagccc cuuguggaau c 31

<210> SEQ ID NO 975
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<400> SEQUENCE: 975

accaucuuau auaaaacaau caaauaaaua c 31

<210> SEQ ID NO 976
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 976

ccaucuuaua uaaaacaauc aaauaaauac a 31

<210> SEQ ID NO 977
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aaaccaucuu auauaaaaca aucaaauaaa u 31

<210> SEQ ID NO 978
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<400> SEQUENCE: 978

aaccaucuua uauaaaacaa ucaaauaaau a 31

<210> SEQ ID NO 979
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 979

caucuuauau aaaacaauca aauaaauaca u 31

<210> SEQ ID NO 980
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<400> SEQUENCE: 980

aucuuauaua aaacaaucaa auaaauacau a 31

<210> SEQ ID NO 981
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<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 981

uauaaaacaa ucaaauaaau acauaaauac a 31

<210> SEQ ID NO 982
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 982

auaaaacaau caaauaaaua cauaaauaca u 31

<210> SEQ ID NO 983
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 983

uaaaacaauc aaauaaauac auaaauacau u 31

<210> SEQ ID NO 984
<211> LENGTH: 31

<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 984

aaacaaucaa auaaauacau aaauacauua a 31

<210> SEQ ID NO 985
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 985

aacaaucaaa uaaauacaua aauacauuaa a 31

<210> SEQ ID NO 986
<211> LENGTH: 31
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 986

acaaucaaau aaauacauaa auacauuaaa a 31

<210> SEQ ID NO 987
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<400> SEQUENCE: 987

aauacauaaa uacauuaaaa aaaugaguca c 31

<210> SEQ ID NO 988
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 988

uaaauacaua aauacauuaa aaaaaugagu c 31

<210> SEQ ID NO 989
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<400> SEQUENCE: 989

aaauacauaa auacauuaaa aaaaugaguc a 31

<210> SEQ ID NO 990
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<400> SEQUENCE: 990

auaaauacau aaauacauua aaaaaaugag u 31

<210> SEQ ID NO 991
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<400> SEQUENCE: 991

ucuuauauaa aacaaucaaa uaaauacaua a 31

<210> SEQ ID NO 992

<211> LENGTH: 31
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<400> SEQUENCE: 992

cuuauauaaa acaaucaaau aaauacauaa a 31

<210> SEQ ID NO 993
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<400> SEQUENCE: 993

auauaaaaca aucaaauaaa uacauaaaua c 31

<210> SEQ ID NO 994
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 994

aaaacaauca aauaaauaca uaaauacauu a 31

<210> SEQ ID NO 995
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<212> TYPE: RNA
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<400> SEQUENCE: 995

caaucaaaua aauacauaaa uacauuaaaa a 31

<210> SEQ ID NO 996
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 996

uuauauaaaa caaucaaaua aauacauaaa u 31

<210> SEQ ID NO 997
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 997

uauauaaaac aaucaaauaa auacauaaau a 31

<210> SEQ ID NO 998
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<400> SEQUENCE: 998

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<400> SEQUENCE: 999

aucaaauaaa uacauaaaua cauuaaaaaa a 31

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<213> ORGANISM: Homo sapiens

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ucaaauaaau acauaaauac auuaaaaaaa u 31

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<400> SEQUENCE: 1001

caaauaaaua cauaaauaca uuaaaaaaau g 31

<210> SEQ ID NO 1002
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<400> SEQUENCE: 1002

aaauaaauac auaaauacau uaaaaaaaug a 31

<210> SEQ ID NO 1003
<211> LENGTH: 31
<212> TYPE: RNA
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<400> SEQUENCE: 1003

aauaaauaca uaaauacauu aaaaaaauga g 31

<210> SEQ ID NO 1004
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<400> SEQUENCE: 1004

ggccucagcg ucuguccgug gugcugaagu u 31

<210> SEQ ID NO 1005
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<400> SEQUENCE: 1005

gccucagcgu cuguccgugg ugcugaaguu u 31

<210> SEQ ID NO 1006
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<400> SEQUENCE: 1006

gaugaagaca ggaagcugca gcuccaggag g 31

<210> SEQ ID NO 1007
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agaugaagac aggaagcugc agcuccagga g 31

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aaugcgacca agcuguguga cacaccgcaa g 31

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caccaccucu caguggcaau gcgaccaagc u 31

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<213> ORGANISM: Mus musculus

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<210> SEQ ID NO 1036
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<210> SEQ ID NO 1039
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<210> SEQ ID NO 1040
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<210> SEQ ID NO 1041
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<210> SEQ ID NO 1042
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uucaccaccu cucaguggca augcgaccaa g 31

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cucaguggca augcgaccaa gcugugugac a 31

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ucaguggcaa ugcgaccaag cugugugaca c 31

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accucucagu ggcaaugcga ccaagcugug u 31

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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1046

cucucagugg caaugcgacc aagcugugug a 31

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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1047

ucucaguggc aaugcgacca agcuguguga c 31

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<400> SEQUENCE: 1048

uaaggccuca cuaaaccacu caucuacacu u 31

<210> SEQ ID NO 1049
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<400> SEQUENCE: 1049

aaggccucac uaaaccacuc aucuacacuu a 31

<210> SEQ ID NO 1050
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1050

aaaccacuca ucuacacuua acaucgaucg u 31

<210> SEQ ID NO 1051
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<400> SEQUENCE: 1051

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<210> SEQ ID NO 1052
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<400> SEQUENCE: 1052

augaagacag gaagcugcag cuccaggagg g 31

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<400> SEQUENCE: 1053

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<400> SEQUENCE: 1054

gcgucugucc guggugcuga aguuuauucg g 31

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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1055

guaaggccuc acuaaaccac ucaucuacac u 31

<210> SEQ ID NO 1056
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1056

aaccacucau cuacacuuaa caucgaucgu g 31

<210> SEQ ID NO 1057
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1057

accacucauc uacacuuaac aucgaucgug a 31

<210> SEQ ID NO 1058
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1058

ccacucaucu acacuuaaca ucgaucguga u 31

<210> SEQ ID NO 1059
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<213> ORGANISM: Mus musculus

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<210> SEQ ID NO 1060
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

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ugcgaccaag cugugugaca caccgcaagg g 31

<210> SEQ ID NO 1061
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<400> SEQUENCE: 1061

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<210> SEQ ID NO 1062
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<400> SEQUENCE: 1062

ugaagacagg aagcugcagc uccaggaggg u 31

<210> SEQ ID NO 1063
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<212> TYPE: RNA
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ccucagcguc uguccguggu gcugaaguuu a 31

<210> SEQ ID NO 1064
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<212> TYPE: RNA
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aagacaggaa gcugcagcuc caggagggua u 31

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<400> SEQUENCE: 1065

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<210> SEQ ID NO 1066
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<400> SEQUENCE: 1066

cagcgucugu ccguggugcu gaaguuuauu c 31

<210> SEQ ID NO 1067
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1067

agcgucuguc cguggugcug aaguuuauuc g 31

<210> SEQ ID NO 1068
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1068

cgucuguccg uggugcugaa guuuauucgg a 31

<210> SEQ ID NO 1069
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1069

ucagcgucug uccguggugc ugaaguuuau u 31

<210> SEQ ID NO 1070
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1070

gucuguccgu ggugcugaag uuuauucgga u 31

<210> SEQ ID NO 1071

<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1071

gguaaggccu cacuaaacca cucaucuaca c 31

<210> SEQ ID NO 1072
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1072

ucuguccgug gugcugaagu uuauucggau u 31

<210> SEQ ID NO 1073
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1073

agguaaggcc ucacuaaacc acucaucuac a 31

<210> SEQ ID NO 1074
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1074

acucaucuac acuuaacauc gaucgugaua g 31

<210> SEQ ID NO 1075
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1075

cucaucuaca cuuaacaucg aucgugauag a 31

<210> SEQ ID NO 1076
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1076

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<210> SEQ ID NO 1077
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1077

ucaucuacac uuaacaucga ucgugauaga u 31

<210> SEQ ID NO 1078
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1078

ccaagcugug ugacacaccg caagggcuug g 31

<210> SEQ ID NO 1079
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1079

gaccaagcug ugugacacac cgcaagggcu u 31

<210> SEQ ID NO 1080
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1080

accaagcugu gugacacacc gcaagggcuu g 31

<210> SEQ ID NO 1081
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1081

uaugcagagu gggagaggua aggccucacu a 31

<210> SEQ ID NO 1082
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1082

augcagagug ggagagguaa ggccucacua a 31

<210> SEQ ID NO 1083
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1083

ggagagguaa ggccucacua aaccacucau c 31

<210> SEQ ID NO 1084
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1084

uauucaccac cucucagugg caaugcgacc a 31

<210> SEQ ID NO 1085
<211> LENGTH: 31
<212> TYPE: RNA
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<400> SEQUENCE: 1085

gagguaaggc cucacuaaac cacucaucua c 31

<210> SEQ ID NO 1086
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1086

uuuccaacug cuuucugaaa ggggugagga u 31

<210> SEQ ID NO 1087
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1087

ugcuuucuga aaggggugag gaucuaccuu a 31

<210> SEQ ID NO 1088
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1088

agagguaagg ccucacuaaa ccacucaucu a 31

<210> SEQ ID NO 1089
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1089

cuuaacaucg aucgugauag augaagacag g 31

<210> SEQ ID NO 1090
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1090

caucuacacu uaacaucgau cgugauagau g 31

<210> SEQ ID NO 1091
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<400> SEQUENCE: 1091

acuuaacauc gaucgugaua gaugaagaca g 31

<210> SEQ ID NO 1092
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<400> SEQUENCE: 1092

aucuacacuu aacaucgauc gugauagaug a 31

<210> SEQ ID NO 1093
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<400> SEQUENCE: 1093

ucuacacuua acaucgaucg ugauagauga a 31

<210> SEQ ID NO 1094
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1094

uacacuuaac aucgaucgug auagaugaag a 31

<210> SEQ ID NO 1095
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<212> TYPE: RNA
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<400> SEQUENCE: 1095

guauucacca ccucucagug gcaaugcgac c 31

<210> SEQ ID NO 1096
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1096

uuccaacugc uuucugaaag gggugaggau c 31

<210> SEQ ID NO 1097
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1097

uccaacugcu uucugaaagg ggugaggauc u 31

<210> SEQ ID NO 1098
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1098

ccaacugcuu ucugaaaggg gugaggaucu a 31

<210> SEQ ID NO 1099
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1099

caacugcuuu cugaaagggg ugaggaucua c 31

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<400> SEQUENCE: 1100

aacugcuuuc ugaaaggggu gaggaucuac c 31

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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1101

acugcuuucu gaaaggggug aggaucuacc u 31

<210> SEQ ID NO 1102
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1102

cugcuuucug aaagggguga ggaucuaccu u 31

<210> SEQ ID NO 1103
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1103

gagagguaag gccucacuaa accacucauc u 31

<210> SEQ ID NO 1104
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1104

cuacacuuaa caucgaucgu gauagaugaa g 31

<210> SEQ ID NO 1105
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1105

acacuuaaca ucgaucguga uagaugaaga c 31

<210> SEQ ID NO 1106
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1106

cacuuaacau cgaucgugau agaugaagac a 31

<210> SEQ ID NO 1107
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1107

gguauucacc accucucagu ggcaaugcga c 31

<210> SEQ ID NO 1108
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1108

ccucacuaaa ccacucaucu acacuuaaca u 31

<210> SEQ ID NO 1109
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cucacuaaac cacucaucua cacuuaacau c 31

<210> SEQ ID NO 1110
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1110

gccucacuaa accacucauc uacacuuaac a 31

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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1111

ucacuaaacc acucaucuac acuuaacauc g 31

<210> SEQ ID NO 1112
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<400> SEQUENCE: 1112

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<210> SEQ ID NO 1113
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cuaaaccacu caucuacacu uaacaucgau c 31

<210> SEQ ID NO 1114
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<400> SEQUENCE: 1114

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<400> SEQUENCE: 1115

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<400> SEQUENCE: 1146

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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1157

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<400> SEQUENCE: 1161

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<210> SEQ ID NO 1162
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<400> SEQUENCE: 1162

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<400> SEQUENCE: 1163

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<210> SEQ ID NO 1164
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<400> SEQUENCE: 1164

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<210> SEQ ID NO 1165
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<400> SEQUENCE: 1165

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<400> SEQUENCE: 1166

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<400> SEQUENCE: 1167

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<210> SEQ ID NO 1168
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<400> SEQUENCE: 1168

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<210> SEQ ID NO 1169
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<400> SEQUENCE: 1169

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<210> SEQ ID NO 1170
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<400> SEQUENCE: 1170

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<210> SEQ ID NO 1171
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<400> SEQUENCE: 1171

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<210> SEQ ID NO 1172
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1172

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<400> SEQUENCE: 1173

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<210> SEQ ID NO 1174
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1174

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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1175

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<210> SEQ ID NO 1176
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1176

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<210> SEQ ID NO 1177
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<210> SEQ ID NO 1178
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1178

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<210> SEQ ID NO 1179
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<212> TYPE: RNA
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<400> SEQUENCE: 1181

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<210> SEQ ID NO 1182
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1182

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<210> SEQ ID NO 1183
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1183

uuuuuuccaa cugcuuucug aaagggguga g 31

<210> SEQ ID NO 1184
<211> LENGTH: 31
<212> TYPE: RNA
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<400> SEQUENCE: 1184

cuuucugaaa ggggugagga ucuaccuuaa u 31

<210> SEQ ID NO 1185
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1185

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<210> SEQ ID NO 1186
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1186

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<210> SEQ ID NO 1187
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1187

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<210> SEQ ID NO 1188
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1188

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<210> SEQ ID NO 1189
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<400> SEQUENCE: 1189

cugcagcucc aggaggguau ucaccaccuc u 31

<210> SEQ ID NO 1190
<211> LENGTH: 31
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<400> SEQUENCE: 1190

ugcagcucca ggaggguauu caccaccucu c 31

<210> SEQ ID NO 1191
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1191

gcagcuccag gaggguauuc accaccucuc a 31

<210> SEQ ID NO 1192
<211> LENGTH: 31
<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1192

cagcuccagg aggguauuca ccaccucuca g 31

<210> SEQ ID NO 1193
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1193

gcuccaggag gguauucacc accucucagu g 31

<210> SEQ ID NO 1194
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1194

cuccaggagg guauucacca ccucucagug g 31

<210> SEQ ID NO 1195
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1195

uccaggaggg uauucaccac cucucagugg c 31

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<400> SEQUENCE: 1196

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<400> SEQUENCE: 1197

agcuguguga cacaccgcaa gggcuuggga u 31

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<400> SEQUENCE: 1198

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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1201

gugugacaca ccgcaagggc uugggaucuu u 31

<210> SEQ ID NO 1202
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1202

agcuccagga ggguauucac caccucucag u 31

<210> SEQ ID NO 1203
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1203

ggaggguauu caccaccucu caguggcaau g 31

<210> SEQ ID NO 1204
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1204

gaggguauuc accaccucuc aguggcaaug c 31

<210> SEQ ID NO 1205
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1205

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<210> SEQ ID NO 1206
<211> LENGTH: 31
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1206

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<210> SEQ ID NO 1207
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<400> SEQUENCE: 1207

aggaggguau ucaccaccuc ucaguggcaa u 31

<210> SEQ ID NO 1208
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1208

guggugcuga aguuuauucg gauuuauuuu u 31

<210> SEQ ID NO 1209
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1209

uggugcugaa guuuauucgg auuuauuuuu u 31

<210> SEQ ID NO 1210
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<400> SEQUENCE: 1210

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<210> SEQ ID NO 1211
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1211

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<210> SEQ ID NO 1212
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1212

auucggauuu auuuuuuucc aacugcuuuc u 31

<210> SEQ ID NO 1213
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1213

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<210> SEQ ID NO 1214
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1214

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<210> SEQ ID NO 1215
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1215

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<210> SEQ ID NO 1216
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<400> SEQUENCE: 1216

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<210> SEQ ID NO 1217
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1217

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<210> SEQ ID NO 1218
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1218

ccguggugcu gaaguuuauu cggauuuauu u 31

<210> SEQ ID NO 1219
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<212> TYPE: RNA
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<400> SEQUENCE: 1219

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<210> SEQ ID NO 1220
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1220

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<210> SEQ ID NO 1221
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<212> TYPE: RNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1221

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<400> SEQUENCE: 1222

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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1223

gauuuauuuu uuuccaacug cuuucugaaa g 31

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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1224

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<210> SEQ ID NO 1225
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1225

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<210> SEQ ID NO 1226
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<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1226

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<210> SEQ ID NO 1227
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<400> SEQUENCE: 1227

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What is claimed is:

1. A conditional RNA-sensor complex comprising:

a sensor strand comprising at least one toehold segment, wherein the toehold segment capable of binding a pathological biomarker present in or overexpressed in a target cell, wherein the pathological biomarker comprises a molecule that encodes ANP, BNP, MHCβ, mir-23a-3p, mir-125-6p, or mir-199b-5p; and

a double stranded pro-RNA molecule comprising

a guide strand comprising an RNA molecule capable of binding a therapeutic target molecule in the target cell, wherein the therapeutic target molecule is an RNA molecule that encodes calcineurin or histone deacetylase 2 (HDAC2); and

a core strand comprising

a first portion comprising a passenger strand that is fully or partially complimentary to and binds the guide strand,

a second portion comprising a first protection segment that is fully or partially complimentary to and binds the sensor strand, and

a first linker that joins a first end of the passenger strand to the first protection segment.

2. The conditional RNA-sensor complex of claim 1, wherein the core strand further comprises a third portion comprising a second protection segment that is fully or partially complimentary to and binds the sensor strand, and a second linker that joins a second end of the passenger strand to the second protection segment.

3. The conditional RNA-sensor complex of claim 1, wherein the toehold segment is an aptamer.

4. The conditional RNA-sensor complex of claim 1, wherein the sensor strand is displaced from the double stranded pro-RNA molecule when the pathological biomarker binds the toehold segment and the resulting double stranded pro-RNA molecule is a substrate for Dicer.

5. The conditional RNA-sensor complex of claim 1, wherein the target cell is a cardiac myocyte.

6. The conditional RNA-sensor complex of claim 1, wherein the molecule that encodes ANP, BNP, or MHCβ is an mRNA molecule and the molecule that encodes mir-23a-3p, mir-125-6p, or mir-199b-5p is an miRNA molecule.

7. The conditional RNA-sensor complex of claim 6, wherein the molecule that encodes ANP comprises a sequence selected from SEQ ID Nos: 8-10, the molecule that encodes BNP comprises a sequence selected from SEQ ID Nos: 4-6, the molecule that encodes MHCβ comprises a sequence of SEQ ID NO: 7, and the molecule that encodes mir-23a-3p comprises a sequence selected from SEQ ID Nos: 1-3.

8. The conditional RNA-sensor complex of claim 7, wherein the sensor strand further comprises one or more chemical modifications to the RNA sequence, wherein the one or more chemical modifications are selected from a locked nucleic acid (LNA) modification, a peptide nucleic acid (PNA) modification, a 2'-O-methyl modification, morpholino modification, a phosphorothioate modification, a terminal modification, or a linker modification.

9. The conditional RNA-sensor complex of claim 5, wherein the double stranded pro-RNA molecule is an RNA interference (RNAi) molecule.

10. The conditional RNA-sensor complex of claim 9, wherein the guide strand comprises a sequence selected from SEQ ID NOS: 11-16.

11. The conditional RNA-sensor complex of claim 2, wherein the first linker, the second linker, or both the first and second linkers is a C3 spacer.

12. The conditional RNA-sensor complex of claim 9, wherein the guide strand further comprises one or more chemical modifications to the RNA sequence, wherein the one or more chemical modifications are selected from a locked nucleic acid (LNA) modification, a peptide nucleic acid (PNA) modification, a 2'-O-methyl modification, morpholino modification, a phosphorothioate modification, a terminal modification, or a linker modification.

13. The conditional RNA-sensor complex of claim 2, wherein the core strand comprises

a passenger strand;

a first linker that joins a 3' end of the passenger strand to the first protection segment; and

a second linker that joins a 5' end of the passenger strand to the second protection segment.

14. The conditional RNA-sensor complex of claim 13, wherein the core strand comprises a sequence selected from SEQ ID NOS: 17-26.

15. The conditional RNA-sensor complex of claim 13, wherein the core strand further comprises one or more chemical modifications to the RNA sequence, wherein the one or more chemical modifications are selected from a locked nucleic acid (LNA) modification, a peptide nucleic acid (PNA) modification, a 2'-O-methyl modification, morpholino modification, a phosphorothioate modification, a terminal modification, or a linker modification.

16. The conditional RNA-sensor complex of claim 1, wherein:

(a) the sensor strand comprises a sequence having at least 95% homology to SEQ ID NO:4, the core strand comprises a sequence having at least 95% homology to SEQ ID NO:21, SEQ ID NO: 49, and SEQ ID NO: 50, and the guide strand comprises a sequence having at least 95% homology to SEQ ID NO:15;

(b) the sensor strand comprises a sequence having at least 95% homology to SEQ ID NO:5, the core strand comprises a sequence having at least 95% homology to SEQ ID NO:22, SEQ ID NO: 49, and SEQ ID NO: 51, and the guide strand comprises a sequence having at least 95% homology to SEQ ID NO:15;

(c) the sensor strand comprises a sequence having at least 95% homology to SEQ ID NO:6, the core strand comprises a sequence having at least 95% homology to SEQ ID NO:23, SEQ ID NO: 49, and SEQ ID NO: 52, and the guide strand comprises a sequence having at least 95% homology to SEQ ID NO:15;

(d) the sensor strand comprises a sequence having at least 95% homology to SEQ ID NO:7, the core strand comprises a sequence having at least 95% homology to SEQ ID NO:24, SEQ ID NO: 49, and SEQ ID NO: 53,

and the guide strand comprises a sequence having at least 95% homology to SEQ ID NO:15;

(e) the sensor strand comprises a sequence having at least 95% homology to SEQ ID NO:8, the core strand comprises a sequence having at least 95% homology to SEQ ID NO:25, and the guide strand comprises a sequence having at least 95% homology to SEQ ID NO:16;

(f) the sensor strand comprises a sequence having at least 95% homology to SEQ ID NO:8, the core strand comprises a sequence having at least 95% homology to SEQ ID NO:18, SEQ ID NO: 45, and SEQ ID NO: 47, and the guide strand comprises a sequence having at least 95% homology to SEQ ID NO:11;

(g) the sensor strand comprises a sequence having at least 95% homology to SEQ ID NO:10, the core strand comprises a sequence having at least 95% homology to SEQ ID NO:19, SEQ ID NO: 45, and SEQ ID NO: 48, and the guide strand comprises a sequence having at least 95% homology to SEQ ID NO:12;

(h) the sensor strand comprises a sequence having at least 95% homology to SEQ ID NO:1, the core strand comprises a sequence having at least 95% homology to SEQ ID NO: 41, SEQ ID NO: 45, and SEQ ID NO: 56, and the guide strand comprises a sequence having at least 95% homology to SEQ ID NO:12;

(i) the sensor strand comprises a sequence having at least 95% homology to SEQ ID NO:2, the core strand comprises a sequence having at least 95% homology to SEQ ID NO: 41, SEQ ID NO: 45, and SEQ ID NO: 56, and the guide strand comprises a sequence having at least 95% homology to SEQ ID NO: 12; or

(j) the sensor strand comprises a sequence having at least 95% homology to SEQ ID NO:39, the core strand comprises a sequence having at least 95% homology to SEQ ID NO: 41, SEQ ID NO: 45, and SEQ ID NO: 56, and the guide strand comprises a sequence having at least 95% homology to SEQ ID NO:12.

17. The conditional RNA-sensor complex of claim **16**, wherein the sensor strand, the guide strand and/or the core strand further comprises one or more chemical modifications to the RNA sequence, wherein the one or more chemical modifications are selected from a locked nucleic acid (LNA) modification, a peptide nucleic acid (PNA) modification, a 2'-O-methyl modification, morpholino modification, a phosphorothioate modification, a terminal modification, or a linker modification.

18. A pharmaceutical composition comprising:

a conditional RNA-sensor complex of claim **1**; and

a pharmaceutically acceptable carrier or excipient.

19. A method of treating a pathological condition comprising administering a therapeutically effective amount of a conditional RNA-sensor complex of claim **1** to a subject suffering from the pathological condition, wherein the pathological condition is myocardial infarction (MI), or cardiac hypertrophy.

20. The method of claim **19**, wherein administering a therapeutically effective amount comprises an intramyocardial injection of the conditional RNA-sensor complex or the pharmaceutical composition after detection of MI.

21. The conditional RNA-sensor complex of claim **1**, wherein the passenger strand bound to the guide strand forms a duplex between 15 and 30 base pairs in length.

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