Glyphosate N-acetylation

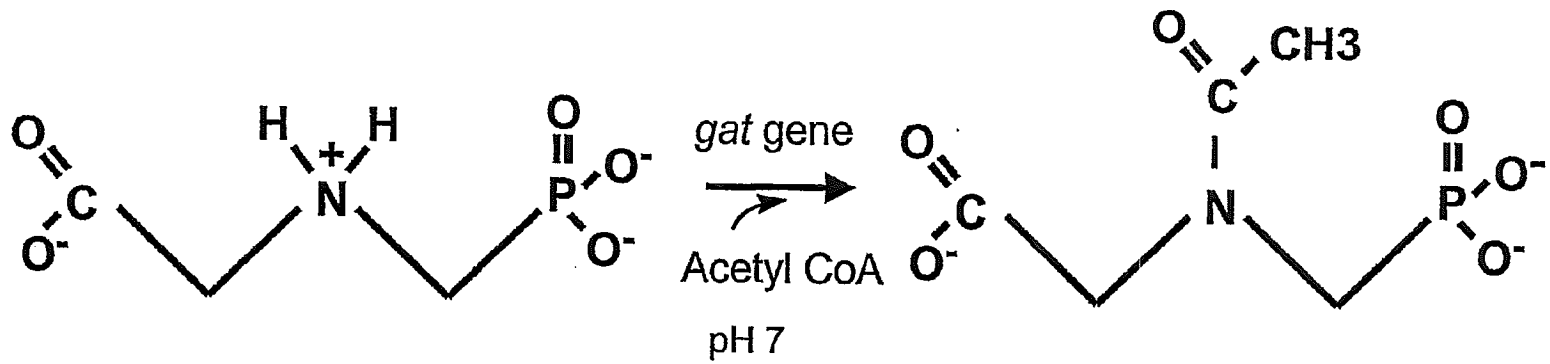


Fig. 1

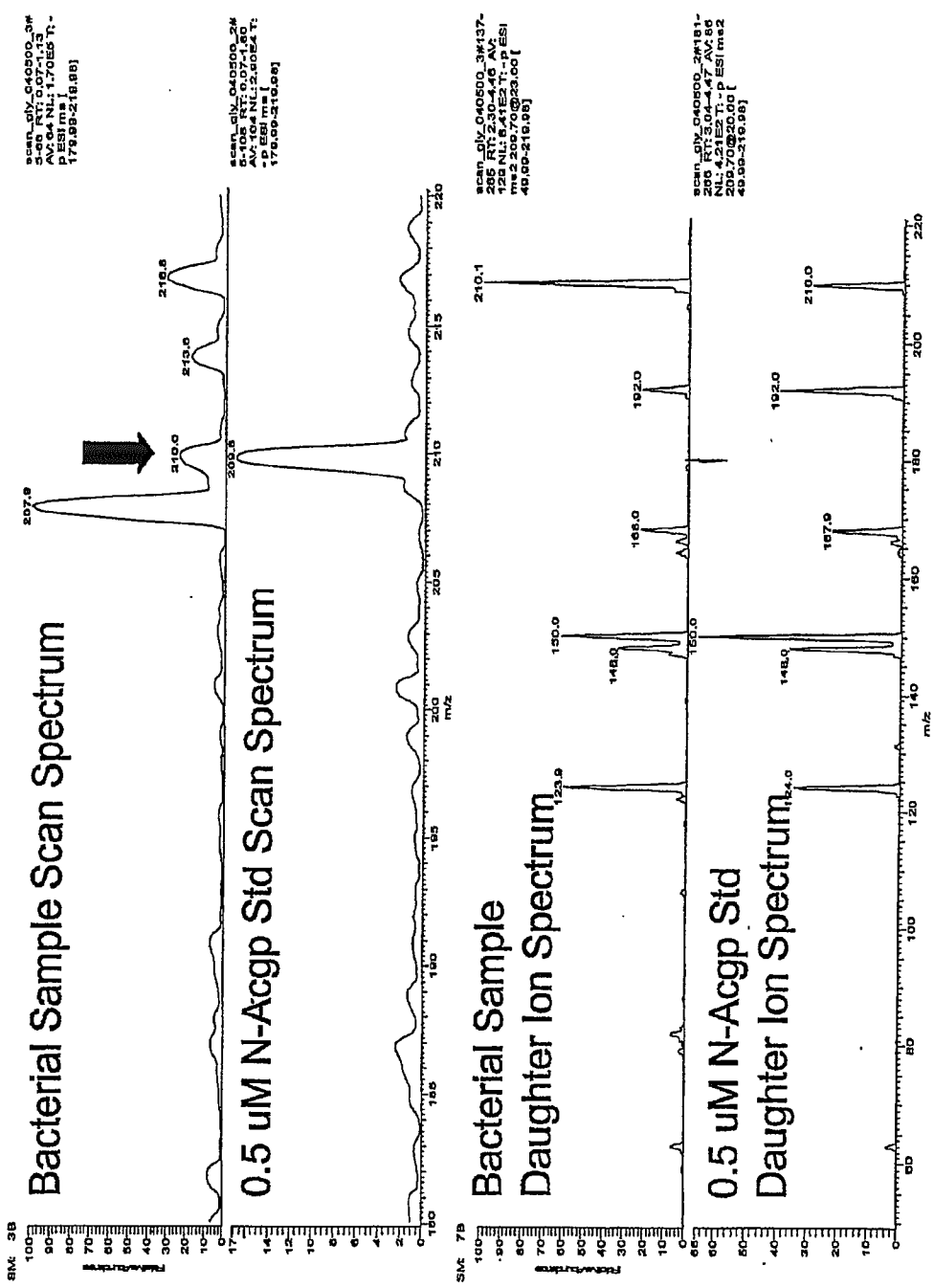

Bacterial Sample Scan Spectrum
0.5 uM N-Acgp Std Scan Spectrum
Bacterial Sample
Daughter Ion Spectrum
0.5 uM N-Acgp Std
Daughter Ion Spectrum
m/z

Fig. 2

Nucleotide identity between sequence pairs

	B6	DS3	ST401	NHA-2	NH5-2	yitl
B6	***	**95.0**	**93.2**	**94.8**	**92.8**	**62.0**
DS3		***	**95.5**	**99.8**	**95.0**	**61.8**
ST401			***	**95.2**	**99.5**	**62.4**
NHA-2				***	**94.8**	**61.5**
NH5-2					***	**62.9**
yitl						***

Fig. 3

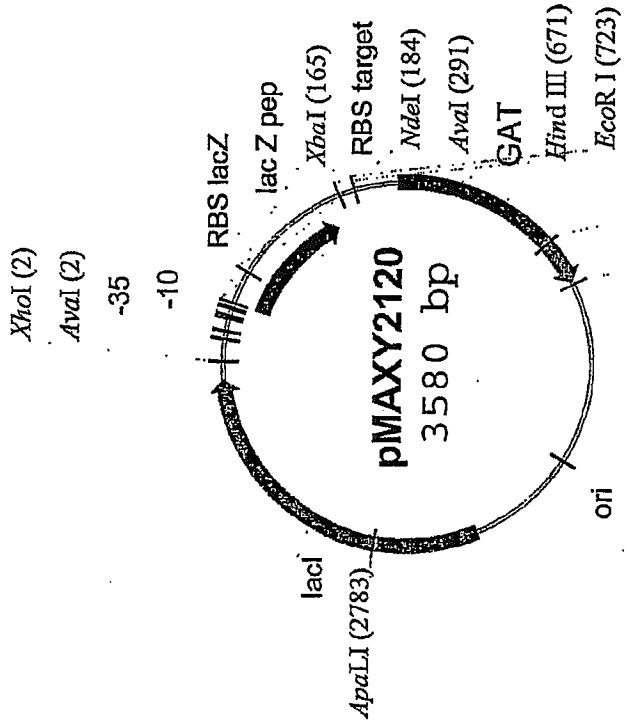
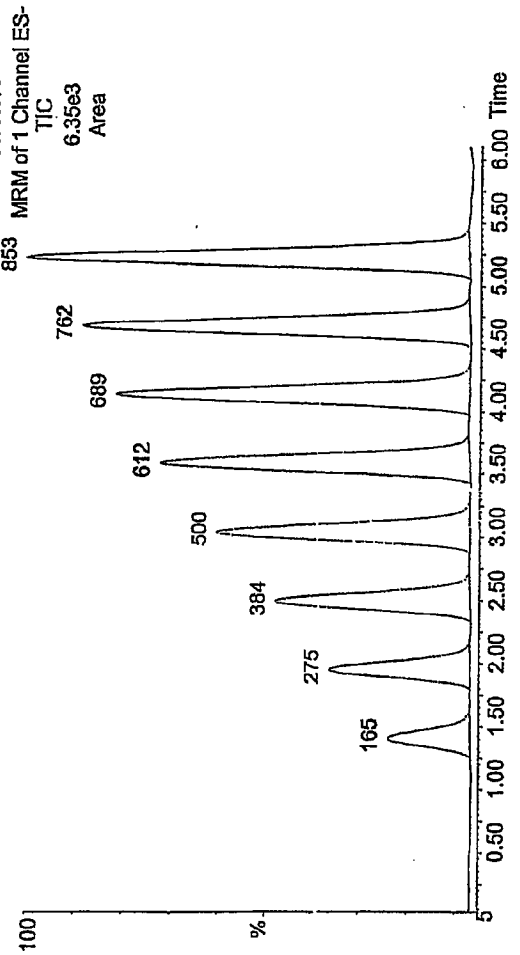

pMAXY2120
3580 bp
XhoI (2)
AvaI (2)
-35
-10
RBS lacZ
lac Z pep
XbaI (165)
RBS target
NdeI (184)
AvaI (291)
GAT
HindIII (671)
EcoR I (723)
camR
NcoI (1377)
PstI (1527)
ori
lacI
ApaLI (2783)

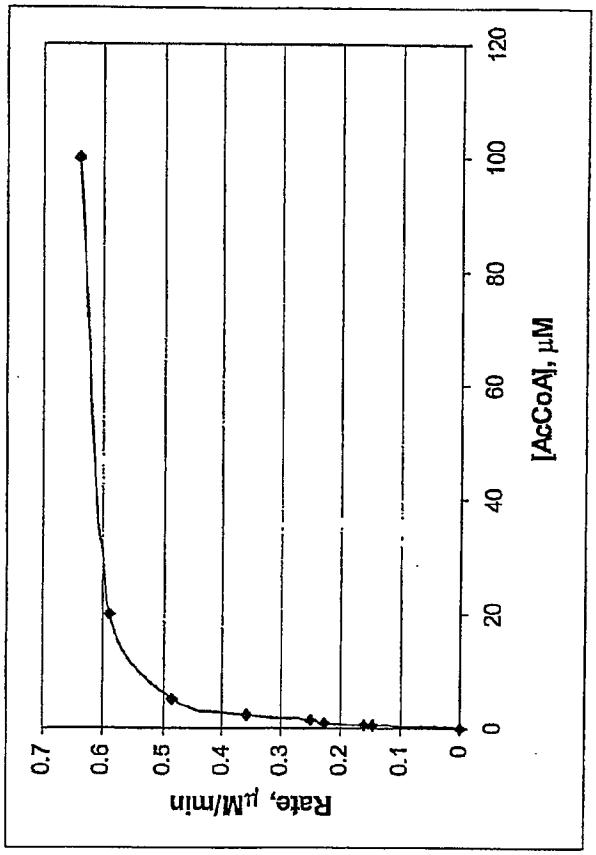
Fig. 4



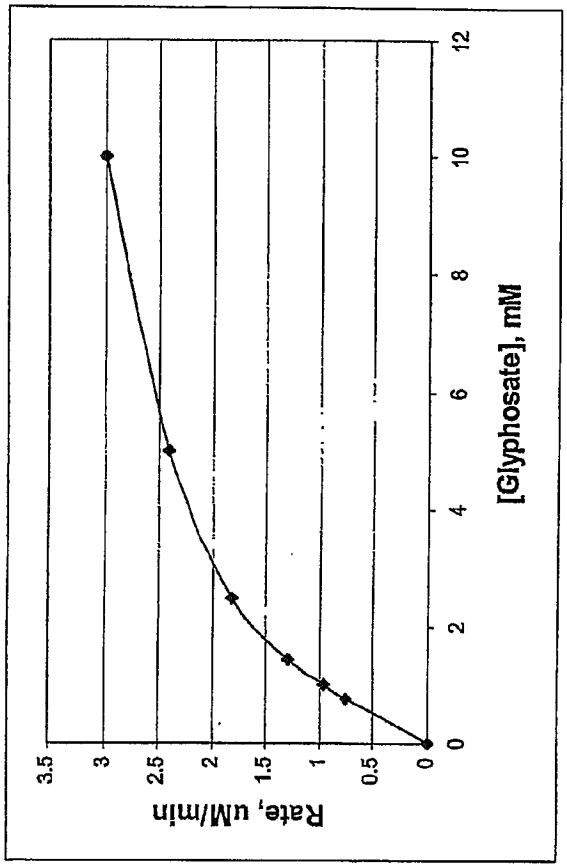
Purified B6 GAT catalyzes
N-acetylglyphosate production

Fig. 5

Fig. 6



B6 GAT K_M for Acetyl CoA = 2 µM



B6 GAT K_M for glyphosate = 2.9 mM

Fig. 7

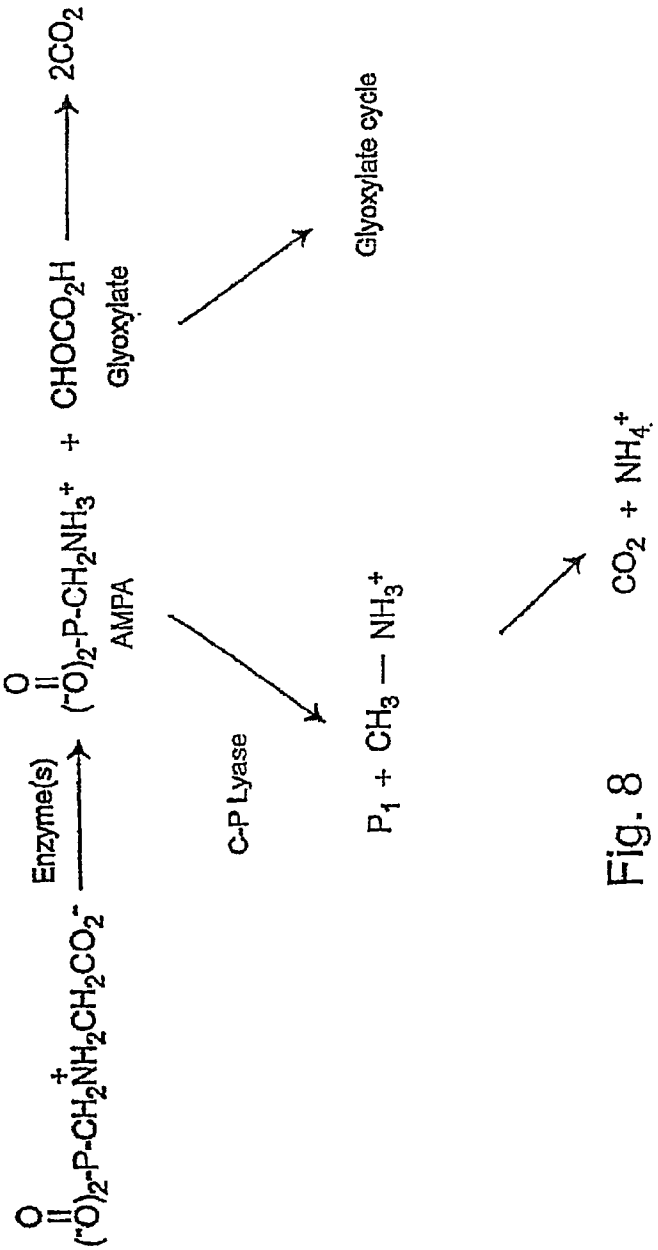

Enzyme(s)
AMPA
Glyoxylate
2CO2
Glyoxylate cycle
C-P Lyase
P1 + CH3 — NH3+
CO2 + NH4+

Fig. 8

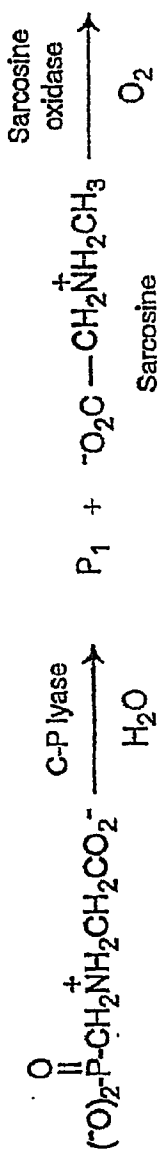

C-P lyase
H2O
P1
Sarcosine oxidase
O2
Sarcosine
Glycine
CH2O
THF cycle
CO2
CO2 + NH4+

Fig. 9

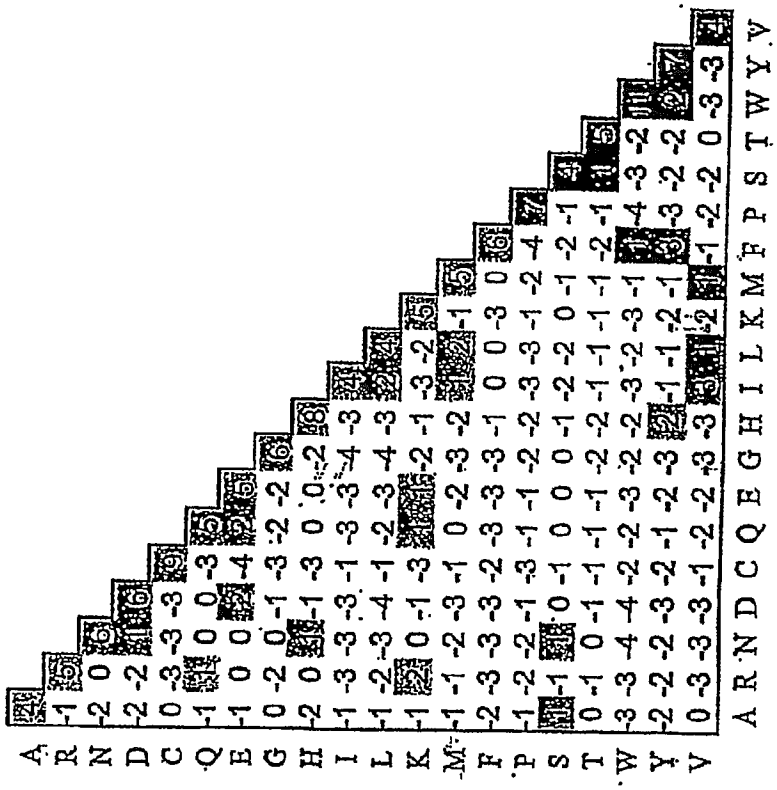

A R N D C Q E G H I L K M F P S T W Y V
A 4
R -1 5
N -2 0 6
D -2 -2 1 6
C 0 -3 -3 -3 9
Q -1 0 0 0 -3 5
E -1 0 0 2 -4 2 5
G 0 -2 0 -1 -3 -2 -2 6
H -2 0 1 -1 -3 0 0 -2 8
I -1 -3 -3 -3 -1 -3 -3 -4 -3 4
L -1 -2 -3 -4 -1 -2 -3 -4 -3 2 4
K -1 2 0 -1 -3 1 1 -2 -1 -3 -2 5
M -1 -1 -2 -3 -1 0 -2 -3 -2 1 2 -1 5
F -2 -3 -3 -3 -2 -3 -3 -3 -1 0 0 -3 0 6
P -1 -2 -2 -1 -3 -1 -1 -2 -2 -3 -3 -1 -2 -4 7
S 1 -1 0 -1 0 0 0 -1 -2 -2 0 -1 -2 -1 4
T 0 -1 0 -1 -1 -1 -2 -2 -1 -1 -1 -1 -2 -1 1 5
W -3 -3 -4 -4 -2 -2 -3 -2 -3 -2 -3 -1 1 -4 -3 -2 11
Y -2 -2 -2 -3 -2 -1 -2 -3 2 -1 -1 -2 -1 3 -3 -2 -2 7
V 0 -3 -3 -3 -1 -2 -2 -3 -3 3 1 -2 1 -1 -2 -2 0 -3 -1 4

Fig. 10

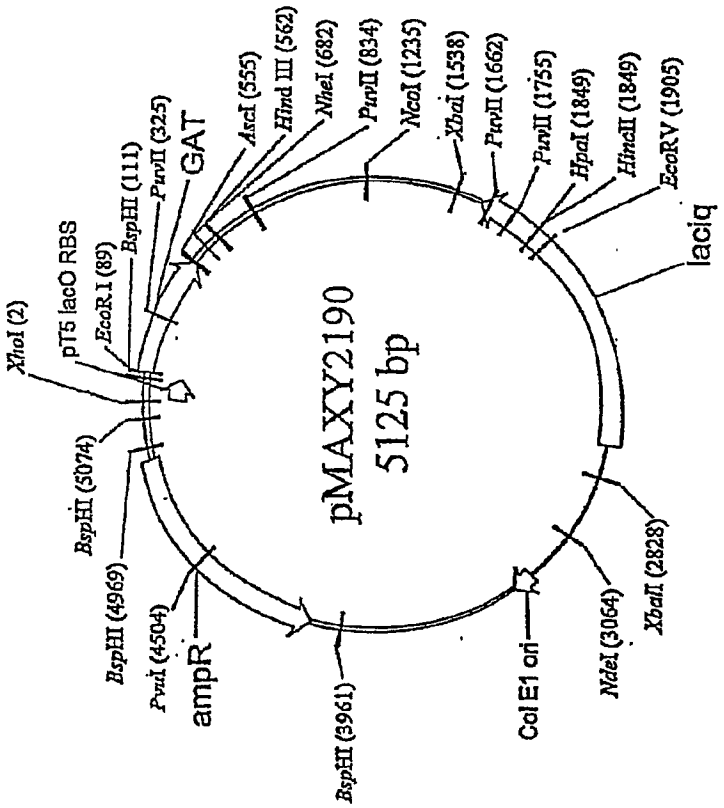
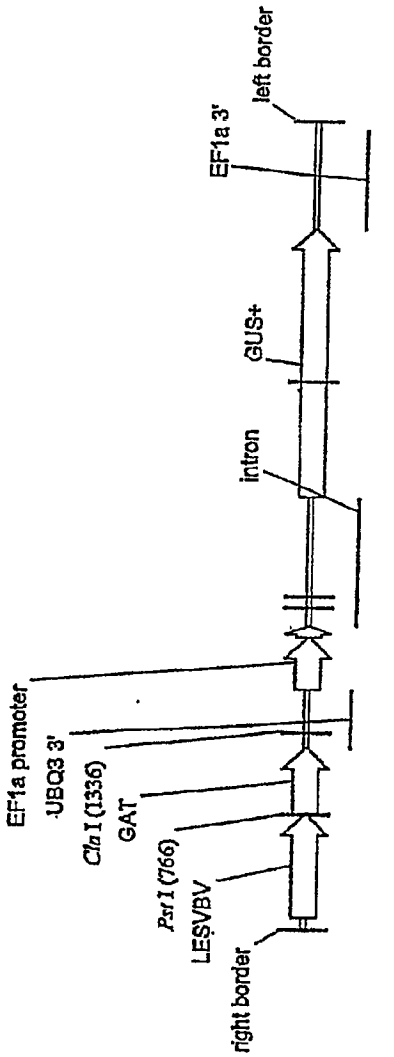

pMAXY2190
5125 bp
XhoI (2)
pT5 lacO RBS
EcoR.I (89)
BspHI (111)
PvuII (325)
GAT
AscI (555)
HindIII (562)
NheI (682)
PvuII (834)
NcoI (1235)
XbaI (1538)
PvuII (1662)
PvuII (1755)
HpaI (1849)
HincII (1849)
EcoRV (1905)
laciq
XbaII (2828)
NdeI (3064)
Col E1 ori
BspHI (3961)
PvuI (4504)
ampR
BspHI (4969)
BspHI (5074)

Fig. 11



GAT T-DNA
5546 bp

Fig. 12

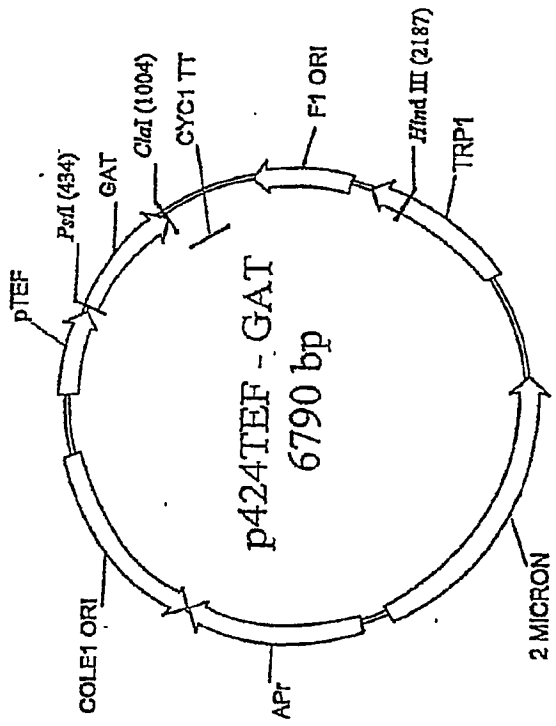

p424TEF - GAT
6790 bp
pTEF
PstI (434)
GAT
ClaI (1004)
CYC1 TT
F1 ORI
HindIII (2187)
TRP1
2 MICRON
APr
COLE1 ORI

Fig. 13

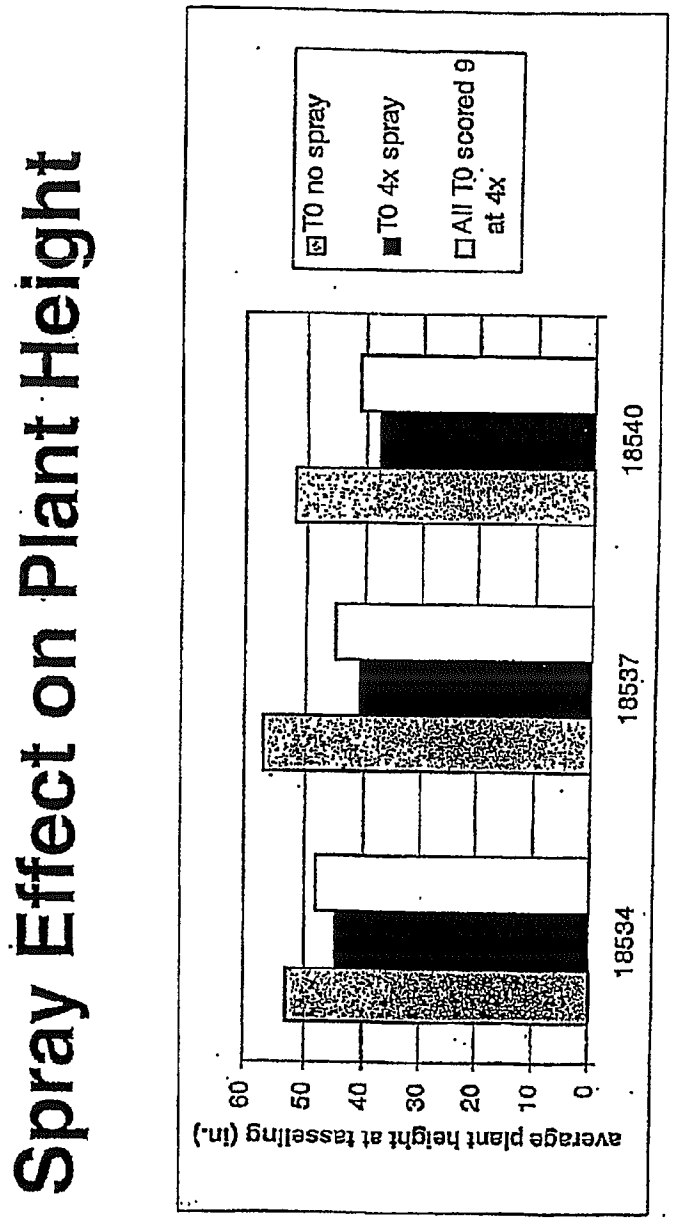

Spray Effect on Plant Height
average plant height at tasselling (in.)
60
50
40
30
20
10
0
18534
18537
18540
T0 no spray
T0 4x spray
All T0 scored 9 at 4x

Fig. 14

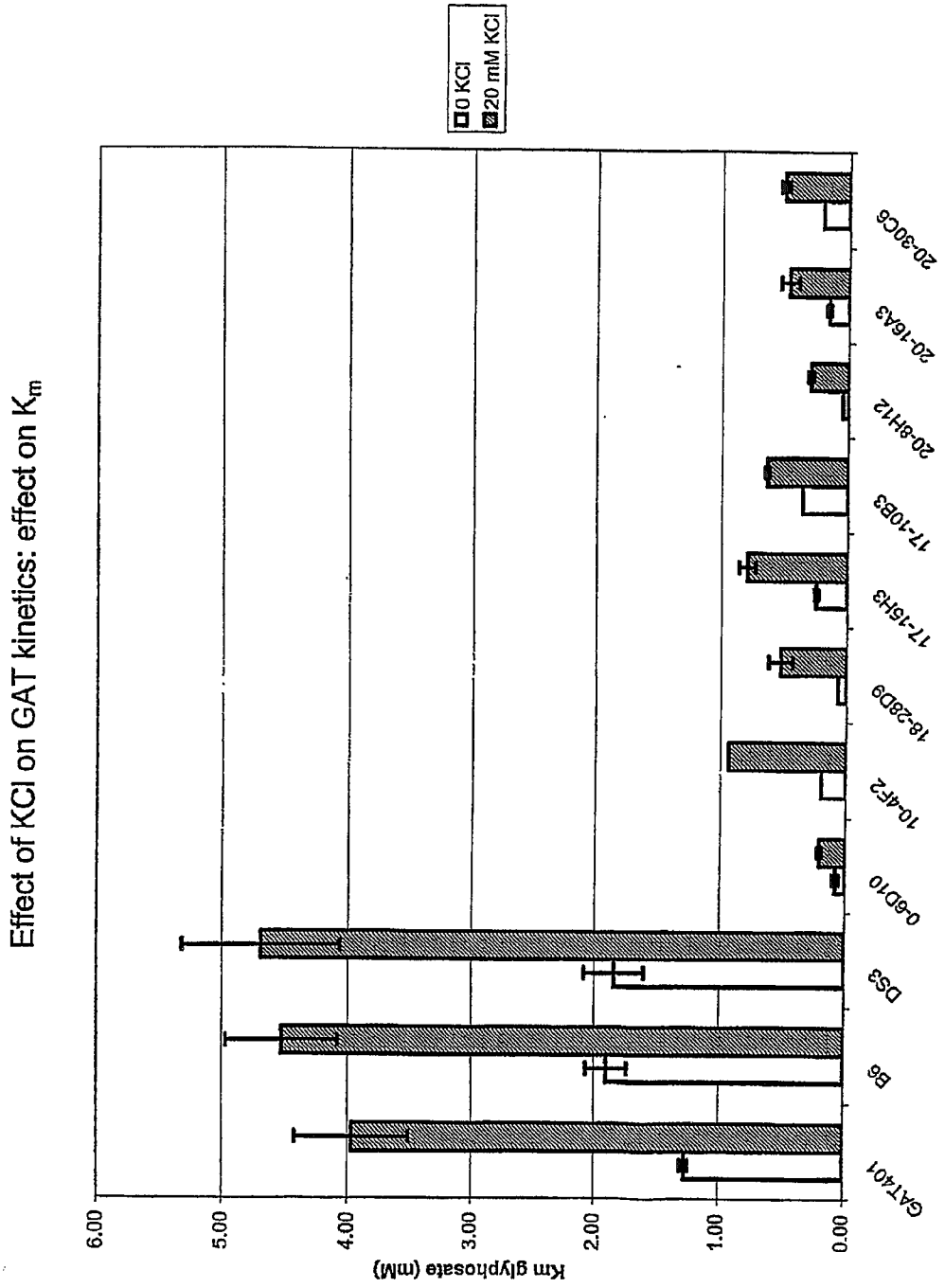

Effect of KCl on GAT kinetics: effect on K_m
0 KCl
20 mM KCl
Km glyphosate (mM)
6.00
5.00
4.00
3.00
2.00
1.00
0.00
GAT401
B6
DS3
0-6D10
10-4F2
18-2BD9
17-15H3
17-10B3
20-8H12
20-16A3
20-30C6
GAT enzyme

Fig. 15A

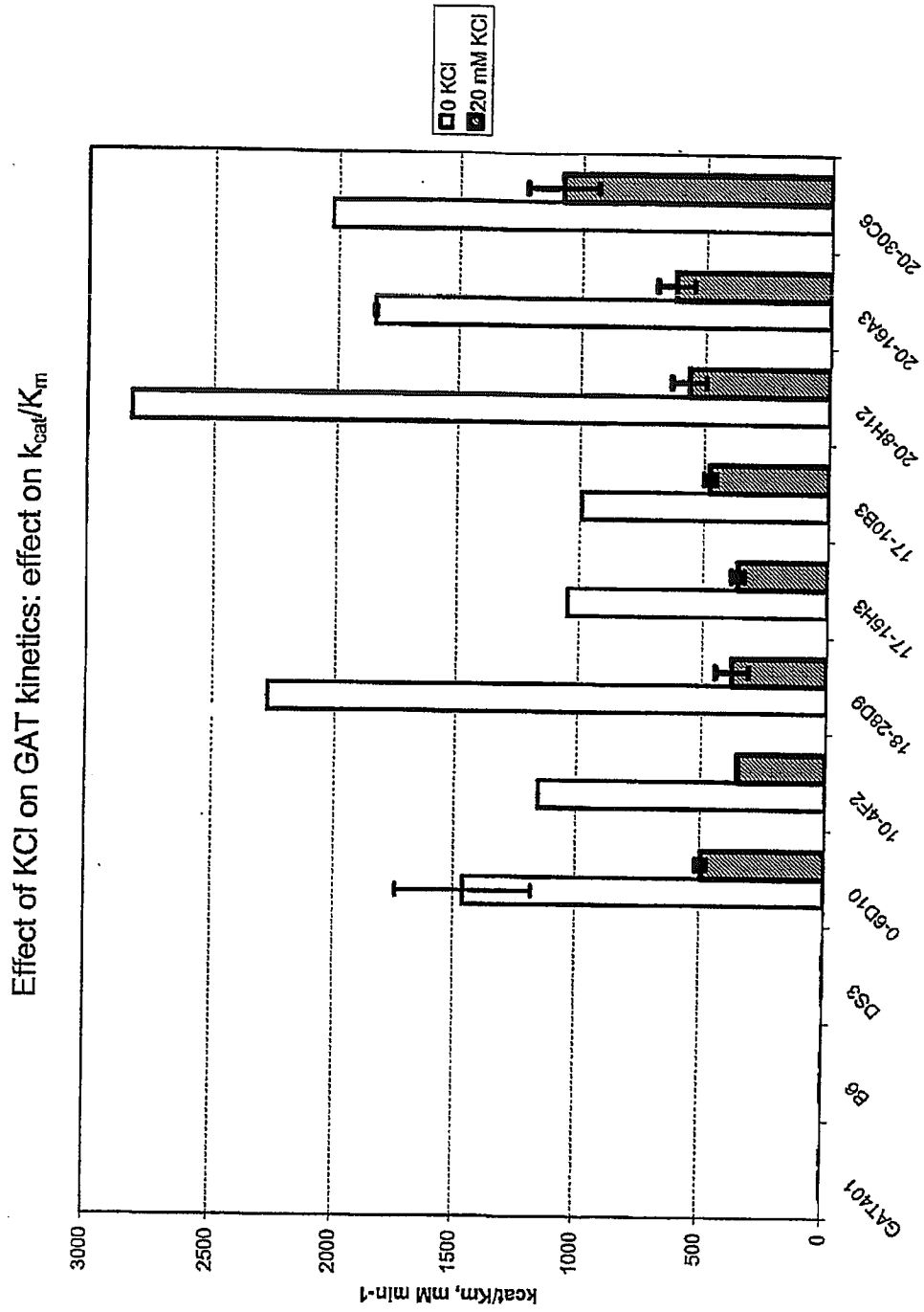

Effect of KCl on GAT kinetics: effect on k_{cat}/K_m
0 KCl
20 mM KCl
kcat/Km, mM min-1
3000
2500
2000
1500
1000
500
0
GAT401
B6
DS3
0-6D10
10-4F2
18-28D9
17-16H3
17-10B3
20-8H12
20-16A3
20-30C6
GAT enzyme

Fig. 15B

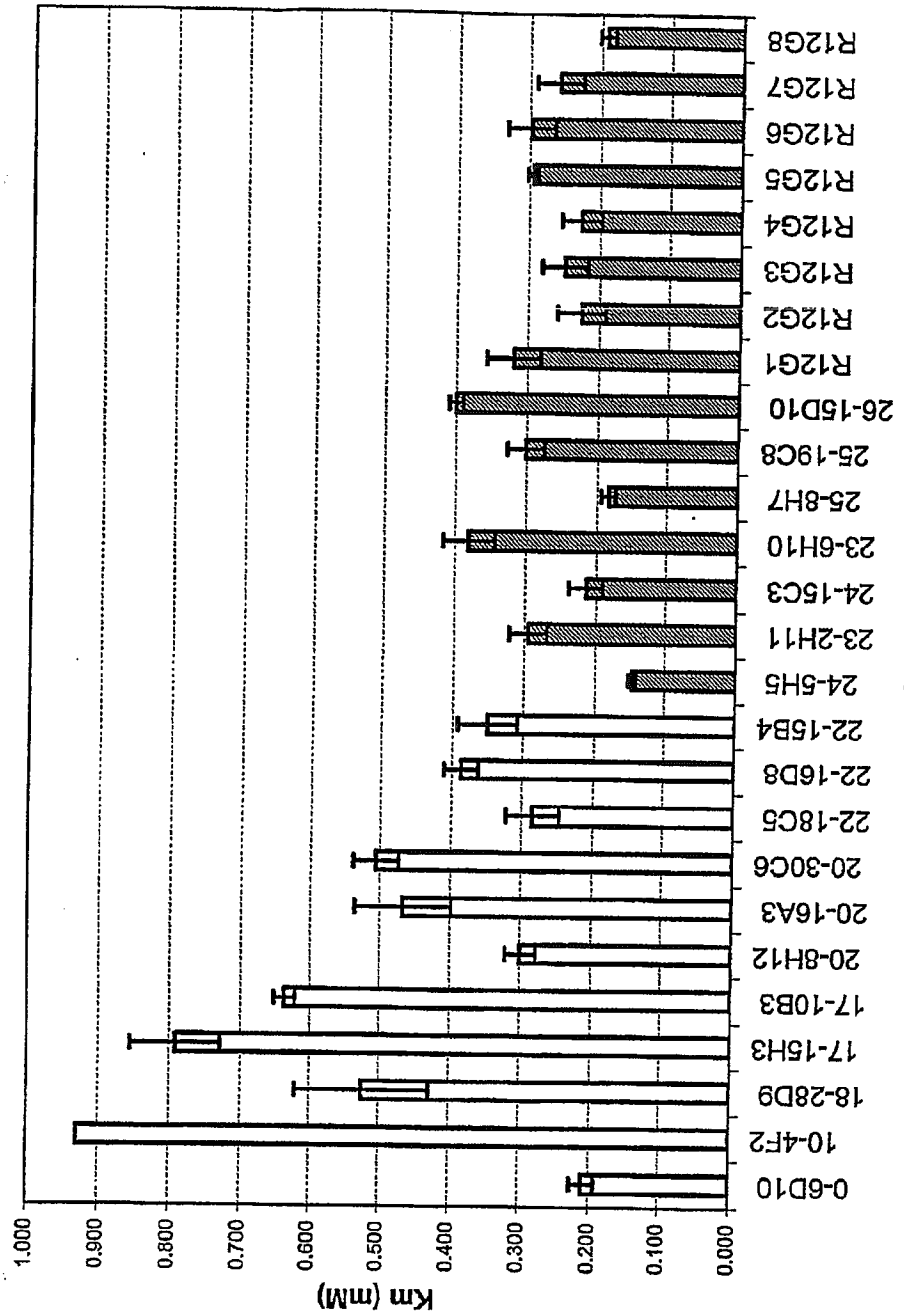

Km (mM)
1.000
0.900
0.800
0.700
0.600
0.500
0.400
0.300
0.200
0.100
0.000
0-6D10
10-4F2
18-28D9
17-15H3
17-10B3
20-8H12
20-16A3
20-30C6
22-18C5
22-16D8
22-15B4
24-5H5
23-2H11
24-15C3
23-6H10
25-8H7
25-19C8
26-15D10
R12G1
R12G2
R12G3
R12G4
R12G5
R12G6
R12G7
R12G8
GAT enzyme

Fig. 16A

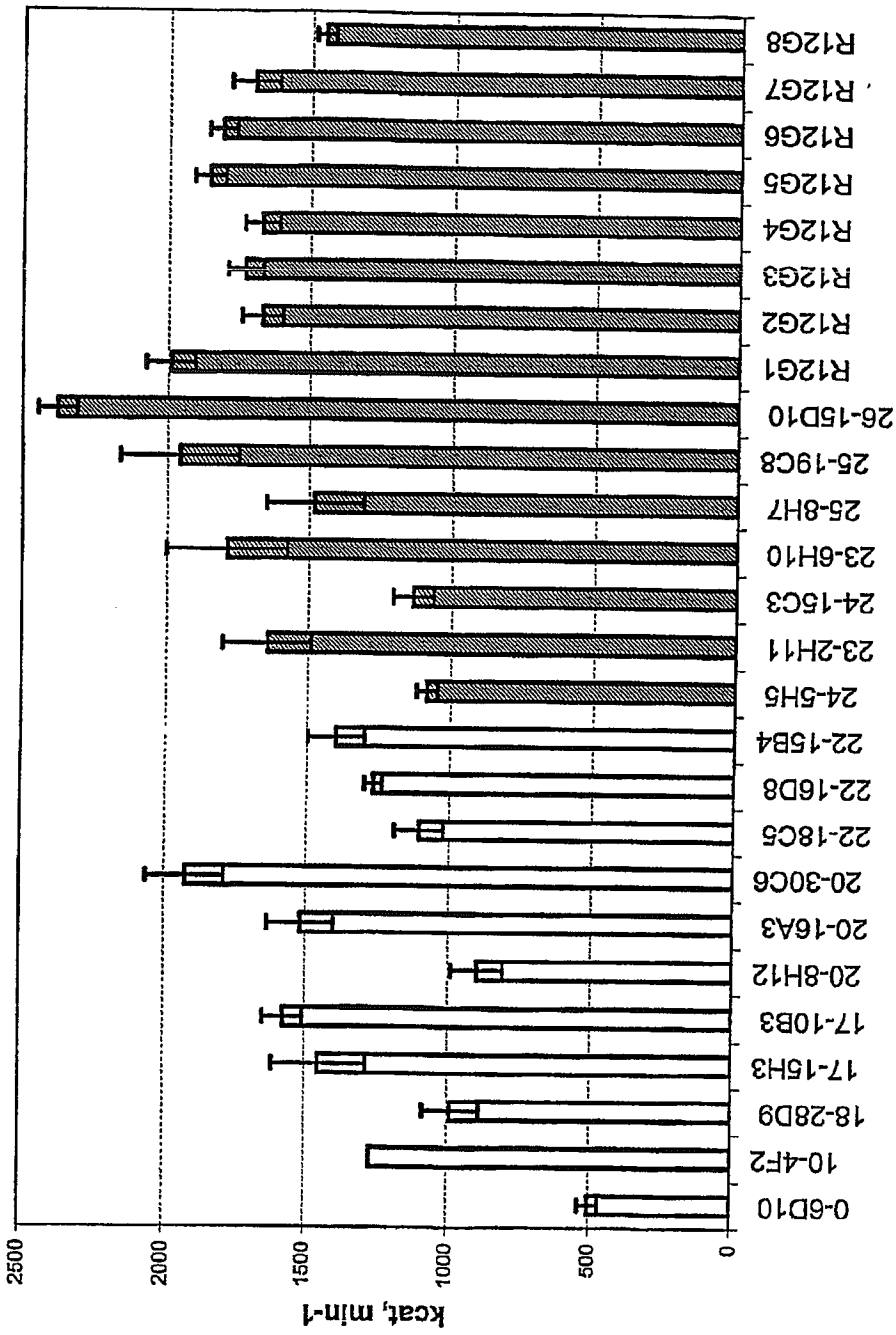

kcat, min-1
2500
2000
1500
1000
500
0
GAT enzyme
0-6D10
10-4F2
18-28D9
17-15H3
17-10B3
20-8H12
20-16A3
20-30C6
22-18C5
22-16D8
22-15B4
24-5H5
23-2H11
24-15C3
23-6H10
25-8H7
25-19C8
26-15D10
R12G1
R12G2
R12G3
R12G4
R12G5
R12G6
R12G7
R12G8

Fig. 16B

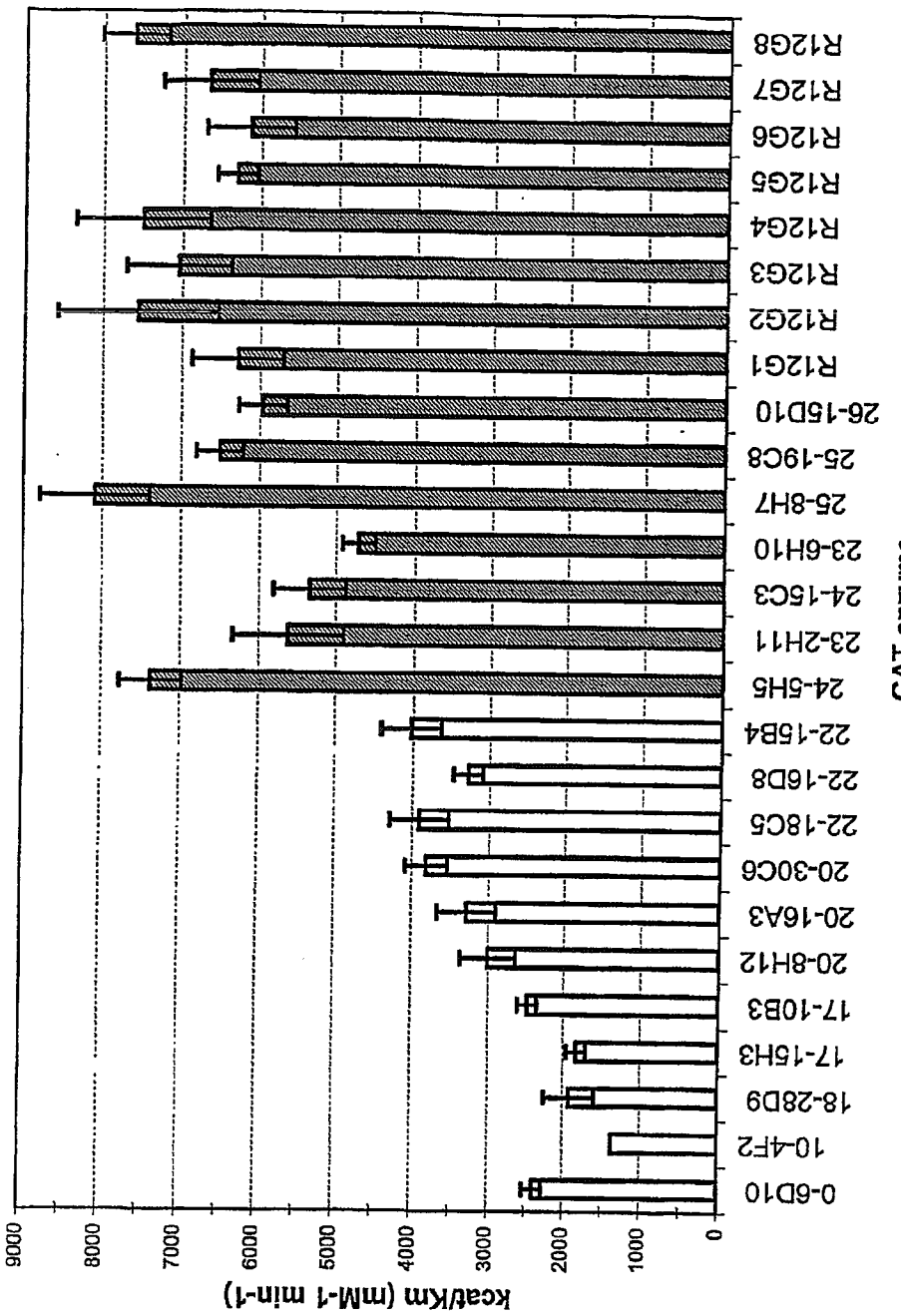

kcat/Km (mM-1 min-1)
0
1000
2000
3000
4000
5000
6000
7000
8000
9000
GAT enzyme
0-6D10
10-4F2
18-28D9
17-15H3
17-10B3
20-8H12
20-16A3
20-30C6
22-18C5
22-16D8
22-15B4
24-5H5
23-2H11
24-15C3
23-6H10
25-8H7
25-19C8
26-15D10
R12G1
R12G2
R12G3
R12G4
R12G5
R12G6
R12G7
R12G8

Fig. 16C

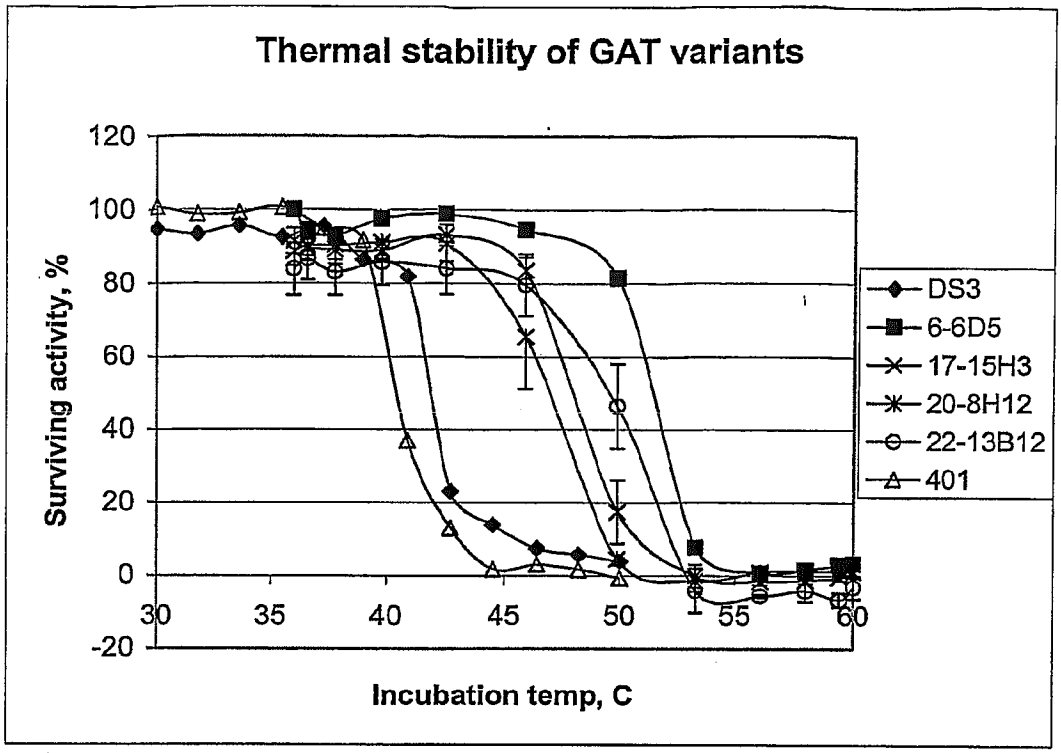

Thermal stability of GAT variants
Surviving activity, %
120
100
80
60
40
20
0
-20
30
35
40
45
50
55
60
Incubation temp, C
DS3
6-6D5
17-15H3
20-8H12
22-13B12
401

FIGURE 17

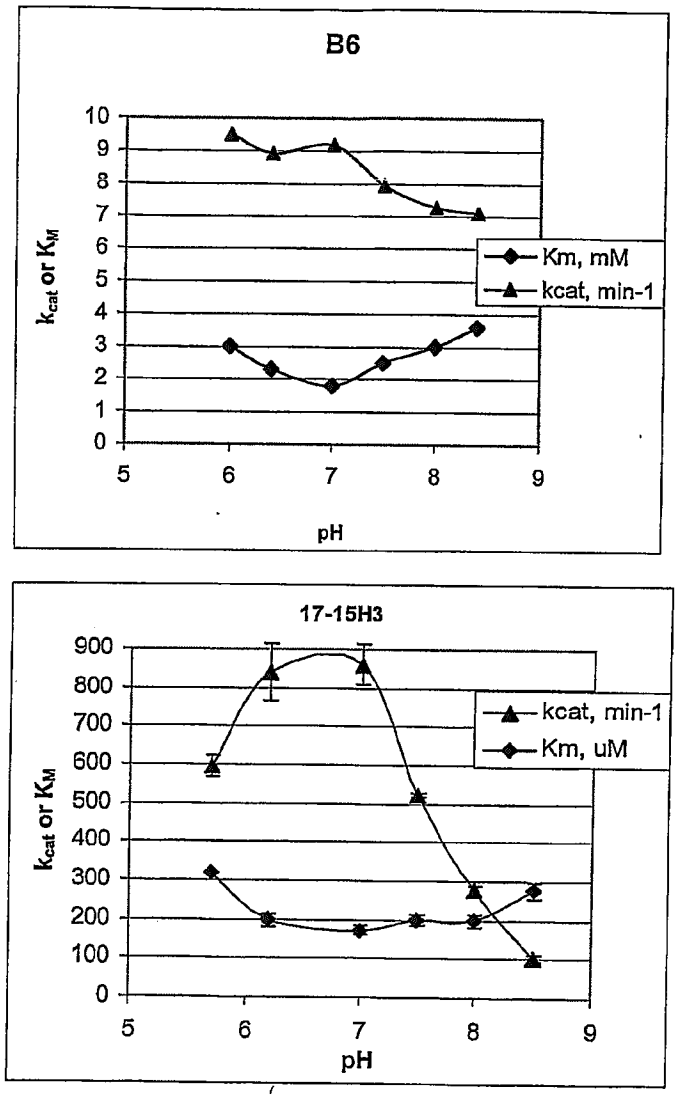

B6
10
9
8
7
6
5
4
3
2
1
0
5
6
7
8
9
pH
k_{cat} or K_M
Km, mM
kcat, min-1
17-15H3
900
800
700
600
500
400
300
200
100
0
5
6
7
8
9
pH
k_{cat} or K_M
kcat, min-1
Km, uM

FIGURE 18

SEQUENCE LISTING

<110> Castle, Linda A.
Siehl, Daniel
Giver, Lorraine
Minshull, Jeremy
Ivy, Christina
Chen, Yong Hong
Patten, Phillip
Gordon, Rebecca
Duck, Nicholas B.
McCutchen, Billy Fred
Kemble, Roger

<120> NOVEL GLYPHOSATE-N-ACETYLTRANSFERASE (GAT) GENES

<130> 035718/277848

<140>
<141> 2004-04-29

<150> US 10/427,692
<151> 2003-04-30

<150> CL 863-2003
<151> 2003-04-29

<160> 972

<170> FastSEQ for Windows Version 4.0

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<211> 441
<212> DNA
<213> Bacillus licheniformis

<220>
<223> ST401 gat

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cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca taaagccgaa 180
cattcagagc ttgaaggcga agaacagtat cagctgagag ggatggcgac gcttgaagga 240
taccgtgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaggggcag accttttatg gtgcaatgcc aggacatctg tgagcggcta ctatgaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 2
<211> 441
<212> DNA
<213> Unknown

<220>

<223> Unidentified microorganism derived from soil
sample.

<220>
<223> B6 gat

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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggcg gatattatcg ggacaggctg atcagcatcg cctcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcag acctttttatg gtgcaacgcc aggacatctg tgagcgggta ctataaaaag 360
ctcggcttca gcgaacaagg cggggtctac gatataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacata a 441

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<212> DNA
<213> Unknown

<220>
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sample.

<220>
<223> DS3

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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcgg gggtacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca taatgccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaaggg 240
taccgcgagc aaaaagcggg aagtacgctt atccgccatg ccgaagagct tcttcgaaaa 300
aaaggcgcgg acctttttatg gtgcaacgcc aggatatctg tgagcggcta ctatgaaaag 360
ctcggcttca gcgaacaagg cgggatctac gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattggcata a 441

<210> 4
<211> 441
<212> DNA
<213> Unknown

<220>
<223> Unidentified microorganism derived from soil
sample.

<220>
<223> NHA-2

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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcgg gggtacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca taatgccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaaggg 240
taccgcgagc aaaaagcggg aagtacgctt atccgccatg ccgaagagct tcttcgaaaa 300

aaaggcgcgg acctttttatg gtgcaacgcc aggatatctg tgagcggcta ctatgaaaag 360
ctcggcctca gcgaacaagg cgggatctac gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattggcata a 441

<210> 5
<211> 441
<212> DNA
<213> Unknown

<220>
<223> Unidentified microorganism derived from soil sample.

<220>
<223> NH5-2

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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcgg gggtgcgttt 120
cacctcggtg gatattacca gggcaagctg atcagcatcg cttcctttca taaagccgaa 180
cattcagagc ttgagggcga agaacagtat cagctgagag ggatggcgac gcttgaagga 240
taccgtgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaatgcc aggacatctg tgagcggcta ctatgaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 6
<211> 146
<212> PRT
<213> Bacillus licheniformis

<220>
<223> ST401 GAT

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 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Glu Glu Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Val Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 7
<211> 146
<212> PRT
<213> Unknown

<220>
<223> Unidentified microorganism derived from soil
sample.

<220>
<223> B6 GAT

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1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Asp
35 40 45
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
115 120 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 8
<211> 146
<212> PRT
<213> Unknown

<220>
<223> Unidentified microorganism derived from soil
sample.

<220>
<223> DS3 GAT

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Asn Ala Glu His Ser Glu Leu

```
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Ile
            100                 105                 110
Ser Val Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Ile Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Ala
145
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<210> 9
<211> 146
<212> PRT
<213> Unknown

<220>
<223> Unidentified microorganism derived from soil sample.

<220>
<223> NHA-2 GAT

<400> 9

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 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Asn Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Ile
            100                 105                 110
Ser Val Ser Gly Tyr Tyr Glu Lys Leu Gly Leu Ser Glu Gln Gly Gly
        115                 120                 125
Ile Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Ala
145
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<210> 10
<211> 146
<212> PRT
<213> Unknown

<220>

<223> Unidentified microorganism derived from soil sample.

<220>
<223> NH5-2 GAT

<400> 10
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Ala Phe His Leu Gly Gly Tyr Tyr Gln Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Glu Glu Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Val Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 11
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<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 13_10F6

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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac actcgaagga 240
taccgtgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttttatg gtgcaacgcc aggacgtctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a   441

<210> 12
<211> 441
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic nucleic acid sequence

<220>
<223> 13_12G6

<400> 12
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cacctcggtg gatattaccg gggcaagctg gtcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aagacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggcag acctcttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgactgggcc ccatattttg 420
atgtataaga aattgacata a 441

<210> 13
<211> 441
<212> DNA
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<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 14_2A5

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cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttaa tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgtgagc aaaaagcggg aagcacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttttatg gtgcaacgcc aggacgtctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 14
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 14_2C1

<400> 14
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cacctcggtg gatattaccg gggcaagctg gtcagcatcg cttcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac actcgaagga 240
taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacacaccgc cgactgggcc ccatattttg 420
atgtataaga aattgacgta a 441

<210> 15
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 14_2F11

<400> 15
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcag gggtgcgttt 120
caccttggtg gatattaccg gggcaagctg gtcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac actcgaagga 240
taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagcgct tcttcggaaa 300
aaggggggcag acctcttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacacaccgc cggccggacc ccatattttg 420
atgtataaga aattgacgta a 441

<210> 16
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> CHIMERA

<400> 16
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagga 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacacaccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 17
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_12D7

<220>
<221> misc_feature

<222> 54
<223> n = A,T,C or G

<400> 17
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagag 240
taccgcgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctcttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 18
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_15F4

<400> 18
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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcag gggtacgttt 120
cacctcggtg ggtattaccg gggcaagctg gtcagcatcg cttcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagag 240
taccgcgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 19
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_17D1

<400> 19
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aagggcgcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 20

<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_17F6

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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg gtcagcatcg cttcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagag 240
taccgcgagc aaaaagcggg aagcacgctt atccgccatg ccgaagagct tcttcggaaa 300
aagggcgcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 21
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_18G9

<400> 21
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cggccgaatc agccgctgga agcatgcaag tatgaaactg atttgctcgg tggcacgttt 120
cacctcggtg gatattaccg gggcaagctg gtcagcatcg cttcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagag 240
taccgcgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctcttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 22
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_1H3

<400> 22
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggtacgttt 120
cacctcggtg gatattatcg gggcaagctg gtcagcatcg cttcctttca tcaagccgaa 180

catccagagc ttgaaggccg aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgaccggacc ccatattttg 420
atgtataaga aattgacata a 441

<210> 23
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_20D10

<400> 23
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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcgg gggcacgctt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagag 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggcag acctttttatg gtgcaacgcc aggacatctg cgagcggcta ctataaaaag 360
ctcggcttca gcgaacaagg cggggtctac gacataccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 24
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_23F2

<400> 24
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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg gtcagcatcg cttcctttca tcaagccgaa 180
cacccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac actcgaagga 240
taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggcag acctcttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacacaccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 25
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_2B8

<400> 25
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggtacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagag 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctcttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacacaccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 26
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_2C7

<400> 26
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcag gggtgcgttt 120
cacctcggcg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac actcgaaggg 240
taccgtgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 27
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_3G5

<400> 27
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg gtcagcatcg cttcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgcgagc aaaaagcggg aagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 28

<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_4H7

<400> 28
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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg gtcagcatcg cttcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgaccggacc ccatattttg 420
atgtataaga aattgacgta a 441

<210> 29
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_6D11

<400> 29
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggcacgctt 120
cacctcggtg gatattaccg gggcaagctg gtcagcatcg cttcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaaggg 240
taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 30
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_8C6

<400> 30
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggtgcgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180

catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac actcgaagga 240
taccgcgagc aaaaagcggg aagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaagg cggggtctac gacataccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 31
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 11C3

<400> 31
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cggccgaatc agccgcttga agcatgcaag tatgaaaccg atttgctcgg gggtacgttt 120
cacctcggtg gatattacca gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaaggg 240
taccgcgagc aaaaagcggg aagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggcag acctttttatg gtgcaacgcc aggacatctg tgagcgggta ctataaaaag 360
ctcggcttca gcgaacaagg cggggtctac gatataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacata a 441

<210> 32
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 11G3

<400> 32
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cggccgaatc agccgcttga agcgtgtatg tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggcg gatattacca gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaaggg 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggcag acctttttatg gtgcaacgcc aggacatctg cgagcggcta ctatgaaaag 360
ctcggcttca gcgaacaagg cggggtctac gatataccgc cgatcggacc tcatattttg 420
atgtataaga aattggcata a 441

<210> 33
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 11H3

<400> 33
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcag gggtgcgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
cacccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagcgct tcttcggaaa 300
aaaggcgcgg acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc caactgggcc ccatattttg 420
atgtataaga aattgacgta a 441

<210> 34
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 12_1F9

<400> 34
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgcgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtccac gacataccgc cgaccggacc ccatattttg 420
atgtataaga aattgacgta a 441

<210> 35
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 12_2G9

<400> 35
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggtacgttt 120
cacctcggcg gatattaccg gggcaagctg gtcagcatcg cttcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagga 240
taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctcttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 36

<211> 441
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<220>
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<220>
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
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taccgtgagc aaaaagcggg aagtacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 37
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 12_5C10

<400> 37
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattatcg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
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taccgcgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 38
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 12_6A10

<400> 38
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggcg gatattaccg gggcaagctg gtcagcatcg cctcctttca tcaagccgaa 180

catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagga 240
taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggcag acctttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaagg cggggtctac gacataccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 39
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 12_6D1

<400> 39
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagag 240
taccgcgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaggggcag acctttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaagg cggggtctac gacataccgc ctgtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 40
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 12_6F9

<400> 40
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac actcgaagga 240
taccgcgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaggggcag acctttatg gtgcaacgcc aggacatctg cgagcggcta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgaccggacc ccatattttg 420
atgtataaga aattgacgta a 441

<210> 41
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 12_6H6

<400> 41
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg gtcagcatcg cctcctttca ccaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagcgct tcttcggaaa 300
aaaggcgcgg acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgaccggacc ccatattttg 420
atgtataaga aattgacata a 441

<210> 42
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 12_7D6

<400> 42
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cggccgaatc agccgctgga agcatgcaag tatgaaactg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaagg cggggtctac gacataccgc cgaccggacc ccatattttg 420
atgtataaga aattgacgta a 441

<210> 43
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 12_7G11

<400> 43
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagga 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacacaccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 44

<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 12F5

<400> 44
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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcgg gggtacgttt 120
cacctcggtg gatattacca gggcaagctg atcagcatcg cttcctttca taaagccgaa 180
cattcagagc ttgagggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaatgcc aggacatctg tgagcgggta ctataaaaag 360
ctcggcttca gcgaacaagg cgggatctac gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 45
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 12G7

<400> 45
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cggccgaatc agccgcttga agcatgcaag tatgaaaccg atttgctcgg gggtacgttt 120
cacctcggtg gatattacca gggcaagctg atcagcatcg cttcctttca taaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaagga 240
taccgtgagc aaaaagcggg aagcacactc atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcag acctttttatg gtgcaacgcc aggacatctg tgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 46
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 1_2H6

<400> 46
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cggccgaatc agccgctgga agcatgtatg tatgaaaccg atttgctcgg gggtgcgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180

cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgcgagc aaaaagcggg aagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggcag acctttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaagg cggggtctac gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 47
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 13_12G12

<400> 47
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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcgg gggtacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttaa tcaagccgaa 180
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ctcggcttca gcgaacaggg cgaagtctac gacataccgc cggtcggacc tcatattttg 420
atgcataaga aattgacgta a 441

<210> 48
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 13_6D10

<400> 48
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cggccgaatc agccgcttga agcatgtatg tatgaaaccg attcgctcgg aggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttaa tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac actcgaaggg 240
taccgtgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
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ctcggcttca gcgaacaggg cgaagtctac gacacaccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 49
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 13_7A7

<400> 49
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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcag gagtgcgttt 120
cacctcggcg gatattaccg gggcaagctg atcagcatcg cctcctttca ccaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgaggg ggatggcgac acttgaagag 240
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ctcggcttca gcgaacaggg cgaagtctac gacacaccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 50
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 13_7B12

<400> 50
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
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atgtataaga agttgacgta a 441

<210> 51
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 13_7C1

<400> 51
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atgtataaga aattgacgta a 441

<210> 52

<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 13_8G6

<400> 52
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atgtataaga aattgacgta a 441

<210> 53
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 13_9F6

<400> 53
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<210> 54
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 14_10C9

<400> 54
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagctgaa 180

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atgtataaga agttgacgta a 441

<210> 55
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 14_10H3

<400> 55
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcag gggtgcgttt 120
cacctcggcg gatattaccg gggcaagctg gtcagcatcg cctcctttca tcaagccgaa 180
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atgtataaga agttgacgta a 441

<210> 56
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 14_10H9

<400> 56
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<210> 57
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 14_11C2

<400> 57
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cacctcggcg gatattaccg gggcaagctg gtcagcatcg cttcctttca tcaagccgaa 180
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<210> 58
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 14_12D8

<400> 58
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aaaggcgcgg acctttttgtg gtgcaacgcc aggacatctg cgagcggcta ctataaaaag 360
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<210> 59
<211> 441
<212> DNA
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<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 14_12H6

<400> 59
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagag 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttttgtg gtgcaacgcc aggacgtctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 60

<211> 441
<212> DNA
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<220>
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<220>
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<400> 60
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttaa tcaagccgaa 180
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aaaggcgcgg acctttatg gtgcaacgcc aggacgtctg cgagcgggta ctataaaaag 360
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<210> 61
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 61
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cacctcggtg gatattaccg gggcaagctg gtcagcatcg cctcctttca tcaagccgaa 180
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atgtataaga aattgacgta a 441

<210> 62
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 14_3B2

<400> 62
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cacctcggtg gatattaccg gggcaagctg gtcagcatcg cctcctttca tcaggccgaa 180

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atgtataaga aattgacgta a 441

<210> 63
<211> 441
<212> DNA
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<220>
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<220>
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<400> 63
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atgtataaga aattgacgta a 441

<210> 64
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 14_6A8

<400> 64
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cacctcggtg gatattaccg gggcaagcta gtcagcatcg cttcctttaa tcaagccgaa 180
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atgtataaga aattgacgta a 441

<210> 65
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<212> DNA
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<220>
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<220>
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caccttggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
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taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
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atgtataaga agttgacgta a 441

<210> 66
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 14_6D4

<400> 66
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttaa tcaagccgaa 180
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taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagcgct tcttcggaaa 300
aaggggcag acctcttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 67
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 14_7A11

<400> 67
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcag gggtgcgttt 120
cacctcggtg gatattaccg gggcaagctg gtcagcatcg cctcctttca tcaagccgaa 180
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taccgtgagc aaaaagcggg aagtacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaggggcag acctcttatg gtgcaacgcc aggacgtctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacacaccgc cgaccggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 68

<211> 441
<212> DNA
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<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 14_7A1

<400> 68
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcag gggtgcgttt 120
cacctcggtg gatattaccg gggcaagctg gtcagcatcg cctcctttca tcaagccgaa 180
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atgtataaga aattgacgta a 441

<210> 69
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 14_7A9

<400> 69
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggtacgttt 120
cacctcggcg gatattaccg gggcaagttg gtcagcatcg cctcctttca tcaagccaaa 180
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atgtataaga aattgacgta a 441

<210> 70
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<212> DNA
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<220>
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<223> 14_7G1

<400> 70
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcag gggtgcgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttaa tcaagccgaa 180

catccagagc ttgaaggcca aaaacagtat cagttgagag ggatggcgac acttgaagag 240
taccgtgagc aaaaagcggg aagtacgctt atccgccatg ccgaagcgct tcttcggaaa 300
aaggggcag acctcttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacacaccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 71
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 14_7H9

<400> 71
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cacctcggcg gatattaccg gggcaagctg gtcagcatcg cttcctttca tcaagccgaa 180
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atgtataaga aattgacgta a 441

<210> 72
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 14_8F7

<400> 72
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cggccgaatc agccgcttga agcatgcaag tatgaaaccg atttgctcgg gggtacgttt 120
cacctcggcg gatattaccg gggcaagctg gtcagcatcg cctcctttca tcaagccgaa 180
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<210> 73
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<212> DNA
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<220>
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<223> 15_10C2

<400> 73
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atgtataaga aattgacgta a 441

<210> 74
<211> 441
<212> DNA
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<220>
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<220>
<223> 15_10D6

<400> 74
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cacctaggtg gatattaccg gggcaagctg gtcagcatcg cctcctttca tcaagccgaa 180
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aaggggcag acctcttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 75
<211> 441
<212> DNA
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<220>
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<220>
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<400> 75
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<210> 76

<211> 441
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<220>
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<210> 77
<211> 441
<212> DNA
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<220>
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<220>
<223> 15_12A8

<400> 77
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<210> 78
<211> 441
<212> DNA
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<220>
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<400> 78
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<210> 79
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<212> DNA
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<220>
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<212> DNA
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<220>
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atgtataaga aattgacata a 441

<210> 81
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 15_3F10

<400> 81
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atgtatacga aattgacgta a 441

<210> 82
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
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<400> 82
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<210> 83
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<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<400> 83
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<210> 84

<211> 441
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<220>
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<220>
<223> 15_4H3

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cacctcggcg gatattaccg gggcaagctg gtcagcatcg cttcctttca tcaagccgaa 180
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aaaggcgcgg acctttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgactgggcc ccatattttg 420
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<210> 85
<211> 441
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<220>
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<220>
<223> 15_6D3

<400> 85
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
cacccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagag 240
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<210> 86
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<213> Artificial Sequence

<220>
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<220>
<223> 15_6G11

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cacctcggtg gatattaccg gggcaagctg gtcagcatcg cctcctttca tcaagccgaa 180

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atgtataaga agttgacgta a 441

<210> 87
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 15_9F6

<400> 87
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<210> 88
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 15F5

<400> 88
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ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc tcatattttg 420
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<210> 89
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<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 16A1

<400> 89
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cacctcggtg gatattacca gggcaagctg atcagcatcg cttcctttca taaagccgaa 180
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atgtataaga aattgacgta a 441

<210> 90
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<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 16H3

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<210> 91
<211> 441
<212> DNA
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<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 17C12

<400> 91
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<210> 92

<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 18D6

<400> 92
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aaggggggcag acctttttatg gtgcaacgcc aggacatctg cgagcggcta ctatgaaaag 360
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atgtataaga aattggcata a 441

<210> 93
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

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<400> 93
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<210> 94
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<212> DNA
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<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 19D5

<400> 94
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cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaaggg 240
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aaggggcag acctttatg gtgcaatgcc aggacatctg tgagcggcta ctataaaaag 360
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<210> 95
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<220>
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<223> 20A12

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<210> 96
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<220>
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<400> 96
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ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc tcatattttg 420
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<210> 97
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

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<210> 98
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<220>
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<210> 99
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<212> DNA
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<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 24C1

<400> 99
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<210> 100

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<220>
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<220>
<223> 24C6

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<210> 101
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<220>
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<223> 24E7

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<210> 102
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<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 2_8C3

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<210> 103
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<212> DNA
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<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 2H3

<400> 103
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<210> 104
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
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<210> 105
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<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<210> 106
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

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<223> 3B_10G7

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<210> 107
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<212> DNA
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<220>
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<220>
<223> 3B_12B1

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<210> 108

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<220>
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<220>
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tccagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagga 240
taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttatg gtgcaacgcc aggatatctg cgagcgggta ctatgaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc ccatattttg 420
atgtataaga aattgacgta a 441

<210> 109
<211> 441
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<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 3B_2E5

<400> 109
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagga 240
taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aagggcgcgg acctttatg gtgcaacgcc aggacatctg cgagcggcta ctatgaaaag 360
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atgtataaga aattgacgta a 441

<210> 110
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<220>
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180

cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagga 240
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aaggggcag acctttatg gtgcaacgcc aggatatctg cgagcggcta ctataaaaag 360
ctcggcttca gcgaacaagg cggggtctac gacataccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 111
<211> 441
<212> DNA
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<220>
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<220>
<223> 3C_12H10

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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgtgggc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttatg gtgcaacgcc aggacatctg cgagcggcta ctatgaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 112
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 3C_9H8

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cacctcggcg gatattatca ggacaggctg atcagcatcg cctcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
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aaaggcgcgg acctttatg gtgcaacgcc aggatatctg cgagcggcta ctatgaaaag 360
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<210> 113
<211> 441
<212> DNA
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<220>
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<220>
<223> 4A_1B11

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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaaggg 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggcag acctttatg gtgcaacgcc aggacatctg cgagcggcta ctatgaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 114
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 4A_1C2

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cacctcggcg gatattatcg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaagag 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcag acctttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 115
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 4B_13E1

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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagag 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttttgtg gtgcaacgcc aggatatctg cgagcggcta ctatgaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 116

<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 4B_13G10

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ccataaaagg tccgcgcctt ttttccgaag aagctcttcg gcatggcgga tgagcgtgct 180
tcccgctttt tgctcgcggt acccttcaag cgtcgccatc cctctcagct gatactgttt 240
ttggccttca agctctgaat gttcggcttg atgaaaggag gcgatgctga tcagcttgcc 300
ccggtaatat ccaccgaggt gaaacgtgcc cccgagcaaa tcagtttcat acttgcatgc 360
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tattggtttg gcttcaatca t 441

<210> 117
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 4B_16E1

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cacctcggcg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
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taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 118
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 4B_17A1

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cacctcggcg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgag 180

catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaagag 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggcag acctttatg gtgcaacgcc aggacatctg cgagcggcta ctatgaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacata a 441

<210> 119
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<212> DNA
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<220>
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<220>
<223> 4B_18F11

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cacctcggcg gatattaccg gggcaagctg atcagcatcg cttcctttca taatgccgaa 180
cattcagagc ttgatggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgcgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcag acctttatg gtgcaacgcc aggacatctg tgagcggcta ctatgaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc tcatatttcg 420
atgtataaga aattgacgta a 441

<210> 120
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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cacctcggcg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
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aaggggcag acctttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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<210> 121
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 4B_1G4

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cacctcggcg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaatccgaa 180
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taccgcgagc taaaagcggg aagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
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atgtataaga aattgacgta a 441

<210> 122
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 4B_21C6

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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagag 240
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<210> 123
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<212> DNA
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<220>
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<220>
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
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aaggggggcag acctttttatg gtgcaacgcc aggacatctg cgagcggcta ctataaaaag 360
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atgtataaga aattgacata a 441

<210> 124

<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 4B_2H8

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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
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<210> 125
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<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 4B_6D8

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cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
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<210> 126
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 4B_7E8

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<210> 127
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<213> Artificial Sequence

<220>
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<210> 128
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<212> DNA
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<220>
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<223> 4H1

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<212> DNA
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<220>
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<220>
<223> 6_14D10

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<210> 130
<211> 441
<212> DNA
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<220>
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<220>
<223> 6_15G7

<400> 130
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atgtataaga aattgacgta a 441

<210> 131
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_16A5

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<210> 132

<211> 441
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<220>
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgag 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagga 240
aaccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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<220>
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<220>
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<400> 134
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cacctcggtg gatattatcg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180

catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaagga 240
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aaggggcag acctttatg gtgcaacgcc aggatatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 135
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<220>
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<220>
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
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atgtataaga aattgacgta a 441

<210> 136
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<212> DNA
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<220>
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<220>
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<400> 136
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
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aaggggcag acctttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgaccggacc ccatattttg 420
atgtataaga aattgacgta a 441

<210> 137
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 6_19B6

<400> 137
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cacctcggtg gatattatcg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
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taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aagggcgcag acctttttatg gtgcaacgcc aggacatctg cgagcggcta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 138
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<212> DNA
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<220>
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<220>
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<400> 138
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cacctcggcg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagga 240
taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 139
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_19C8

<400> 139
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagga 240
taccgtgagc aaaaagcggg cagtacgctt atccgccaag ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataagg aattgacgta a 441

<210> 140

<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_20A7

<400> 140
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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcag gggcacgttt 120
cacctcggcg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
cattcagatc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagag 240
taccgcgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 141
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_20A9

<400> 141
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tctacggaaa 300
aaaggcgcgg acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 142
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<220>
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<223> 6_20H5

<400> 142
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggcg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180

cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagga 240
taccgtgagc aaaaagcggg aagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttttatg gtgcaacgcc aggacatctg cgagcggcta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 143
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 6_21F4

<400> 143
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cggccgaatc agccgctgga agcatgtatg tatgaaaccg atttgctcgg gggtgcgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 144
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 6_22C9

<400> 144
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cggccgaatc ggccgcttga agcatgtatg tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
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taccgcgagc aaaaagcggg aagcacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttttatg gtgcaacgcc aggacttccg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 145
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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cggccgaatc agccgctgga agcatgcatg tatgaaaccg atttgctcga gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgag 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagga 240
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atgtataaga aattgacgta a 441

<210> 146
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_22H9

<400> 146
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
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ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc ccatattttg 420
atgtataaga aattgacgta a 441

<210> 147
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_23H3

<400> 147
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cggccgaatc agccgcttga agcatgtatg tatggaactg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgag 180
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aaggggggcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 148

<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_23H7

<400> 148
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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaagga 240
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atgtataaga aattgacgta a 441

<210> 149
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_2H1

<400> 149
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atgtataaga aattgacgta a 441

<210> 150
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_3D6

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cacctcggtg gatattaccg aggcaagctg atcagcatcg cctcctttca tcaagccgaa 180

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ctcggcttca gcgaacaggg cgaggtctac gacataccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 151
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 6_3G3

<400> 151
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atgtataaga aattgacgta a 441

<210> 152
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
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atgtataaga aattgacata a 441

<210> 153
<211> 441
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<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_4A10

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atgtataaga aattgacgta a 441

<210> 154
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 6_4B1

<400> 154
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atgtataaga aattgacata a 441

<210> 155
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_5D11

<400> 155
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atgtataaga aattgacgta a 441

<210> 156

<211> 441
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<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_5F11

<400> 156
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atgtataaga aattgacgta a 441

<210> 157
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 6_5G9

<400> 157
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atgtataaga aattgacgta a 441

<210> 158
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_6D5

<400> 158
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cacctcggcg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180

cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttttgtg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaagg cggggtctac gacataccgc cggtcggacc tcatattttg 420
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<220>
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<220>
<223> 6_7D1

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cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagga 240
taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggcag acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaagg cggggtctac gacataccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 160
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<220>
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<220>
<223> 6_8H3

<400> 160
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaaggg 240
taccgcgagc aaaaagcggg aagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 161
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<213> Artificial Sequence

<220>
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<220>
<223> 6_9G11

<400> 161
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaaggg 240
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aaaggcgcgg acctttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaagg cgaagtctac gacataccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 162
<211> 441
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<220>
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<220>
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<400> 162
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cacctcggtg gatattaccg gggcaagctg gtctgcatcg cttcctttca taaagccgaa 180
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atgtataaga aattgacgta a 441

<210> 163
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 7_1C4

<400> 163
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgag 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagag 240
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aaaggcgcgg acctttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

<210> 164

<211> 441
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<213> Artificial Sequence

<220>
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<220>
<223> 7_2A10

<400> 164
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catctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaaggg 240
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atgtataaga aattgacgta a 441

<210> 165
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 7_2A11

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cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgcgagc aaaaagcggg aagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaagg cggggtctac gacataccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 166
<211> 441
<212> DNA
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<220>
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<220>
<223> 7_2D7

<400> 166
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180

catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaaggg 240
taccgtgagc aaaaagcggg aagtacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttttatg gtgcaacgcc aggacatctg cgagtgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 167
<211> 441
<212> DNA
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<220>
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<223> 7_5C7

<400> 167
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
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taccgtgagc aaaaagtggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
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atgtataaga aattgacgta a 441

<210> 168
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 7_9C9

<400> 168
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
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taccgcgagc aaaaagcggg aagtacgctc atccgccatg ccgaagagct tctacggaaa 300
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atgtataaga aattgacgta a 441

<210> 169
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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caccttggtg gatattaccg gggcaagctg gtcagcatcg cctcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagag 240
taccgcgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaggggcag acctcttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgactgggcc ccatattttg 420
atgtataaga aattgacgta a 441

<210> 170
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 9_13F1

<400> 170
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caccttggtg gatattaccg gggcaagctg gtcagcatcg cctcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagag 240
taccgcgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
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<210> 171
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 9_15D5

<400> 171
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cggccgaatc agccgctgga cgcatgcaag tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
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taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
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atgtataaga aattgacgta a 441

<210> 172

<211> 441
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<213> Artificial Sequence

<220>
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<223> 9_15D8

<400> 172
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cacctcggcg gatattaccg gggcaagctg gtcagcatcg cctcctttca tcaagctgaa 180
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atgtataaga agttgacgta a 441

<210> 173
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

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<223> 9_15H3

<400> 173
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cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
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ctcggcttta gcgaacaggg cgaagtctac aacacaccgc cggttggacc tcatattttg 420
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<210> 174
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<220>
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<223> 9_18H2

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cggccgaatc agccgctgga agcatgtatg tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggcg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180

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aaggggcag acctttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
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atgtataaga aattgacgta a 441

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<220>
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atgtataaga aattgacgta a 441

<210> 176
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 9_21C8

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<210> 177
<211> 441
<212> DNA
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<220>
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<220>
<223> 9_22B1

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<210> 178
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<212> DNA
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<220>
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<220>
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<220>
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atgtataaga aattgacgta a 441

<210> 180

<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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atgtataaga aattgacata a 441

<210> 181
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<212> DNA
<213> Artificial Sequence

<220>
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<220>
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atgtataaga aattgacata a 441

<210> 182
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<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 9_8H1

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atgtataaga aattgacgta a 441

<210> 183
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 9_9H7

<400> 183
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gagcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagag 240
taccgcgagc aaaaagcggg aagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc ctgtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 184
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 9C6

<400> 184
atgattgaag tcaaaccaat aaacgcggaa gatacgtatg agatcaggca ccgcattctc 60
cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggtacgttt 120
cacctcggtg gatattaccg gggcaagctg atctgcatcg cctcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaaggg 240
taccgcgagc aaaaagcggg aagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggcag acctttatg gtgcaatgcc aggacatctg tgagaggcta ctatgaaaag 360
ctcggcttca gcgaacaagg cggggtctac gatataccgc cgatcggacc tcatattttg 420
atgtataaga aattggcgta a 441

<210> 185
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 9H11

<400> 185
atgattgaag tcaaaccaat aaacgcggaa gatacgtatg agatcaggca ccgcattctc 60
cggccgaatc agccgttgga agcatgcaag tatgaaaccg atttgctcgg gggtacgttt 120
cacctcggcg gatattaccg gggcaagctg atcagcatcg cttcctttca taaagccgaa 180
cattcagagc ttgagggcga agaacagtat cagctgagag ggatggcgac gcttgaagga 240
taccgtgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaatgcc aggacatctg tgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 186
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 0_4B10

<400> 186
atgatagaag tgaaaccgat taacgcagag gatacctatg aactaaggca taaaatactc 60
agaccaaacc agccgataga agcgtgtatg tatgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tcgaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgactcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acatgctttg gtgcaatgcg cggacaaccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 187
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 0_5B11

<400> 187
atgatagagg tgaaaccgat taacgcagag gatacctatg aactaaggca taaaatactc 60
agaccaaacc agccgataga agcgtgtatg tatgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gcttttacgg gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tcgaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgactcta attaaacacg ctgaacaact tcttcgtaag 300
agggggggcgg acatgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa agatcaca 438

<210> 188

<211> 438
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 0_5B3

<400> 188
atgctagagg tgaaaccgat taacgcagag gatacctatg aactaaggca tagaatactc 60
agaccaaacc agccgataga agcgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta attaaacacg ctgaacaact tcttcgtaag 300
agggggggcgg acttgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcaca 438

<210> 189
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 0_5B4

<400> 189
atgctagagg tgaaactgat taacgcagag gatacctatg aactaaggca tagaatactc 60
agaccaaacc agccgttaga agcgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tcgaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tttcgtgatc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggggcga acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcaca 438

<210> 190
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 0_5B8

<400> 190
atgatagagg tgaaaccgat taacgcagag gatacctatg aactaaggca taaaatactc 60
agaccaaacc agccgataga agcgtgtatg tatgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180

cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta attagacacg ctgaacaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcaca 438

<210> 191
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 0_5C4

<400> 191
atgatagagg tgaaaccgat taacgcagag gatacctatg aactaaggca taaaatactc 60
agaccaaacc agccgttaga agcgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcaggcc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtata attaaacacg ctgaagaaat tcttcgtaag 300
aaggggggcgg acttgctttg gtgcaatgcg cggacgtccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gacacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcaca 438

<210> 192
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 0_5D11

<400> 192
atgatagagg tgaaaccgat taacgcagag gatacctatg aactaaggca tagaatactc 60
agaccaaacc agccgataga agcgtgtatg tatgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgactcta attagacacg ctgaacaact tcttcgtaag 300
agggggggcgg acttgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaagg 360
ttaggcttca gcgagcaggg agaggtattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcaca 438

<210> 193
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 0_5D3

<400> 193
atgctagagg tgaaaccgat taacgcagag gatacctatg aactaaggca tagaatactc 60
agaccaaacc agccgataga agcgtgtatg tatgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 194
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 0_5D7

<400> 194
atgatagaag tgaaaccgat taacgcagag gagacctatg aactaaggca tagaatactc 60
agaccaaacc agccgataga agcgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tcgaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta attagacacg ctgaacaact tcttcgtaag 300
aaggggcga atatgctttg gtgtaatgcg cggacaaccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcaca 438

<210> 195
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 0_6B4

<400> 195
atgctagagg tgaaaccgat taacgcagag gatacctatg aactaaggca tagaatactc 60
agaccaaacc agccgataga agcgtgtatg tatgaaagcg atttacttcg tggtgcactt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tttcgtgatc agaaagcggg atcgagtcta attagacacg ctgaacaaat tcttcgtaag 300
agggggcgg acttgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg aaaggtattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcaca 438

<210> 196

<211> 438
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 0_6D10

<400> 196
atgctagagg tgaaaccgat taacgcagag gatacctatg aactaaggca taaaatactc 60
agaccaaacc agccgttaga agtgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta attagacacg ctgaacaaat tcttcgtaag 300
agggggcgg acatgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcaca 438

<210> 197
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 0_6D11

<400> 197
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggcacgctt 120
cacctcggtg gatattaccg gggcaagctg gtcagcatcg cttcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaaggg 240
taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag accttttatg gtgcaacgcc aggacatctg cgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cggtcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 198
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 0_6F2

<400> 198
atgatagagg tgaaaccgat taacgcagag gatacctatg aactaaggca tagaatactc 60
agaccaaacc agccgataga agcgtgtatg tatgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacag gggcaaactg atttccatag cttcattcca ccaggccgag 180

cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tttcgtgagc agaaagcggg atcgactcta attagacacg ctgaacaaat tcttcgtaag 300
agggggggcgg acatgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcaca 438

<210> 199
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 0_6H9

<400> 199
atgatagagg tgaaaccgat taacgcagag gatacctatg aactaaggca taaaatactc 60
agaccaaacc agccgataga agcgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacgg gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tcgaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgactcta attagacacg ctgaagaaat tcttcgtaag 300
aaggggggcga acttgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gacacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcaca 438

<210> 200
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_4C10

<220>
<221> misc_feature
<222> 134, 313
<223> n = A,T,C or G

<400> 200
atgatagagg tgaaaccgat taacgcagag gatacctatg aactaaggca taaaatactc 60
agaccaaacc agccgttaga agtgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gctnttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta attaaacacg ctgaacaaat tcttcgtaag 300
agggggggcgg acntgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 201
<211> 441
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_4D5

<400> 201
atgatagagg tgaaaccgat taacgcagag gatacctatg aactaaggca tagaatactc 60
agaccaaacc agccgataga agtgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgactcta attagacacg ctgaacaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 202
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_4F2

<400> 202
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attagacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acatgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 203
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_4F9

<400> 203
atgatagagg tgaaaccgat taacgcagag gatacctatg aactaaggca tagaatactc 60
agaccaaacc agccgataga agtgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tttcgtgagc agaaagcggg atcgagtcta attagacacg ctgaacaaat tcttcgtaag 300

agggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 204
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_4G5

<400> 204
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
taccgcgatc agaaagcggg atcgagtcta attagacacg ctgaacaaat tcttcgtaag 300
agggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 205
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 10_4H4

<400> 205
atgctagagg tgaaaccgat taacgcagag gatacctatg aactaaggca taaaatactc 60
agaccaaacc agccgttaga agtgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggcgg acttgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 206
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 11_3A11

<400> 206
atgatagaag tgaaaccgat taacgcagag gatacctatg aactgaggca taaaatactc 60
agaccaaacc agccgataga agtgtgtatg tatgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cgtcattcca ccaggccgag 180
cacccagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta attaaacacg ctgaacaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 207
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 11_3B1

<400> 207
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agaccaaacc agccgataga agcgtgtatg tttgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac caactccgag gtatggctac cttggaaggt 240
tttcgtgagc agaaagcggg atcgactcta attagacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaagg 360
ttaggcttca gcgagcaggg agagatattt gacacgccgc cagtagggcc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 208
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 11_3B5

<400> 208
atgatagagg tgaaaccgat taacgcagag gatacctatg aactaaggca tagaatactc 60
agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacag gggcaaactg atttccatag cgtcattcca ccaggccgag 180
cactcggaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta attagacacg ctgaacaaat tcttcgtaag 300
agggggggcgg acatgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 209
<211> 441
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 11_3C12

<400> 209
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cacttgggcg gcttttacgg gggcaaactg atttccatag cgtcattcca ccaggccgag 180
cacccagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta attagacacg ctgaacaact tcttcgtaag 300
agggggggcgg acttgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattc gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 210
<211> 441
<212> DNA
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<220>
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<220>
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<400> 210
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cacttaggcg gctattacag gggcaaactg atttccatag cgtcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gacacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 211
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 11_3C6

<400> 211
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cacttaggcg gcttttacgg gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tcgaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgactcta attagacacg ctgaagaaat tcttcgtaag 300

agggggcgg acttgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 212
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 11_3D6

<400> 212
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cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaacaaat tcttcgtaag 300
agggggcgg acttgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
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atgtataaaa ggctcacata a 441

<210> 213
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 1_1G12

<400> 213
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cacttaggcg gcttttacgg gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 214
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 1_1H1

<400> 214
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cgccctaatc agccgataga ggcatgcatg tatgaaagcg atctgctgcg gggctcgttc 120
catttgggcg ggttctatcg tggccaattg atctcgattg cgagtttcca caaagctgaa 180
cactcagaac tgcaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
ttccgtgagc agaaggctgg ctcttcgctt attaggcacg ccgaggagat actacggaat 300
aaaggggcag atctgctttg gtgtaatgca cgcacgacag cctccggtta ctataaaagg 360
cttggtttta gtgagcacgg cgaagttttc gaaaccccgc cggttgggcc gcacattctt 420
atgtacaaaa gaatcact 438

<210> 215
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 1_1H2

<400> 215
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cgccctaatc agccgttaga ggcatgcatg tatgaaagcg atctgctgcg gggctcgttc 120
catttgggcg ggttctatcg tggcaaattg atctcgattg cgagtttcca ccaagctgaa 180
cactcagaac tggaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
ttccgtgagc agaaggctgg ctcttcgctt attaggcacg ccgaggagat actacggaaa 300
agaggggcag atctgctttg gtgtaatgca cgcacgacag ccgccggtta ctataaaaag 360
cttggtttta gtgagcaggg cgaaattttc gacaccccgc cggttgggcc gcacattctt 420
atgtacaaaa gaatcact 438

<210> 216
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 1_1H5

<400> 216
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cgccctaatc agccgttaga ggcatgcatg tatgaaagcg atctgctgcg gggctcgttc 120
catttgggcg ggttctatcg tggcaaattg atctcgattg cgagtttcca ccaagctgaa 180
cactcagacc tggaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
taccgtgatc agaaggctgg ctcttcgctt attaggcacg ccgagcagat actacggaaa 300
agaggggcag atctgctttg gtgcaatgca cgcacgacag ccgccggtta ctataaaagg 360
cttggtttta gtgagcaggg cgaagttttc gacaccccgc cggttgggcc gcacattctt 420
atgtacaaaa aactcact 438

<210> 217
<211> 438
<212> DNA

<213> Artificial Sequence

<220>
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<220>
<223> 1_2A12

<400> 217
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catttgggcg ggttctatcg tggcaaattg atctcgattg cgagtttcca ccaagctgaa 180
cagtcagaac tggaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
taccgtgatc agaaggctgg ctctacgctt attaagcacg ccgaggagat actacggaaa 300
aaaggggcag atctgctttg gtgcaatgca cgcacgtcag ccgccggtta ctataaaagg 360
cttggtttta gtgagcaggg cgaaattttc gacaccccgc cggttgggcc gcacattctt 420
atgtacaaaa gactcact 438

<210> 218
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 1_2B6

<400> 218
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cgccctaatc agccgttaga ggcatgcatg tatgaaaccg atctgctgcg gggctcgttc 120
catttgggcg ggttctatcg tggcaaattg atctcgattg cgagtttcca ccaagctgaa 180
cactcagaac tggaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
ttccgtgatc agaaggctgg ctcttcgctt attaagcacg ccgaggagat actacggaaa 300
agaggggcag atctgctttg gtgcaatgca cgcacgtcag cctccggtta ctataaaaag 360
cttggtttta gtgagcaggg cgaaattttc gaaaccccgc cggttgggcc gcacattctt 420
atgtacaaaa gactcact 438

<210> 219
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 1_2C4

<400> 219
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cgccctaatc agccgataga ggcatgcatg tatgaaaccg atctgctgcg gggctcgttc 120
catttgggcg ggttctatcg tggccaattg atctcgattg cgagtttcca ccaagctgaa 180
cactcagacc tgcaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
taccgtgagc agaaggctgg ctctacgctt attaagcacg ccgaggagct actacggaaa 300

aaaggggcag atctgctttg gtgcaatgca cgcacgacag ccgccggtta ctataaaaag 360
cttggtttta gtgagcaggg cgaagttttc gacaccccgc cggttgggcc gcacattctt 420
atgtacaaaa aaatcact 438

<210> 220
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 1_2D2

<400> 220
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cgccctaatc agccgttaga ggcatgcatg tatgaaagcg atctgctgcg gagcgcattc 120
catttgggcg ggttctatcg tggcaaattg atctcgattg cgagtttcca caaagctgaa 180
cactcagaac tgcaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
taccgtgatc agaaggctgg ctcttcgctt attaggcacg ccgaggagat actacggaaa 300
agaggggcag atatgctttg gtgcaatgca cgcacgtcag ccgccggtta ctataaaagg 360
cttggtttta gtgagcaggg cgaagttttc gacaccccgc cggttgggcc gcacattctt 420
atgtacaaaa gaatcactta a 441

<210> 221
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 1_2D4

<400> 221
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cgccctaatc agccgataga ggcatgcatg tatgaaagcg atctgctgcg gggctcgttc 120
catttgggcg ggttctatcg tggcaaattg atctcgattg cgagtttcca ccaagctgaa 180
cactcagacc tgcaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
taccgtgagc agaaggctgg ctcttcgctt attaagcacg ccgagcagct actacggaaa 300
aaaggggcag atatgctttg gtgtaatgca cgcacgtcag ccgccggtta ctataaaagg 360
cttggtttta gtgagcacgg cgaaattttc gaaaccccgc cggttgggcc gcacattctt 420
atgtacaaaa gaatcact 438

<210> 222
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 1_2F8

<400> 222
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catttgggcg ggttctatcg tggcaaattg atctcgattg cgagtttcca ccaagctgaa 180
cattcagaac tggaagggca aaagcagtat caattacgag ggatggcgac tctcgaagga 240
taccgtgatc agaaggctgg ctcttcgctt attaggcacg ccgaggagat actacggaaa 300
agaggggcag atatgctttg gtgcaatgca cgcacgacag ccgccggtta ctataaaaag 360
cttggtttta gtgagcaggg cgaaatttac gacaccccgc cggttgggcc gcacattctt 420
atgtacaaaa aactcact 438

<210> 223
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<212> DNA
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<220>
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<220>
<223> 1_2H8

<400> 223
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catttgggcg ggttctatcg tggcaaattg atctcgattg cgagtttcca ccaagctgac 180
cactcagaac tgcaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
taccgtgagc agaaggctgg ctctacgctt attaggcacg ccgagcagat actacggaaa 300
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cttggtttta gtgagcacgg cgaaattttc gaaaccccgc cggttgggcc gcacattctt 420
atgtacaaaa gactcactta a 441

<210> 224
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 1_3A2

<400> 224
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cgccctaatc agccgataga ggcatgcatg tatgaaagcg atctgctgcg gggcgcgttc 120
catttgggcg ggttctatcg tggcaaattg atctcgattg cgagtttcca ccaagctgaa 180
cactcagacc tgcaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
taccgtgagc agaaggctgg ctcttcgctt attaggcacg ccgaggagat actacggaaa 300
aaaggggcag atatgctttg gtgcaatgca cgcacgacag ccgccggtta ctataaaagg 360
cttggtttta gtgagcaggg cgaagttttc gacaccccgc cggttgggcc gcacattctt 420
atgtacaaaa gaatcact 438

<210> 225
<211> 441
<212> DNA

<213> Artificial Sequence

<220>
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<220>
<223> 1_3D6

<400> 225
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cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
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agggggggcgg acttgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 226
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 1_3F3

<400> 226
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cgccctaatc agccgataga ggcatgcatg tatgaaagcg atctgctgcg gggctcgttc 120
catttgggcg ggttctatcg tggccaattg atctcgattg cgagtttcca ccaagctgaa 180
cactcagaac tgcaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
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cttggtttta gtgagcacgg cgaaattttc gacaccccgc cggttgggcc gcacattctt 420
atgtacaaaa gaatcact 438

<210> 227
<211> 438
<212> DNA
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<220>
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<220>
<223> 1_3H2

<400> 227
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aaaggggcag atatgctttg gtgcaatgca cgcacgtcag ccgccggtta ctataaaagg 360
cttggtttta gtgagcaggg cgaagttttc gacaccccgc cggttgggcc gcacattctt 420
atgtacaaaa aactcact 438

<210> 228
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 1_4C5

<400> 228
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cactcagacc tggaagggca aaaccagtat caattacgag ggatggcgac cctcgaagga 240
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agaggggcag atatgctttg gtgcaatgca cgcacgtcag cctccggtta ctataaaagg 360
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atgtacaaaa gactcactta a 441

<210> 229
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 1_4D6

<400> 229
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cactcagacc tggaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
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atgtacaaaa gactcact 438

<210> 230
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 1_4H1

<400> 230
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catttgggcg ggttctatcg tggcaaattg atctcgattg cgagtttcca ccaagctgaa 180
cactcagacc tgcaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
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agaggggcag atctgctttg gtgcaatgca cgcacgtcag cctccggtta ctataaaagg 360
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atgtacaaaa gactcact 438

<210> 231
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 1_5H5

<400> 231
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catttgggcg ggtactatcg tggccaattg atctcgattg cgagtttcca ccaagctgaa 180
cactcagaac tggaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
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cttggtttta gtgagcacgg cgaaattttc gacaccccgc cggttgggcc gcacattctt 420
atgtacaaaa aactcactta a 441

<210> 232
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<400> 232
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cactcagacc tagaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
taccgtgatc agaaggctgg ctctacgctt attaagcacg ccgaggagct actacggaaa 300
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cttggtttta gtgagcacgg cgaaatttac gaaaccccgc cggttgggcc gcacattctt 420
atgtacaaaa aaatcact 438

<210> 233
<211> 438
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 1_6H6

<400> 233
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cgccctaatc agccgataga ggcatgcatg tatgaaagcg atctgctgcg gggctcgttc 120
catttgggcg ggttctatcg tggccaattg atctcgattg cgagtttcca ccaagctgaa 180
cactcagacc tggaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
taccgtgatc agaaggctgg ctcttcgctt attaagcacg ccgaggagat actacggaaa 300
agaggggcag atctgctttg gtgcaatgca cgcacgtcag ccgccggtta ctataaaagg 360
cttggtttta gtgagcaggg cgaaattttc gacaccccgc cggttgggcc gcacattctt 420
atgtacaaaa aaatcact 438

<210> 234
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 3_11A10

<400> 234
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agaccaaacc agccgataga agcgtgtatg tatgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta gttaaacacg ctgaagaaat tcttcgtaag 300
agggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 235
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 3_14F6

<400> 235
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agaccaaacc agccgataga agcgtgtatg tatgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300

aggggggcgg acttgctttg gtgtaatgcg cggacgtccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 236
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> 3_15B2

<400> 236
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agaccaaacc agccgttaga agtgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gctattacgg gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
aggggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 237
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 3_6A10

<400> 237
atgatagaag tgaaaccgat taacgcagag gatacctatg aactaaggca tagaatactc 60
agaccaaacc agccgataga agcgtgtatg tatgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
aggggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 238
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 3_6B1

<400> 238
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agaccaaacc agccgataga agcgtgtatg tatgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cacccagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 239
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 3_7F9

<400> 239
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agaccaaacc agccgataga agcgtgtatg tatgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacgg gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 240
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 3_8G11

<400> 240
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agacccaacc agccgataga agtgtgtatg tatgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 241
<211> 441
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 4_1B10

<400> 241
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agaccaaacc agccgataga agtgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacgg gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta attagacacg ctgaacaaat tcttcgtaag 300
agggggggcgg acatgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 242
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 5_2B3

<400> 242
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agaccaaacc agccgttaga agtgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacgg gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta attagacacg ctgaacaaat tcttcgtaag 300
agggggggcgg acatgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 243
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 5_2D9

<220>
<221> misc_feature
<222> 9, 76, 98
<223> n = A,T,C or G

<400> 243

atgctagang tgaaaccgat taacgcagag gatacctatg aactaaggca taaaatactc 60
agaccaaacc agccgntaga agtgtgtatg tatgaaancg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta attaaacacg ctgaacaaat tcttcgtgag 300
agggggggcgg acatgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gacacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 244
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 5_2F10

<400> 244
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agaccaaacc agccgataga agtgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacgg gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta attagacacg ctgaacaaat tcttcgtaag 300
agggggggcgg acatgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 245
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_1A11

<400> 245
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agaccaaacc agccgttaga agtgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cgtcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta attagacacg ctgaacaaat tcttcgtaag 300
agggggggcgg acatgctttg gtgcaatgcg cggacatccg cctcaggcta ctacagaaag 360
ttaggcttca gcgagcaggg agaggtattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 246
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_1D5

<400> 246
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agaccaaacc agccgttaga agtgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta attagacacg ctgaacaaat tcttcgtaag 300
agggggcgg acatgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg ggaggtattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 247
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_1F11

<400> 247
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agaccaaacc agccgttaga agtgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attagacacg ctgaacaaat tcttcgtaag 300
agggggcgg acatgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 248
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_1F1

<400> 248
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agaccaaacc agccgttaga agtgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attagacacg ctgaacaaat tcttcgtaag 300
agggggcgg acatgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gaaacgccgc cagtaggacc tcacatcctg 420

atgtataaaa ggctcacata a 441

<210> 249
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_1H10

<400> 249
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agaccaaacc agccgttaga agtgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacgg gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcggacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta attagacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acatgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gacacgccgc cagtaggacc tcacatcctg 420
atgtataaaa agatcacata a 441

<210> 250
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 6_1H4

<400> 250
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agaccaaacc agccgttaga agtgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacgg gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgactcta attaaacacg ctgaacaaat tcttcgtaag 300
agggggggcgg acatgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 251
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 8_1F8

<400> 251

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agaccaaacc agccgttaga agtgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
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ttaggcttca gcgagcaggg agagatattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 252
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 8_1G2

<400> 252
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cacttaggcg gctattacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gagacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacgta a 441

<210> 253
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 8_1G3

<400> 253
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agaccaaacc agccgataga agtgtgtatg tatgaaaccg atttacttcg tggtgcattt 120
cacttaggcg gctattacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attagacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacgta a 441

<210> 254
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 8_1H7

<400> 254
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cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
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ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 255
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 8_1H9

<400> 255
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cacttaggcg gctattacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attagacacg ctgaagaaat tcttcgtaag 300
agggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 256
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> GAT1_21F12

<400> 256
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cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggcg gatattaccg gggcaagctg atcagcatcg cttcctttca taatgccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaagga 240
taccgtgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcgg acctttttatg gtgcaacgcc aggacatctg tgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc tcatattttg 420

atgtataaga aattgacgta a 441

<210> 257
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> GAT1_24G3

<400> 257
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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cctcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaatgcc aggacatttg tgagcggtta ctatgaaaag 360
ctcggtttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc ttatattttg 420
atgtattaga aattgacata a 441

<210> 258
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> GAT1_29G1

<400> 258
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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcgg gggtacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgcgagc aaaaagcggg tagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaacgcc aggacatctg tgagcgggta ctataaaaag 360
ctcggcttca gcgaacaagg cggggtctgc gatataccgc cgatcggacc tcatattttg 420
atgtataaga aattggcata a 441

<210> 259
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> GAT1_32G1

<400> 259

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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcag acctttttatg gtgcaacgcc aggacatctg tgagcggcta ctatgaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacata a 441

<210> 260
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> GAT2_15G8

<400> 260
atgattgaag tcaaaccaat aaacgcggaa gatacgtatg agatcaggca ccgcattctc 60
cggccgaatc agccgctgga agcatgcaag tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca taatgccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac gcttgaaggg 240
taccgcgagc aaaaagcggg aagcacgctc atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcag acctttttatg gtgcaacgcc aggacatctg tgagcgggta ctataaaaag 360
ctcggcttca gcgaacaggg cgaagtctac gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 261
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> GAT2_19H8

<400> 261
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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
catccagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaaggg 240
taccgcgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaaggcgcag acctttttatg gtgcaacgcc aggacatctg tgagcggcta ctatgaaaag 360
ctcggcttca gcgaacaggg cgaagtctgc gacataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacata a 441

<210> 262
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<223> GAT2_21F1

<400> 262
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cggccgaatc agccgcttga agcatgtatg tatgaaaccg atttgctcgg gggcacgttt 120
cacctcggtg gatattaccg gggcaagctg atcagcatcg cttcctttca tcaagccgaa 180
cattcagagc ttgaaggcca aaaacagtat cagctgagag ggatggcgac acttgaagga 240
taccgtgagc aaaaagcggg cagtacgctt atccgccatg ccgaagagct tcttcggaaa 300
aaggggggcag acctttttatg gtgcaacgcc aggacatctg tgagcgggta ctataaaaag 360
ctcggcttca gcgaacaagg cggggtctac gatataccgc cgatcggacc tcatattttg 420
atgtataaga aattgacgta a 441

<210> 263
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 13_10F6

<400> 263
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 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 264
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Protein Sequence

<220>
<223> 13_12G6

<400> 264
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Arg Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 265
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_2A5

<400> 265
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Ser Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe Asn Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125

Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 266
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_2C1

<400> 266
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Thr Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 267
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_2F11

<400> 267
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30

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Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Ala
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Thr Pro Pro Ala Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 268
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> CHIMERA

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<400> 268
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 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 269
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_12D7

<400> 269
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Leu His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 270
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_15F4

<400> 270
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110

Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
115 120 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 271
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_17D1

<400> 271
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 272
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_17F6

<400> 272
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15

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His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 273
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_18G9

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<400> 273
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 274
<211> 146

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_1H3

<400> 274
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Arg Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 275
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_20D10

<400> 275
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Leu His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95

Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
115 120 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 276
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_23F2

<400> 276
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 277
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_2B8

<400> 277

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 278
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_2C7

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<400> 278
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 279
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_3G5

<400> 279
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 280
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_4H7

<400> 280
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80

Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 281
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_6D11

<400> 281
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Gly Thr Leu His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 282
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_8C6

<400> 282
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 283
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 11C3

<400> 283
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Gln Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 284
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 11G3

<400> 284
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Gln Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Ala
145

<210> 285
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 11H3

<400> 285
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Ala Phe His Leu Gly Gly Tyr Tyr Gln Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50   55   60

Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Val Arg Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Gly
115 120 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 286
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 12_1F9

<400> 286
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val His Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 287
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 12_2G9

<400> 287
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 288
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 12_3F1

<400> 288
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140

Leu Thr
145

<210> 289
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 12_5C10

<400> 289
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ala Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 290
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 12_6A10

<400> 290
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45

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Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 291
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 12_6D1

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<400> 291
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 292
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Protein Sequence

<220>
<223> 12_6F9

<400> 292
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 293
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 12_6H6

<400> 293
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Ala
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125

Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 294
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 12_7D6

<400> 294
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
115 120 125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 295
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 12_7G11

<400> 295
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30

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Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 296
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 12F5

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<400> 296
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Gln Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Ile Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 297
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 12G7

<400> 297
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Gln Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 298
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_2H6

<400> 298
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110

Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
115 120 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 299
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 13_12G12

<400> 299
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe Asn Gln Ala Glu His Pro Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met His Lys Lys
130 135 140
Leu Thr
145

<210> 300
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 13_6D10

<400> 300
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15

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His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Ser Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe Asn Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 301
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 13_7A7

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<400> 301
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Ser Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 302
<211> 146

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 13_7B12

<400> 302
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Ser Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 303
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 13_7C1

<400> 303
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95

Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Arg Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 304
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 13_8G6

<400> 304
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30
Thr Asp Ser Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe Asn Gln Ala Glu His Pro Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
115 120 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 305
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 13_9F6

<400> 305

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 306
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_10C9

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<400> 306
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 307
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_10H3

<400> 307
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 308
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_10H9

<400> 308
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80

Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 309
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_11C2

<400> 309
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Ser Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Ala
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Thr Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 310
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_12D8

<400> 310
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Ala
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Arg Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 311
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_12H6

<400> 311
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 312
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_2B6

<400> 312
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe Asn Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 313
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_2G11

<400> 313
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60

Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 314
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_3B2

<400> 314
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Ala
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
115 120 125
Val Tyr Asp Ile Pro Pro Ala Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 315
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_4H8

<400> 315
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Ser Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 316
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_6A8

<400> 316
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe Asn Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Val Leu Met Tyr Lys Lys
    130   135   140

Leu Thr
145

<210> 317
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_6B10

<400> 317
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Met Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 318
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_6D4

<400> 318
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45

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Lys Leu Ile Ser Ile Ala Ser Phe Asn Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Ala
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 319
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_7A11

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<400> 319
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Leu Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Thr Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 320
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Protein Sequence

<220>
<223> 14_7A1

<400> 320
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Thr Pro Pro Ala Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 321
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_7A9

<400> 321
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Lys His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125

Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 322
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_7G1

<400> 322
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe Asn Gln Ala Glu His Pro Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Ala
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 323
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_7H9

<400> 323
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30

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Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 324
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 14_8F7

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<400> 324
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Ala
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 325
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 15_10C2

<400> 325
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Thr Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 326
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 15_10D6

<400> 326
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110

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Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145


<210> 327
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 15_11F9

<400> 327
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Val Ser Ile Ala Ser Phe Asn Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Arg Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145


<210> 328
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 15_11H3

<400> 328
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
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His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Ala
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 329
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 15_12A8

<400> 329

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Ala
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 330
<211> 146

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 15_12D6

<400> 330
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 331
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 15_12D8

<400> 331
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95

Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Lys
115 120 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 332
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 15_12D9

<400> 332
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30
Thr Asp Leu Leu Arg Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 333
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 15_3F10

<400> 333

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Val Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Thr Pro Pro Ala Gly Pro His Ile Leu Met Tyr Thr Lys
    130                 135                 140
Leu Thr
145
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<210> 334
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 15_3G11

<400> 334

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 335
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 15_4F11

<400> 335
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Lys Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe Asn Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Ala
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 336
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 15_4H3

<400> 336
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80

Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 337
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 15_6D3

<400> 337
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 338
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 15_6G11

<400> 338
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Lys
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 339
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 15_9F6

<400> 339
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Arg Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 340
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 15F5

<400> 340
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Glu Glu Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg Tyr Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 341
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 16A1

<400> 341
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Leu His Leu Gly Gly Tyr Tyr Gln Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Gly Leu
    50   55   60

Glu Gly Glu Glu Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Val Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 342
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 16H3

<400> 342
Met Ile Asp Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Gln Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Val Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 343
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 17C12

<400> 343
Met Ile Glu Val Lys Pro Ile Ser Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Ala Phe His Leu Gly Gly Tyr Tyr Gln Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Val Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 344
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 18D6

<400> 344
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140

Leu Ala
145

<210> 345
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 19C6

<400> 345
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Cys Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Val Arg Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Ala
145

<210> 346
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 19D5

<400> 346
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Cys Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Gln Gly
        35   40   45

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Lys Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 347
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 20A12

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<400> 347
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Gln Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Asn Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Ile Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Ala
145
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<210> 348
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Protein Sequence

<220>
<223> 20F2

<400> 348
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Val Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 349
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 21E11

<400> 349
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Ala Phe His Leu Gly Gly Tyr Tyr Gln Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125

Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 350
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 23H11

<400> 350
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Gln Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Ala
145

<210> 351
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 24C1

<400> 351
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30

Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Asp
        35   40   45
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 352
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 24C6

<400> 352
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Ile
            100   105   110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Ala
145

<210> 353
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 24E7

<400> 353
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Asn Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Ala
145

<210> 354
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 2_8C3

<400> 354
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Asp
        35   40   45
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110

Ser Ala Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 355
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 2H3

<400> 355
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Gln Gly
35 40 45
Lys Leu Ile Ser Thr Ala Ser Phe His Gln Ala Gly His Ser Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Arg Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Ile
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
115 120 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 356
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 30G8

<400> 356
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15

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His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Phe Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Ala Phe His Leu Gly Gly Tyr Tyr Gln Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 357
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 3B_10C4

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<400> 357
Met Ile Glu Val Arg Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ala Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 358
<211> 146

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 3B_10G7

<400> 358
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 359
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 3B_12B1

<400> 359
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95

Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 360
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 3B_12D10

<400> 360
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Pro Ala Glu His Ser Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Ile
100 105 110
Ser Ala Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 361
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 3B_2E5

<400> 361

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Lys Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 362
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 3C_10H3

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<400> 362
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Ile
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 363
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 3C_12H10

<400> 363
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Gly Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 364
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 3C_9H8

<400> 364
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Gln Asp
        35   40   45
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80

Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg Tyr Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Ile
100 105 110
Ser Ala Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 365
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 4A_1B11

<400> 365
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 366
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 4A_1C2

<400> 366
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 367
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 4B_13E1

<400> 367
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Ile
            100   105   110
Ser Ala Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 368
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 4B_13G10

<400> 368
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro Tyr Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 369
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 4B_16E1

<400> 369
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60

Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
115 120 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 370
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 4B_17A1

<400> 370
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 371
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 4B_18F11

<400> 371
Met Ile Glu Val Asn Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Ser His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Asn Ala Glu His Ser Glu Leu
    50   55   60
Asp Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Val Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Ser Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 372
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 4B_19C8

<400> 372
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140

Leu Ala
145

<210> 373
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 4B_1G4

<400> 373
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ser Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Leu Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Ile
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 374
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 4B_21C6

<400> 374
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45

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Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Ile
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 375
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 4B_2H7

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<400> 375
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Val Tyr Gly Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 376
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Protein Sequence

<220>
<223> 4B_2H8

<400> 376
Met Ile Glu Ala Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 377
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 4B_6D8

<400> 377
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu His Gly Glu
        115   120   125

Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 378
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 4B_7E8

<400> 378
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 379
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 4C_8C9

<400> 379
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
20 25 30

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Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
```

<210> 380
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 4H1

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<400> 380
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Ala Phe His Leu Gly Gly Tyr Tyr Gln Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Val His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 381
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_14D10

<400> 381
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly His Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 382
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_15G7

<400> 382
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110

Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 383
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_16A5

<400> 383
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
20 25 30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
115 120 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 384
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_16F5

<400> 384
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15

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His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Val His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
```

<210> 385
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_17C5

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<400> 385
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Ala Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Asn Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Val Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 386
<211> 146

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_18C7

<400> 386
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Arg Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Ile
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 387
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_18D7

<220>
<221> VARIANT
<222> 17
<223> Xaa = Any Amino Acid

<400> 387
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
Xaa Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu

```
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
```

<210> 388
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_19A10

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<400> 388
Met Ile Glu Ala Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
```

<210> 389
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_19B6

<400> 389
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 390
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_19C3

<400> 390
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys

```
    130                 135                 140
Leu Thr
145


<210> 391
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_19C8

<400> 391
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Leu His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg Gln Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Glu
    130                 135                 140
Leu Thr
145


<210> 392
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_20A7

<400> 392
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
```

```
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
```

<210> 393
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_20A9

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<400> 393
Met Ile Glu Val Lys Pro Ile Asn Ala Gly Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 394
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_20H5

<400> 394
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 395
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_21F4

<400> 395
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu

```
        115                 120                 125
Val Tyr Asp Val Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145


<210> 396
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_22C9

<400> 396
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Arg Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Gly Leu
    50                  55                  60
Glu Gly Lys Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145


<210> 397
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_22D9

<400> 397
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
```

```
            20                  25                  30
Thr Asp Leu Leu Glu Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145


<210> 398
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_22H9

<400> 398
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Asp Glu
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145


<210> 399
<211> 146
<212> PRT
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<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_23H3

<400> 399
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Gly
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu Gln Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 400
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_23H7

<400> 400
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr

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            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145


<210> 401
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_2H1

<400> 401
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Pro Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145


<210> 402
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_3D6

<400> 402
Met Ile Glu Ile Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
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 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 403
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_3G3

<400> 403

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 404

<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_3H2

<400> 404
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 405
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_4A10

<400> 405
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu

```
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 406
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_4B1

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<400> 406
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Gly Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Gly Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 407
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_5D11

<400> 407
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 408
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_5F11

<400> 408
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val His Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 409
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_5G9

<400> 409
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Ile
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 410
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_6D5

<400> 410
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Ala Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly

65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
115 120 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 411
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_7D1

<400> 411
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
20 25 30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
115 120 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 412
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>

<223> 6_8H3

<400> 412
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 413
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_9G11

<400> 413
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Leu His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr

145

<210> 414
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6F1

<400> 414
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Cys Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Asp Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Val Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 415
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 7_1C4

<400> 415
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu

```
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 416
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 7_2A10

<400> 416

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 417
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 7_2A11

<400> 417
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 418
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 7_2D7

<400> 418
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys

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    130                 135                 140
Leu Thr
145


<210> 419
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 7_5C7

<400> 419
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Val Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145


<210> 420
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 7_9C9

<400> 420
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
```

```
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 421
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 9_13F10

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<400> 421
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 422
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 9_13F1

<400> 422
Met Ile Glu Ala Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 423
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 9_15D5

<400> 423
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Asp Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu

```
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145


<210> 424
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 9_15D8

<400> 424
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Ala
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145


<210> 425
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 9_15H3

<400> 425
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
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            20                  25                  30
Thr Asp Met Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65                  70                  75                  80
Tyr His Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asn Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 426
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 9_18H2

<400> 426

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Val Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 427
<211> 146
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 9_20F12

<400> 427
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Glu Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 428
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 9_21C8

<400> 428
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr

```
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Asp Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145


<210> 429
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 9_22B1

<400> 429
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Leu Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145


<210> 430
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 9_23A10

<400> 430
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
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 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Leu His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Gly Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 431
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 9_24F6

<400> 431

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Ala
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 432

<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 9_4H10

<400> 432
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Leu His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Ile Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 433
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 9_4H8

<400> 433
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe Asn Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu

```
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 434
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 9_8H1

<400> 434

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Met Ile Glu Val Lys Pro Ile Thr Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Thr Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 435
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 9_9H7

<400> 435
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Ala Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Ser Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Glu
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 436
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 9C6

<400> 436
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Gln Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Asn Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Val Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Ala
145

<210> 437
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 9H11

<400> 437
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Glu Glu Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 438
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 0_4B10

<400> 438
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly

65 70 75 80
Tyr Arg Asp Gln Lys Ala Gly Ser Thr Leu Ile Lys His Ala Glu Glu
85 90 95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
100 105 110
Thr Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140
Leu Thr
145

<210> 439
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 0_5B11

<400> 439
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
20 25 30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Asp Gln Lys Ala Gly Ser Thr Leu Ile Lys His Ala Glu Gln
85 90 95
Leu Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Ile Thr
145

<210> 440
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>

<223> 0_5B3

<400> 440
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Gln
                85   90   95
Leu Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 441
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 0_5B4

<400> 441
Met Leu Glu Val Lys Leu Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Phe Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asn Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr

145

<210> 442
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 0_5B8

<400> 442
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Leu Thr
145

<210> 443
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 0_5C4

<400> 443
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Gly Leu

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    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Ile Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 444
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 0_5D11

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<400> 444
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Gln
                85                  90                  95
Leu Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145
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<210> 445
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 0_5D3

<400> 445
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 446
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 0_5D7

<400> 446
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Glu Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asn Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Thr Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg

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    130                 135                 140
Ile Thr
145


<210> 447
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 0_6B4

<400> 447
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Leu His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Phe Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Lys
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 448
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 0_6D10

<400> 448
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
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        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145
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<210> 449
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 0_6D11

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<400> 449
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Phe Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 450
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 0_6F2

<400> 450
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Phe Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Gln
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 451
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 0_6H9

<400> 451
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Lys Gly Ala Asn Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu

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        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145


<210> 452
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_4C10

<220>
<221> VARIANT
<222> 45, 105
<223> Xaa = Any Amino Acid

<400> 452
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Xaa Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Gln
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Xaa Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145


<210> 453
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_4D5
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<400> 453
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Gln
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 454
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_4F2

<400> 454
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Leu Thr
145

<210> 455
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_4F9

<400> 455
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Phe Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Leu Thr
145

<210> 456
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_4G5

<400> 456
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60

Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
85 90 95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140
Leu Thr
145

<210> 457
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 10_4H4

<400> 457
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
20 25 30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
50 55 60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
85 90 95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140
Ile Thr
145

<210> 458
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 11_3A11

<400> 458
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Gln
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Leu Thr
145

<210> 459
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 11_3B1

<400> 459
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Phe Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140

Leu Thr
145

<210> 460
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 11_3B5

<400> 460
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 461
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 11_3C12

<400> 461
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45

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Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Asp Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
                85                  90                  95
Leu Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 462
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 11_3C3

<400> 462
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Leu His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 463
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
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<223> Synthetic Protein Sequence

<220>
<223> 11_3C6

<400> 463
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 464
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 11_3D6

<400> 464
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Gln
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125

Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140
Leu Thr
145

<210> 465
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_1G12

<400> 465
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
20 25 30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
50 55 60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
85 90 95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140
Leu Thr
145

<210> 466
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_1H1

<400> 466
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Glu Thr Tyr Glu Leu Arg
1 5 10 15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
20 25 30

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Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Gln Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Phe Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Asn Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Thr Ala Ser Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu His Gly Glu
        115                 120                 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 467
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_1H2

<400> 467

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Phe Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Thr Ala Ala Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 468
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_1H5

<400> 468
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Thr Ala Ala Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 469
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_2A12

<400> 469
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu Gln Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Asp Gln Lys Ala Gly Ser Thr Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110

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Ser Ala Ala Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145
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<210> 470
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_2B6

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<400> 470
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Glu Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Phe Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145
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<210> 471
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_2C4

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<400> 471
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Glu Thr Tyr Glu Leu Arg
 1               5                  10                  15
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His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Gln Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Thr Ala Ala Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Ile Thr
145


<210> 472
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_2D2

<400> 472
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Ser Asp Leu Leu Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ala Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 473
<211> 146
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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_2D4

<400> 473
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Gln
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ala Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu His Gly Glu
        115   120   125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 474
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_2F8

<400> 474
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85   90   95

Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
100 105 110
Thr Ala Ala Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Ile Tyr Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 475
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_2H8

<400> 475
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Glu Thr Tyr Glu Leu Arg
1 5 10 15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
20 25 30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Asp His Ser Glu Leu
50 55 60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Gln
85 90 95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ala Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu His Gly Glu
115 120 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140
Leu Thr
145

<210> 476
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_3A2

<400> 476

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Lys Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Thr Ala Ala Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 477
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_3D6

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<400> 477
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20                  25                  30
Ser Asp Leu Leu Gln Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Gln Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Phe Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ala Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu His Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Ala Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 478
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_3F3

<400> 478
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Glu Thr Tyr Glu Leu Arg
 1   5   10   15
Gln Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Gln Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ala Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu His Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 479
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_3H2

<400> 479
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Gln Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80

Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Lys His Ala Glu Gln
                85   90   95
Leu Leu Arg Glu Lys Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ala Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 480
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_4C5

<400> 480
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Asp Leu
    50   55   60
Glu Gly Gln Asn Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu His Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Leu Thr
145

<210> 481
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_4D6

<400> 481
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Gln Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Asp Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Gln
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ala Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Leu Thr
145

<210> 482
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_4H1

<400> 482
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Gln
                85   90   95
Leu Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu His Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Leu Thr
145

<210> 483
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_5H5

<400> 483
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Glu Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Gln Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Phe Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Lys His Ala Glu Gln
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ala Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu His Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 484
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_6F12

<400> 484
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Glu Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60

Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Asp Gln Lys Ala Gly Ser Thr Leu Ile Lys His Ala Glu Glu
85 90 95
Leu Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ala Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu His Gly Glu
115 120 125
Ile Tyr Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Ile Thr
145

<210> 485
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 1_6H6

<400> 485
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
20 25 30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
35 40 45
Gln Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
85 90 95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ala Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Ile Thr
145

<210> 486
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 3_11A10

<400> 486
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 487
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 3_14F6

<400> 487
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140

Leu Thr
145

<210> 488
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 3_15B2

<400> 488
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 489
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 3_6A10

<400> 489
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45

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Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 490
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 3_6B1

<400> 490
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 491
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
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<223> Synthetic Protein Sequence

<220>
<223> 3_7F9

<400> 491
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 492
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 3_8G11

<400> 492
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125

Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140
Ile Thr
145

<210> 493
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 4_1B10

<400> 493
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
20 25 30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
50 55 60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
85 90 95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140
Ile Thr
145

<210> 494
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 5_2B3

<400> 494
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
20 25 30

Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 495
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 5_2D9

<220>
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<222> 3, 26, 33
<223> Xaa = Any Amino Acid

<400> 495
Met Leu Xaa Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Xaa Glu Val Cys Met Tyr Glu
            20   25   30
Xaa Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Gln
                85   90   95
Ile Leu Arg Glu Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Leu Thr
145

<210> 496
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 5_2F10

<400> 496
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Leu Thr
145

<210> 497
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_1A11

<400> 497
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly

65 70 75 80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
85 90 95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140
Leu Thr
145

<210> 498
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_1D5

<400> 498
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
20 25 30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
50 55 60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
85 90 95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140
Ile Thr
145

<210> 499
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>

<223> 6_1F11

<400> 499
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Leu Thr
145

<210> 500
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_1F1

<400> 500
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Leu Thr

145

<210> 501
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_1H10

<400> 501
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Ile Thr
145

<210> 502
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 6_1H4

<400> 502
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu

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    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Asp Gln Lys Ala Gly Ser Thr Leu Ile Lys His Ala Glu Gln
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145
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<210> 503
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 8_1F8

<400> 503

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 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 504
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 8_1G2

<400> 504
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Leu Thr
145

<210> 505
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 8_1G3

<400> 505
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg

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    130                 135                 140
Ile Thr
145


<210> 506
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 8_1H7

<400> 506
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145


<210> 507
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> 8_1H9

<400> 507
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
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        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145
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<210> 508
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> GAT1_21F12

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<400> 508
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Asn Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 509
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> GAT1_24G3

<400> 509
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Phe Val Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro Tyr Ile Leu Met Tyr Glu Lys
    130   135   140
Leu Thr
145

<210> 510
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> GAT1_29G1

<400> 510
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly

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        115                 120                 125
Val Cys Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Ala
145


<210> 511
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> GAT1_32G1

<400> 511
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Val Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145


<210> 512
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> GAT2_15G8

<400> 512
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Lys Tyr Glu
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            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Asn Ala Glu His Ser Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 513
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> GAT2_19H8

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<400> 513
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Val Ser Gly Tyr Tyr Glu Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Cys Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 514
<211> 146
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> GAT2_21F1

<400> 514
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Ile Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Gly Gly Thr Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Arg His Ala Glu Glu
                85   90   95
Leu Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Val Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Gly
        115   120   125
Val Tyr Asp Ile Pro Pro Ile Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 515
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> RBS
<222> (0)...(0)
<223> B. licheniformis ribosome binding site

<400> 515
aactgaagga ggaatctc 18

<210> 516
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>

<223> GY12_7G1

<400> 516
atgattgagg tgaaaccgat taacgcagag gatacctatg aactaaggca taggatactc 60
agaccaaacc agccgataga ggtttgtatg tatgaaaccg atttacttcg tggtgcgttt 120
cacttaggcg gcttttacag gggcaagctg atttccatag cttcattcca ccaggccgag 180
cattcagatc tcgagggcca gaaacaatac caactccgag gtatggctac cttggaaggt 240
tatcgtgaac agaaagcggg atcgacccta attcaacacg ctgaacagat ccttcggaag 300
cgggggggcgg acatgctatg gtgcaatgcg cggacaaccg ccgctggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gatacgccgc cagtaggacc tcacatccta 420
atgtataaac gcctcacata a 441

<210> 517
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> GY12_5A11

<400> 517
atgattgaag tgaaaccgat taacgcagag gatacctatg aactaaggca taggatactc 60
agaccaaacc agccgataga ggtttgtatg tatgaaagcg atttacttcg tggtgcgttt 120
cacttaggcg gcttttacag gggcaagctg atttccatag cttcattcca ccaggccgag 180
cattcagaac tccagggcca gaaacaatac caactccgag gtatggctac cttggaaggt 240
tatcgtgacc agaaagcggg atcgagccta attagacacg ctgaacagat ccttcggaag 300
cgggggggcgg acatgctatg gtgcaatgcg cggacatccg cctctggcta ctacaaaaag 360
ttaggcttca gtgagcaggg agaggtattt gatacgccgc cagtaggacc tcacatccta 420
atgtataaac gcatcacata a 441

<210> 518
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> GY12_4H12

<400> 518
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agaccacacc agccgataga ggtttgtatg tatgaaaccg atttacttcg tggtgcgttt 120
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cgggggggcgg acatgctatg gtgcaatgcg cggacatccg ccgctggcta ctacaaaaag 360
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catttgggcg ggttctatcg tggccaattg atctcgattg cgagtttcca caaagctgaa 180
cacccagaac tgcaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
ttccgtgagc agaaggctgg ctcttcgctt attaggcacg ccgaggagat actacggaat 300
aaaggggcag atctgctttg gtgtaatgca cgcacgacag cctccggtta ctataaaagg 360
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atgtacaaaa aactcactta a 441

<210> 520
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catttgggcg ggttctatcg tggccaattg atctcgattg cgagtttcca caaagctgaa 180
cacccagaac tgcaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
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aaaggggcag atctgctttg gtgtaatgca cgcacgacag cctccggtta ctataaaagg 360
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atgtacaaaa gaatcactta a 441

<210> 521
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catttgggcg ggttctatcg tggccaattg atctcgattg cgagtttcca caaagctgaa 180
cactcagaac tgcaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240

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cttggtttta gtgagcacgg cgaagttttc gaaaccccgc cggttgggcc gcacattctt 420
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<210> 522
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catttgggcg ggttctatcg tggccaattg atctcgattg cgagtttcaa caaagctgaa 180
cactcagaac tgcaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
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<223> D_S00218540_B-4B5

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atgtacaaaa aactcactta a 441

<210> 525
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<212> DNA
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<220>
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<220>
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cacccagaac tgcaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
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<210> 527
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<212> DNA
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atgtacaaaa aactcactta a 441

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cactcagaac tgcaagggca aaagcagtat caattacgag ggatggcgac cctcgaagga 240
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atgtacaaaa aactcactta a 441

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cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tcgaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240

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ttaggcttca gcgagcaggg agaggtattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

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<223> D_S00221106_C7A8

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atgtataaaa ggatcacata a 441

<210> 535
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<212> DNA
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<210> 538
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<223> D_S00224766_17-10B3

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agggggggcgg acatgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 543
<211> 441

<212> DNA
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<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00260491_17-12B10

<400> 543
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcgttt 120
cacttaggcg gctattacgg gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggcgg acttgctttg gtgtaatgcg cggacgtccg cctcaggcta ctacaaaaag 360
ctaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 544
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00260546_17-12H5

<400> 544
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gcttttacgg gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggagggt 240
tatcgtgagc agaaagcggg atcgagtcta attagacacg ctgaagaaat tcttcgtaag 300
agggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 545
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00260588_17-13C11

<400> 545
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacgg gggcaaactg atttccatag cttcattcca ccgggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240

tatcgtgagc agaaagcggg atcgagtcta gttaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gacacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 546
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00260694_17-14F9

<400> 546
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacgg gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcggaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 547
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00260743_17-15B10

<400> 547
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gcttttacgg gggcaaactg atttccatag cttcattcca ccaggccgag 180
cacttagacc tcgaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 548
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>

<223> D_S00260793_17-15G12

<400> 548
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttgggcg gctattacag gggcaaactg atttccgtag cgtcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta gttaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 549
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00260796_17-15H3

<400> 549
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacgg gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaggcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattc gacacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 550
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> 17-16A10

<400> 550
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacag gggcaaactg atttccatag cgtcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta gttaaacacg ctgaagaaat tcttcgtaag 300
aggggggcgg acatgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacatg a 441

<210> 551
<211> 441

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00260847_17-16D6

<400> 551
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttgggcg gctattacag gggcaaactg atttccgtag cgtcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgatc agaaagcggg atcgagtcta gttaaacacg ctgaagaaat tcttcgtaag 300
agggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggctcacata a 441

<210> 552
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00260855_17-16F2

<400> 552
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttgggcg gcttttacag gggcaaactg atttccatag cgtcattcca ccaggccgag 180
cactcagacc tcgaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggcgg acatgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg ggagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 553
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00260862_17-16F9

<400> 553
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca ggaacagtac cagctccgag gtatggctac cttggaaggt 240

tatcgtgatc agaaagcggg atcgagtcta gttaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgcaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 554
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00260904_17-17B3

<400> 554
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcactt 120
cacttaggcg gctattacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtctg gttaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 555
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00260929_17-17D4

<400> 555
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacag gggcaaactg atttccatag cgtcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta gttaaacacg ctgaagaaat tctccgtaag 300
agggggggcgg acttgctttg gtgtaatgcg cggacgtccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 556
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>

<223> D_S00260940_17-17F3

<400> 556
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cgctcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggagggt 240
tatcgtgatc agaaagcggg atcgagtcta attagacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgtaatgcg cggacgtccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 557
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00260942_17-17F5

<400> 557
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcactt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta gttaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 558
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00260945_17-17F8

<400> 558
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacag gggcaaactg atttccatag cttcattcca tcaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta gttaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acatgctttg gtgtaatgcg cggacgtccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gacacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 559
<211> 441

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00224368_18-8A7

<400> 559
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcactt 120
cacttaggcg gcttttacgg gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 560
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00224350_18-8B7

<400> 560
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacag gggcaaactg atttccatag cgtcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attagacacg ctgaagaaat tcttcgtaag 300
agggggcgg acatgctttg gtgcaacgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 561
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00224416_18-9A1

<400> 561
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcactt 120
cacttaggcg gctattacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tcgaaggccg gaaacagtac cagctccgag gtatggctac cttggaaggt 240

tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gacacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 562
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00224422_18-9A7

<400> 562
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agaccaaacc agccgataga agcgtgtatg tatgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacag aggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcggaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acatgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agaggtattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 563
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00224466_18-9F3

<400> 563
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agaccaaacc agccgataga agcgtgtatg tatgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta gttaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acatgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggtttca gcgagcaggg agaggtattt gacacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 564
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>

<223> D_S00261096_18-24D3

<400> 564
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agaccaaacc agccgatgga agcgtgtatg tatgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tcgaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attaaacacg ctgaagaaat tcttcgtaag 300
agggggggcgg acttgctttg gtgtaatgcg cggacgtccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gatacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 565
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00261192_18-25F3

<400> 565
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gctattacgg gggcaaactg atttccatag cgtcattcca ccaggccgag 180
cactcggaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attagacacg ctgaagaaat tctccgtaag 300
agggggggcgg acatgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 566
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00261438_18-28D9

<400> 566
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcggaac tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcaactcta gttaaacacg ctgaagaaat ccttcgtaag 300
agggggggcgg acatgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gacacgccgc cagtaggacc tcacatcctg 420
atgtataaaa ggatcacata a 441

<210> 567
<211> 441

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_S00261440_18-28D11

<400> 567
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agaccaaacc agccgataga agcgtgtatg tttgaaagcg atttacttcg tggtgcattt 120
cacttaggcg gcttttacag gggcaaactg atttccatag cttcattcca ccaggccgag 180
cactcagacc tccaaggcca gaaacagtac cagctccgag gtatggctac cttggaaggt 240
tatcgtgagc agaaagcggg atcgagtcta attagacacg ctgaagaaat tcttcgtaag 300
agggggcgg acttgctttg gtgtaatgcg cggacatccg cctcaggcta ctacaaaaag 360
ttaggcttca gcgagcaggg agagatattt gaaacgccgc cagtaggacc tcacatcctg 420
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<220>
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<220>
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 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Ile Gln His Ala Glu Gln
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Thr Ala Ala Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Leu Thr
145

<210> 569
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<212> PRT

<213> Artificial Sequence

<220>
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<220>
<223> GY12_5A11

<400> 569
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 570
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> GY12_4H12

<400> 570
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 1   5   10   15
His Arg Ile Leu Arg Pro His Gln Pro Ile Glu Val Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Gln
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr

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            100                 105                 110
Ser Ala Ala Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Val Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145


<210> 571
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<223> D_S00218358_B-2A3

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 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Gln Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Pro Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Phe Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Asn Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Thr Ala Ser Gly Tyr Tyr Lys Arg Leu Gly Phe Cys Glu His Gly Glu
        115                 120                 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145


<210> 572
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00218372_B-2B5

<400> 572
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 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Gln Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Pro Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Phe Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Asn Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Thr Ala Ser Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu His Gly Glu
        115                 120                 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 573
<211> 146
<212> PRT
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<220>
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<220>
<223> D_S00218373_B-2B6

<400> 573

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 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Gln Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Phe Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Asn Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Thr Ala Ser Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu His Gly Glu
        115                 120                 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 574

<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00267061_B-3B8

<400> 574
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Glu Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Gln Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Phe Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85   90   95
Ile Leu Arg Asn Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Thr Ala Ser Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu His Gly Glu
        115   120   125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 575
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00218516_B-3H5

<400> 575
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Glu Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Gln Leu Ile Ser Ile Ala Ser Phe Asn Lys Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Phe Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu

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                85                  90                  95
Ile Leu Arg Asn Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Thr Ala Ser Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu His Gly Glu
        115                 120                 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 576
<211> 146
<212> PRT
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<220>
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<220>
<223> D_S00218540_B-4B5

<400> 576

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 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Gln Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Phe Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Asn Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Thr Ala Ser Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu His Gly Glu
        115                 120                 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130                 135                 140
Leu Thr
145
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<210> 577
<211> 146
<212> PRT
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<220>
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<220>
<223> D_S00218549_B-4C2

<400> 577
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Glu Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Gln Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Pro Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Phe Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85   90   95
Ile Leu Arg Asn Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Thr Ala Ser Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu His Gly Glu
        115   120   125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 578
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00267186_B-4G1

<400> 578
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 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Gln Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Pro Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Phe Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85   90   95
Ile Leu Arg Asn Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Thr Ala Ser Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu His Gly Glu
        115   120   125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 579
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00218594_B-4G11

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 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Val Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Gln Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Gln Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Phe Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85   90   95
Ile Leu Arg Asn Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Thr Ala Ser Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu His Gly Glu
        115   120   125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
    130   135   140
Leu Thr
145

<210> 580
<211> 146
<212> PRT
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<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00267527_B-8G6

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 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Asp Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Gln Leu Ile Ser Ile Ala Ser Phe His Lys Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly

65 70 75 80
Phe Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
85 90 95
Ile Leu Arg Asn Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Thr Ala Ser Gly Tyr Tyr Lys Arg Leu Gly Phe Ser Glu His Gly Glu
115 120 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Lys
130 135 140
Leu Thr
145

<210> 581
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00220826_C3G4

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His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
20 25 30
Thr Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
50 55 60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
85 90 95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140
Ile Thr
145

<210> 582
<211> 146
<212> PRT
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<220>
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<220>

<223> D_S00221015_C6A1

<400> 582
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 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20   25   30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 583
<211> 146
<212> PRT
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<220>
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<220>
<223> D_S00221055_C6D5

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Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr

145

<210> 584
<211> 146
<212> PRT
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<220>
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<220>
<223> D_S00221106_C7A8

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 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 585
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<223> D_S00221021_C7B11

<400> 585
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 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Cys Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu

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    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 586
<211> 146
<212> PRT
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<220>
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<220>
<223> D_S00221095_C8B1

<400> 586

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Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Ala Cys Met Tyr Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Lys Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 587
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00221246_C8G4

<400> 587
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 588
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<223> D_S00221401_C10F3

<400> 588
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Glu Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ser Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Gly Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg

130 135 140
Ile Thr
145

<210> 589
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00224699_17-9C8

<400> 589
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
20 25 30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
50 55 60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
85 90 95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140
Ile Thr
145

<210> 590
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00224736_17-9G9

<400> 590
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
20 25 30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly

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        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys
    130                 135                 140


<210> 591
<211> 146
<212> PRT
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<220>
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<220>
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 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145


<210> 592
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence
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<220>
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<400> 592
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 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 593
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00224783_17-10C8

<400> 593
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Gly Glu Gln Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg

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    130                 135                 140
Leu Thr
145


<210> 594
<211> 146
<212> PRT
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<220>
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<220>
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<400> 594
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 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Gln
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145


<210> 595
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<223> D_S00260491_17-12B10

<400> 595
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
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        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 596
<211> 146
<212> PRT
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<220>
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<220>
<223> D_S00260546_17-12H5

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 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 597
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00260588_17-13C11

<400> 597
Met Leu Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Arg Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 598
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00260694_17

<400> 598
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu

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        115                 120                 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145


<210> 599
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00260743_17-15B10

<400> 599
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Leu Asp Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145


<210> 600
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00260793_17-15G12

<400> 600
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
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            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145


<210> 601
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00260796_17-15H3

<400> 601
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 602
<211> 146
<212> PRT
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<213> Artificial Sequence

<220>
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<220>
<223> 17-16A10

<400> 602
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 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 603
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00260847_17-16D6

<400> 603
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 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr

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            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145


<210> 604
<211> 146
<212> PRT
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<220>
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<220>
<223> D_S00260855_17-16F2

<400> 604
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50                  55                  60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 605
<211> 146
<212> PRT
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<220>
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<220>
<223> D_S00260862_17-16F9

<400> 605
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
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 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Glu Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 606
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<223> D_S00260904_17-17B3

<400> 606
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Leu His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 607
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<211> 146
<212> PRT
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<220>
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<220>
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 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 608
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<223> D_S00260940_17-17F3

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu Arg Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu

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                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 609
<211> 146
<212> PRT
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<220>
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<220>
<223> D_S00260942_17-17F5

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Leu His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 610
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<223> D_S00260945_17-17F8
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<400> 610
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 611
<211> 146
<212> PRT
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<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00224368_18-8A7

<400> 611
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Leu His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 612
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00224350_18-8B7

<400> 612
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 613
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00224416_18-9A1

<400> 613
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Leu His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Glu Gly Arg Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly

65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
85 90 95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140
Ile Thr
145

<210> 614
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00224422_18-9A7

<400> 614
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
20 25 30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
35 40 45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
50 55 60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
85 90 95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140
Ile Thr
145

<210> 615
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>

<223> D_S00224466_18-9F3

<400> 615
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 616
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00261096_18-24D3

<400> 616
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Met Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Glu Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr

145

<210> 617
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00261192_18-25F3

<400> 617
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 618
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00261438_18-28D9

<400> 618
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu

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    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 619
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_S00261440_18-28D11

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<400> 619
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 620
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_GE002256_GAT20-12F7

<220>
<221> CDS
<222> (1)...(441)

<400> 620
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20   25   30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc 144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35   40   45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt 192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50   55   60

caa ggc cag aaa cag tac cag att cga ggt gtg gct acc tta gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Ile Arg Gly Val Ala Thr Leu Glu Gly
 65   70   75   80

tat cgt gag cag aag gcg gga tcc agt cta gtt aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85   90   95

att cta cgt aag agg ggg gcg gac ctg ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag 384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg 432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140

atc aca taa 441
Ile Thr *
145

<210> 621
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> D_GE002256_GAT20-12F7

<220>
<223> Synthetic Protein Sequence

<400> 621
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Ile Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 622
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<223> D_GE003194_GAT20-12F7b

<220>
<221> CDS
<222> (1)...(441)

<400> 622
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20   25   30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35   40   45

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aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag att cga ggt gtg gct acc tta gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Ile Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ctg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
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<210> 623
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<220>
<223> D_GE003194_GAT20-12F7b

<400> 623

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Ile Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
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        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 624
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002257_GAT20-13A2

<400> 624
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga atc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc atc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
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Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                    441
Ile Thr  *
145
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<210> 625
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002257_GAT20-13A2

<220>
<223> Synthetic Protein Sequence

<400> 625

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 626
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002258_GAT20-13H9

<400> 626
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20   25   30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc 144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35   40   45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt 192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50   55   60

caa ggc cag aaa cag tac cag att cga ggt gtg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Ile Arg Gly Val Ala Thr Leu Glu Gly
 65   70   75   80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85   90   95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110

tcc gcc tca ggc ttc tac aga aag tta ggc ttc agc gag cag gga gag 384
Ser Ala Ser Gly Phe Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125

ata ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa tgg 432
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Trp
    130   135   140

atc aca taa 441
Ile Thr *
145

<210> 627
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002258_GAT20-13H9

<220>
<223> Synthetic Protein Sequence

<400> 627
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg

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 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Ile Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Phe Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Trp
    130                 135                 140
Ile Thr
145
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<210> 628
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002259_GAT20-14A6

<400> 628

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60

cca ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Pro Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
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tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc ttc tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Phe Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 629
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002259_GAT20-14A6

<220>
<223> Synthetic Protein Sequence

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<400> 629
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Pro Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Phe Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 630
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002260_GAT20-14A11

<400> 630

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aga ctg att tcc atc gct tca ttc cac cag gcc gag cac tcg gaa att   192
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Ile
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
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<210> 631
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002260_GAT20-14A11

<220>
<223> Synthetic Protein Sequence

<400> 631
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Ile
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 632
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE003195_GAT20-14A11b

<400> 632
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96

```
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45

aga ctg att tcc atc gct tca ttc cac cag gcc gag cac tcg gaa att   192
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Ile
    50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 633
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE003195_GAT20-14A11b

<220>
<223> Synthetic Protein Sequence

<400> 633

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Ile
    50                  55                  60
```

```
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 634
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002261_GAT20-14G7

<400> 634

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35                  40                  45

aga ctg att tcc atc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
```

```
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

ata ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 635
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002261_GAT20-14G7

<220>
<223> Synthetic Protein Sequence

<400> 635

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 636
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002262_GAT20-14H3

<400> 636
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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ttg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35                  40                  45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att ata cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Ile Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc ttc tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Phe Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 637
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> D_GE002262_GAT20-14H3

<220>
<223> Synthetic Protein Sequence

<400> 637
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35   40   45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Ile Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Phe Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 638
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002263_GAT20-16A3

<400> 638
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20   25   30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35   40   45

```
aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ctg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 639
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002263_GAT20-16A3

<220>
<223> Synthetic Protein Sequence

<400> 639

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
```

```
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 640
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE003196_GAT20-16A3b

<400> 640
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ctg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
```

```
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                    441
Ile Thr  *
145
```

<210> 641
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE003196_GAT20-16A3b

<220>
<223> Synthetic Protein Sequence

<400> 641

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 642
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002264_GAT20-16C7

<400> 642
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
20 25 30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc 144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
35 40 45

aaa ctg att tcc atc gct tca ttc cac cag gcc gag cac acg gaa ctt 192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
50 55 60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65 70 75 80

tat cgt gag cag aag gcg gga acc agt cta ctt aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Leu Lys His Ala Glu Glu
85 90 95

att cta cgt aag agg ggg gcg gac ctg ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110

tcc gcc tca ggc ttc tac aaa aag tta ggc ttc agc gag cag gga gag 384
Ser Ala Ser Gly Phe Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg 432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140

atc aca taa 441
Ile Thr *
145

<210> 643
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002264_GAT20-16C7

<220>
<223> Synthetic Protein Sequence

<400> 643
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg

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 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Leu Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Phe Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 644
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002265_GAT20-16G8

<400> 644

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
```

```
tat cgt gag cag aag gcg gga acc agt cta ctt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Leu Lys His Ala Glu Glu
                 85                  90                  95

att ata cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Ile Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc ttc tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Phe Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 645
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002265_GAT20-16G8

<220>
<223> Synthetic Protein Sequence

<400> 645

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Leu Lys His Ala Glu Glu
                85                  90                  95
Ile Ile Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Phe Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 646
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002266_GAT20-17A10

<400> 646

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aga ctg att tcc atc gct tca ttc cac cag gcc gag cac acg gaa ctt   192
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

ata ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
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<210> 647
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002266_GAT20-17A10

<220>
<223> Synthetic Protein Sequence

<400> 647
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20   25   30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 648
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE003197_GAT20-17A10b

<400> 648
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96

```
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aga ctg att tcc atc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

ata ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
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<210> 649
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE003197_GAT20-17A10b

<220>
<223> Synthetic Protein Sequence

<400> 649

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
```

```
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 650
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002267_GAT20-17B11

<400> 650

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atg ata gag ata aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Ile Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Asp
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc atc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
```

```
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 651
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002267_GAT20-17B11

<220>
<223> Synthetic Protein Sequence

<400> 651

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Met Ile Glu Ile Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Asp
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 652
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002268_GAT20-17C1

<400> 652
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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aga ctg att tcc atc gct tca ttc cac cag gcc gag cac acg gaa ctt   192
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

ata ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 653
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> D_GE002268_GAT20-17C1

<220>
<223> Synthetic Protein Sequence

<400> 653
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20   25   30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 654
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002269_GAT20-18D7

<400> 654
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20   25   30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35   40   45

```
aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gat   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Asp
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
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<210> 655
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002269_GAT20-18D7

<220>
<223> Synthetic Protein Sequence

<400> 655

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Asp
```

```
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 656
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002270_GAT20-18D9

<400> 656
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aga ctg att tcc atc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
```

```
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                    441
Ile Thr  *
145
```

<210> 657
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002270_GAT20-18D9

<220>
<223> Synthetic Protein Sequence

<400> 657

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 658
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002271_GAT20-20H10

<400> 658
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
20 25 30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc 144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
35 40 45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt 192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
50 55 60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65 70 75 80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
85 90 95

att cta cgt aag agg ggg gcg gac ctg ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag 384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg 432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140

atc aca taa 441
Ile Thr *
145

<210> 659
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002271_GAT20-20H10

<220>
<223> Synthetic Protein Sequence

<400> 659
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg

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 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 660
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002272_GAT20-22G5

<400> 660

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
```

```
tat cgt gag cag aag gcg gga tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145


<210> 661
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002272_GAT20-22G5

<220>
<223> Synthetic Protein Sequence

<400> 661
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 662
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002273_GAT20-22H1

<400> 662

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35                  40                  45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gat   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Asp
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 663
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002273_GAT20-22H1

<220>
<223> Synthetic Protein Sequence

<400> 663
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35   40   45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Asp
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 664
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002274_GAT19-11C8

<400> 664
atg ata gaa gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga ata ctc aga cca aac cag ccg gta gaa gcg tgt atg ttt gaa   96

```
His Arg Ile Leu Arg Pro Asn Gln Pro Val Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc tat tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35                  40                  45

aaa ctg gtt tcc ata gct tca ttc cac cag gcc gag cac tcg gaa ctc   192
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

cac cgt gag cag aaa gcg gga tcg agt cta att aaa cac gct gaa gaa   288
His Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                 85                  90                  95

atc ctt cgt aag agg ggg gcg gac atg ctt tgg tgc aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 665
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002274_GAT19-11C8

<220>
<223> Synthetic Protein Sequence

<400> 665

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Val Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
```

```
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
His Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 666
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002275_GAT19-11D6

<400> 666

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atg ata gag gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga ata ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc tat tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc ata gct tca ttc cac cag gcc gag cac tca gaa ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag gaa cag tac cag ctc cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Glu Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aaa gcg gga tca act cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Val Lys His Ala Glu Glu
                85                  90                  95

att ctt cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
```

```
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

ata ttt gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 667
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002275_GAT19-11D6

<220>
<223> Synthetic Protein Sequence

<400> 667

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Glu Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 668
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002276_GAT19-11D8

<400> 668
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atg ata gag gtg aaa ccg att aac gca gag gat acc tat gag cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga ata ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc ttt tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tct ata gct tca ttc cac cag gcc gag cac tca gac ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aaa gcg gga tca act cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Val Lys His Ala Glu Glu
                 85                  90                  95

atc ctt cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttt gaa acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

ctc aca taa                                                      441
Leu Thr  *
145
```

<210> 669
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> D_GE002276_GAT19-11D8

<220>
<223> Synthetic Protein Sequence

<400> 669
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Leu Thr
145

<210> 670
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002277_GAT19-11H12

<400> 670
atg ata gaa gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aaa ata ctc aga cca aac cag ccg tta gaa gtg tgt atg tat gaa   96
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
             20   25   30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc tat tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35   40   45

```
aaa ctg att tcc ata gct tca ttc cac cag gct gag cac cca gaa ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gat cag aaa gcg gga tcg agt cta att aga cac gct gaa gaa   288
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                 85                  90                  95

att ctt cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
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<210> 671
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002277_GAT19-11H12

<220>
<223> Synthetic Protein Sequence

<400> 671

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Pro Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Arg His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
```

```
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 672
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002278_GAT20-24F8

<400> 672
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta ctt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Leu Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc ttc tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Phe Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
```

```
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                    441
Ile Thr  *
145
```

<210> 673
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002278_GAT20-24F8

<220>
<223> Synthetic Protein Sequence

<400> 673

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Leu Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Phe Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 674
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002279_GAT20-26A4

<400> 674
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
20 25 30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc 144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
35 40 45

aaa ctg att tcc atc gct tca ttc cac cag gcc gag cac tcg gaa ctt 192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
50 55 60

caa ggc cag aaa cag tac cag att cga ggt gtg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Ile Arg Gly Val Ala Thr Leu Glu Gly
65 70 75 80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
85 90 95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag 384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125

ata ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg 432
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140

atc aca taa 441
Ile Thr *
145

<210> 675
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002279_GAT20-26A4

<220>
<223> Synthetic Protein Sequence

<400> 675
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg

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 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Ile Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 676
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002280_GAT20-27C7

<400> 676

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
```

```
tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc ttc tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Phe Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc atg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Met Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 677
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002280_GAT20-27C7

<220>
<223> Synthetic Protein Sequence

<400> 677

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Phe Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Met Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 678
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002281_GAT20-27F9

<400> 678

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35                  40                  45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ttt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Phe
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att ata cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Ile Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

ata ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 679
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002281_GAT20-27F9

<220>
<223> Synthetic Protein Sequence

<400> 679
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20   25   30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35   40   45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Phe
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Ile Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 680
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002282_GAT20-30B10

<400> 680
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96

```
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc atc gct tca ttc cac cag gcc gag cac acg gaa ctt   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga act agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc ttc tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Phe Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 681
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002282_GAT20-30B10

<220>
<223> Synthetic Protein Sequence

<400> 681

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
```

```
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Phe Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 682
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002283_GAT20-30C6

<400> 682

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
```

```
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 683
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002283_GAT20-30C6

<220>
<223> Synthetic Protein Sequence

<400> 683

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 684
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE003198_GAT20-30C6b

<400> 684
```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 685
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> D_GE003198_GAT20-30C6b

<220>
<223> Synthetic Protein Sequence

<400> 685
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 686
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002284_GAT20-30F7

<400> 686
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga atc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
             20   25   30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35   40   45

```
aaa ctg att tcc atc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 687
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002284_GAT20-30F7

<220>
<223> Synthetic Protein Sequence

<400> 687

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
```

```
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 688
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002285_GAT20-31D6

<400> 688
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Asp
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aga ctg att tcc atc gct tca ttc cac ccg gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Ile Ala Ser Phe His Pro Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc atg atg tat aaa agg   432
```

```
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Met Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                    441
Ile Thr  *
145
```

<210> 689
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002285_GAT20-31D6

<220>
<223> Synthetic Protein Sequence

<400> 689

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Asp
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Ile Ala Ser Phe His Pro Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Met Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 690
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_GE002286_GAT20-31G1

<400> 690
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
1 5 10 15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
20 25 30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc 144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
35 40 45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt 192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
50 55 60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65 70 75 80

tat cgt gag cag aag gcg gga tcc agt cta gtt aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
85 90 95

att cta cgt aag agg ggg gcg gac ctg ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110

tcc gcc tca ggc ttc tac aaa aag tta ggc ttc agc gag cag gga gag 384
Ser Ala Ser Gly Phe Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125

gta ttc gac acg ccg cca gta gga cct cac atc atg atg tat aaa agg 432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Met Met Tyr Lys Arg
130 135 140

atc aca taa 441
Ile Thr *
145

<210> 691
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_GE002286_GAT20-31G1

<220>
<223> Synthetic Protein Sequence

<400> 691
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg

```
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Phe Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Met Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 692
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00339957_GAT19-1A7

<400> 692

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atg ata gag gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga ata ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc tat tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45

aaa ctg att tcc ata gct tca ttc cac cag gcc gag cac tca gaa ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
```

```
tat cgt gag cag aaa gcg gga tcg agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

atc ctc cgt aag agg ggg gcg gac ttg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttt gat acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
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<210> 693
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00339957_GAT19-1A7

<220>
<223> Synthetic Protein Sequence

<400> 693

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 694
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00339989_GAT19-1D3

<400> 694

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atg ata gaa gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga ata ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc ttt tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc ata gct tca ttc cac cag gcc gag cac tca gac ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aaa gcg gga tca act cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Val Lys His Ala Glu Glu
                 85                  90                  95

atc ctt cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ctc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Leu Ser Glu Gln Gly Glu
        115                 120                 125

gta ttt gac acg ccg cca gta ggg cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

ctc aca taa                                                      441
Leu Thr  *
145
```

<210> 695
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00339989_GAT19-1D3

<220>
<223> Synthetic Protein Sequence

<400> 695
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Leu Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Leu Thr
145

<210> 696
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00339991_GAT19-1D5

<400> 696
atg ata gaa gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aaa ata ctc aga cca aac cag ccg tta gaa gtg tgt atg ttt gaa   96

```
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Phe Glu
             20                  25                  30

agc gat tta ctt cgc ggt gca ttt cac tta ggc ggc tat tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc ata gct tca ttc cac cag gcc gag cac tcg gaa ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aaa gcg gga tcg agt cta att aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                 85                  90                  95

att ctt cgt aag agg ggg gtg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

ctc aca taa                                                      441
Leu Thr  *
145


<210> 697
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00339991_GAT19-1D5

<220>
<223> Synthetic Protein Sequence

<400> 697
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
```

```
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Val Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145
```

<210> 698
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00340001_GAT19-1F3

<400> 698

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atg ata gaa gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aaa ata ctc aga cca aac cag ccg tta gaa gtg tgt atg tat gaa   96
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
             20                  25                  30

acc gat tta ctt cgt ggc gca ttt cac tta ggc ggc ttt tac ggg ggc   144
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc ata gct tca ttc cac cag gcc gag cac tca gac ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gat cag aaa gcg gga tcg agt cta att aaa cac gct gaa gaa   288
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                 85                  90                  95

att ctt cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
```

```
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 699
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00340001_GAT19-1F3

<220>
<223> Synthetic Protein Sequence

<400> 699

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Leu Glu Val Cys Met Tyr Glu
            20                  25                  30
Thr Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 700
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00340013_GAT19-1G3

<400> 700
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atg ata gag gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga ata ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc ttt tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc ata gct tca ttc cac cag gcc gag cac tca gaa ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aaa gcg gga tca act cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Val Lys His Ala Glu Glu
                 85                  90                  95

atc ctt cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttt gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 701
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> D_S00340013_GAT19-1G3

<220>
<223> Synthetic Protein Sequence

<400> 701
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 702
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00340017_GAT19-1G7

<400> 702
atg ata gag gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga ata ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc tat tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35   40   45

```
aaa ctg att tcc ata gct tca ttc cac cag gcc gag cac tcg gaa ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aaa gcg gga tca act cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Val Lys His Ala Glu Glu
                 85                  90                  95

atc ctt cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc ggc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Gly Glu Gln Gly Glu
        115                 120                 125

gta ttt gaa acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 703
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00340017_GAT19-1G7

<220>
<223> Synthetic Protein Sequence

<400> 703

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Gly Glu Gln Gly Glu
```

```
        115                 120                 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 704
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00340201_GAT19-3H11

<400> 704
atg ata gaa gtg aaa ccg att aac gca gag gat acc tat gag cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga ata ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc ttt tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc ata gct tca ttc cac cag gcc gag cac tcg gaa ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aaa gcg gga tca act cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att ctt cgt aag agg ggg gcg gac ttg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttt gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
```

```
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                    441
Ile Thr  *
145
```

<210> 705
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00340201_GAT19-3H11

<220>
<223> Synthetic Protein Sequence

<400> 705

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 706
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00340360_GAT19-5H2

<400> 706
atg ata gag gtg aaa ccg att aac gca gag gat acc tat gaa cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15

cat aga ata ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa 96
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
20 25 30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc tat tac ggg ggc 144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
35 40 45

aaa ctg att tcc ata gct tca ttc cac cag gcc gag cac tca gaa ctc 192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
50 55 60

caa ggc cag aaa cag tac cag ctc cga ggt atg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80

tat cgt gat cag aaa gcg gga tcg agt cta gtt aga cac gct gaa caa 288
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Val Arg His Ala Glu Gln
85 90 95

att ctt cgt aag agg ggg gcg gac ttg ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agt gag cag gga gag 384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg 432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140

ctc aca taa 441
Leu Thr *
145

<210> 707
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00340360_GAT19-5H2

<220>
<223> Synthetic Protein Sequence

<400> 707
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg

```
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Asp Gln Lys Ala Gly Ser Ser Leu Val Arg His Ala Glu Gln
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145
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<210> 708
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00340389_GAT19-6B7

<400> 708

```
atg ata gaa gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga ata ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc tat tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45

aaa ctg att tcc ata gct tca ttc cac cag gcc gag cac tca gaa ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
```

```
tat cgt gag cag aag gcg gga tcg agt cta att aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                 85                  90                  95

att ctt cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

ata ttt gac acg ccg cca gta gga ccc cac atc ctg atg tat aaa agg   432
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
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<210> 709
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00340389_GAT19-6B7

<220>
<223> Synthetic Protein Sequence

<400> 709

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 710
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00340420_GAT19-6F2

<400> 710

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atg ata gaa gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga ata ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat ttg ctt cgt ggt gca ttt cac tta ggc ggc ttt tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc ata gct tca ttc cac cag gct gag cac tca gaa ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aaa gcg gga tcg agt cta att aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                 85                  90                  95

atc ctt cgt aag agg ggg gcg gac ttg ctt tgg tgt aat gcg cgg gca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Ala
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttt gat acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

ctc aca taa                                                      441
Leu Thr  *
145
```

<210> 711
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00340420_GAT19-6F2

<220>
<223> Synthetic Protein Sequence

<400> 711
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Ala
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Leu Thr
145

<210> 712
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00340423_GAT19-6F5

<400> 712
atg ata gaa gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga ata ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96

```
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc tat tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc ata gct tca ttc cac cag gcc gag cac tcg gaa ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga tcg agt cta att aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                 85                  90                  95

att ctt cgt aag agg ggg gcg gac atg ctt tgg tgc aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttt gaa acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 713
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00340423_GAT19-6F5

<220>
<223> Synthetic Protein Sequence

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<400> 713
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
```

```
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 714
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00340426_GAT19-6F8

<400> 714

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atg ata gag gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga ata ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc ttt tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc ata gct tca ttc cac cag gct gag cac tca gaa ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aaa gcg gga tcg agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

atc ctt cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
```

```
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttt gaa acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 715
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00340426_GAT19-6F8

<220>
<223> Synthetic Protein Sequence

<400> 715

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 716
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00340428_GAT19-6F10

<400> 716
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atg ata gag gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aaa ata ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc ttt tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc ata gct tca ttc cac cag gcc gag cac tcg gaa ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aaa gcg ggg tcg agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

atc ctt cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aag aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttt gaa acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 717
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> D_S00340428_GAT19-6F10

<220>
<223> Synthetic Protein Sequence

<400> 717
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 718
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00340436_GAT19-6G6

<400> 718
atg ata gaa gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aaa ata ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20   25   30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc ttt tac agg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
         35   40   45

```
aaa ctg att tcc ata gct tca ttc cac cag gcc gag cac tcg gaa ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aaa gcg gga tcg agt cta att aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                 85                  90                  95

atc ctt cgt aag agg ggg gcg gac atg ctt tgg tgc aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttt gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 719
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00340436_GAT19-6G6

<220>
<223> Synthetic Protein Sequence

<400> 719

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
```

```
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 720
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00340437_GAT19-6G7

<400> 720
atg ata gag gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga ata ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc tat tac agg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
         35                  40                  45

aaa ctg gtt tcc ata gct tca ttc cac cag gcc gag cac tca gac ctc   192
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga tcg agt cta att aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                 85                  90                  95

att ctt cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttt gaa acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
```

```
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

ctc aca taa                                                    441
Leu Thr  *
145
```

<210> 721
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00340437_GAT19-6G7

<220>
<223> Synthetic Protein Sequence

<400> 721

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Arg Gly
        35                  40                  45
Lys Leu Val Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Asp Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Glu Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Leu Thr
145
```

<210> 722
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00341190_GAT20-1F8

<400> 722
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
20 25 30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc 144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
35 40 45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt 192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
50 55 60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65 70 75 80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
85 90 95

att cta cgt aag agg ggg gcg gac ctg ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag 384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg 432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140

atc aca taa 441
Ile Thr *
145

<210> 723
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00341190_GAT20-1F8

<220>
<223> Synthetic Protein Sequence

<400> 723
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg

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 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 724
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00341206_GAT20-1G12

<400> 724

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc atc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag att cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Ile Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80
```

```
tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

ata ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 725
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00341206_GAT20-1G12

<220>
<223> Synthetic Protein Sequence

<400> 725

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Ile Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 726
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00341290_GAT20-2G12

<400> 726
```
atg ata gag ata aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Ile Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt act agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc atg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Met Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 727
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00341290_GAT20-2G12

<220>
<223> Synthetic Protein Sequence

<400> 727
Met Ile Glu Ile Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20   25   30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Met Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 728
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00341421_GAT20-4C11

<400> 728
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96

```
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45

aaa ctg ata tcc atc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag caa gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc atg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Met Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 729
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00341421_GAT20-4C11

<220>
<223> Synthetic Protein Sequence

```
<400> 729
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
```

```
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Met Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 730
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00341448_GAT20-4G2

<400> 730

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att ata cgt aag agg ggg gcg gac ctg ctt tgg tgt aat gcg cgg aca   336
Ile Ile Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
```

```
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc atg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Met Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
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<210> 731
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00341448_GAT20-4G2

<220>
<223> Synthetic Protein Sequence

<400> 731

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Ile Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Met Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 732
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00341692_GAT20-7F6

<400> 732
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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac ttg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Leu Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag att cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Ile Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ctg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

ata ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 733
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> D_S00341692_GAT20-7F6

<220>
<223> Synthetic Protein Sequence

<400> 733
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Leu Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Ile Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 734
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00341732_GAT20-8A10

<400> 734
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga atc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
             20   25   30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35   40   45

```
aaa ctg att tcc atc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 735
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00341732_GAT20-8A10

<220>
<223> Synthetic Protein Sequence

<400> 735

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
```

```
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 736
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00341794_GAT20-8G12

<400> 736
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa att   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Ile
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

ata ttc gac acg ccg cca gta gga cct cac atc atg atg tat aaa agg   432
```

```
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Met Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                    441
Ile Thr  *
145
```

<210> 737
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00341794_GAT20-8G12

<220>
<223> Synthetic Protein Sequence

<400> 737

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Ile
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Met Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 738
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00341806_GAT20-8H12

<400> 738
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
20 25 30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc 144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
35 40 45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt 192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
50 55 60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80

tat cgt gag cag aag gcg gga tcc agt cta gtt aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
85 90 95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag 384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg 432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140

atc aca taa 441
Ile Thr *
145

<210> 739
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00341806_GAT20-8H12

<220>
<223> Synthetic Protein Sequence

<400> 739
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg

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 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 740
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00375329_GAT20-8H12b

<400> 740

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
```

```
tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145


<210> 741
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00375329_GAT20-8H12b

<220>
<223> Synthetic Protein Sequence

<400> 741
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 742
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00341822_GAT20-9B4

<400> 742

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35                  40                  45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gat   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Asp
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 743
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00341822_GAT20-9B4

<220>
<223> Synthetic Protein Sequence

<400> 743
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35   40   45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Asp
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 744
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00342013_GAT20-11D3

<400> 744
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96

```
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 745
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00342013_GAT20-11D3

<220>
<223> Synthetic Protein Sequence

<400> 745

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
```

```
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 746
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00342016_GAT20-11D6

<400> 746

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc tac tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
         35                  40                  45

aaa ctg ata tcc atc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
```

```
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag caa gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc atg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Met Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 747
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00342016_GAT20-11D6

<220>
<223> Synthetic Protein Sequence

<400> 747

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Tyr Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Met Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 748
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00392016_GAT22-1C12

<400> 748

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt act agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

ata ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 749
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> D_S00392016_GAT22-1C12

<220>
<223> Synthetic Protein Sequence

<400> 749
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20   25   30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 750
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00392026_22-1D10

<400> 750
atg ata gag ata aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Ile Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20   25   30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35   40   45

```
aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 751
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00392026_22-1D10

<220>
<223> Synthetic Protein Sequence

<400> 751

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Met Ile Glu Ile Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
```

```
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 752
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00392111_GAT22-2D11

<400> 752
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gtg gac ctg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
```

```
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                    441
Ile Thr  *
145
```

<210> 753
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00392111_GAT22-2D11

<220>
<223> Synthetic Protein Sequence

<400> 753

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 754
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00392304_GAT22-4G12

<400> 754
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
1 5 10 15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
20 25 30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc 144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
35 40 45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt 192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
50 55 60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
85 90 95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
100 105 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag 384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg 432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140

atc aca taa 441
Ile Thr *
145

<210> 755
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00392304_GAT22-4G12

<220>
<223> Synthetic Protein Sequence

<400> 755
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg

```
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 756
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00392376_GAT22-5F12

<400> 756

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30

agt gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
```

```
tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ctg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 757
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00392376_GAT22-5F12

<220>
<223> Synthetic Protein Sequence

<400> 757

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 758
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00392449_GAT22-6F1

<400> 758

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt act agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 759
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00392449_GAT22-6F1

<220>
<223> Synthetic Protein Sequence

<400> 759
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 760
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00392474_GAT22-6H2

<400> 760
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96

```
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 761
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00392474_GAT22-6H2

<220>
<223> Synthetic Protein Sequence

<400> 761

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
```

```
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 762
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00392595_GAT22-8C3

<400> 762

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gtg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Ile Leu Trp Cys Asn Ala Arg Thr
```

```
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 763
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00392595_GAT22-8C3

<220>
<223> Synthetic Protein Sequence

<400> 763

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Val Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 764
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00392619_22-8F3

<400> 764
```
atg ata gag ata aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Ile Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt act agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 765
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> D_S00392619_22-8F3

<220>
<223> Synthetic Protein Sequence

<400> 765
Met Ile Glu Ile Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 766
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00392706_GAT22-9F6

<400> 766
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20   25   30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35   40   45

```
aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ctg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 767
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00392706_GAT22-9F6

<220>
<223> Synthetic Protein Sequence

<400> 767

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
```

```
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 768
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00392922_22-12B6

<400> 768
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta atg cgt ggt gca ttg cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Leu His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
```

```
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                    441
Ile Thr  *
145
```

<210> 769
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00392922_22-12B6

<220>
<223> Synthetic Protein Sequence

<400> 769

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Leu His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 770
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00397347_21-15C11

<400> 770
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
1 5 10 15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
20 25 30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc 144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
35 40 45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt 192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
50 55 60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65 70 75 80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
85 90 95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag 384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg 432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140

atc aca taa 441
Ile Thr *
145

<210> 771
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00397347_21-15C11

<220>
<223> Synthetic Protein Sequence

<400> 771
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg

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 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 772
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00397467_21-16G11

<400> 772

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggt ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
```

```
tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
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<210> 773
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00397467_21-16G11

<220>
<223> Synthetic Protein Sequence

<400> 773

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 774
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00397517_GAT21-17D1

<400> 774

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc atc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc tta gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
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<210> 775
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00397517_GAT21-17D1

<220>
<223> Synthetic Protein Sequence

<400> 775
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 776
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00397574_GAT21-18A10

<400> 776
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96

```
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta ggg cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
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<210> 777
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00397574_GAT21-18A10

<220>
<223> Synthetic Protein Sequence

<400> 777

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
```

```
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 778
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00397585_GAT21-18B9

<400> 778

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc tta gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
```

```
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
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<210> 779
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00397585_GAT21-18B9

<220>
<223> Synthetic Protein Sequence

<400> 779

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 780
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00397672_22-13B12

<400> 780
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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcg gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
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<210> 781
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> D_S00397672_22-13B12

<220>
<223> Synthetic Protein Sequence

<400> 781
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 782
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00397680_GAT22-13C8

<400> 782
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga gtt ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20   25   30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35   40   45

```
aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 783
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00397680_GAT22-13C8

<220>
<223> Synthetic Protein Sequence

<400> 783

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
```

```
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 784
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00397762_GAT22-14C6

<400> 784
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
             20                  25                  30

agc gat tta ctg cgc ggt gca ttt cac tta ggg ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt act agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
```

```
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                    441
Ile Thr  *
145
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<210> 785
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00397762_GAT22-14C6

<220>
<223> Synthetic Protein Sequence

<400> 785

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 786
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00397779_GAT22-14D11

<400> 786
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20   25   30

agt gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc 144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35   40   45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt 192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50   55   60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65   70   75   80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85   90   95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag 384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125

gta ttc gac acg ccg cca gta gga cct cac atc cta atg tat aaa agg 432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140

atc aca taa 441
Ile Thr *
145

<210> 787
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00397779_GAT22-14D11

<220>
<223> Synthetic Protein Sequence

<400> 787
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg

```
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 788
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00397832_GAT22-15B4

<400> 788

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atg ata gag gta aaa ccg att aac gca gaa gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30

agc gat tta atg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
```

```
tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 789
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00397832_GAT22-15B4

<220>
<223> Synthetic Protein Sequence

<400> 789

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Met Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 790
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00397844_GAT22-15C4

<400> 790

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt act agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ctg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
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<210> 791
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00397844_GAT22-15C4

<220>
<223> Synthetic Protein Sequence

<400> 791
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 792
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00397944_22-16D8

<400> 792
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96

```
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttt agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 793
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00397944_22-16D8

<220>
<223> Synthetic Protein Sequence

<400> 793

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
```

```
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 794
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00398097_GAT22-18C5

<400> 794

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tat cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
```

```
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 795
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00398097_GAT22-18C5

<220>
<223> Synthetic Protein Sequence

<400> 795

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 796
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00398147_22-18H7

<400> 796
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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

cag ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aga agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Arg Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 797
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> D_S00398147_22-18H7

<220>
<223> Synthetic Protein Sequence

<400> 797
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20   25   30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Arg Arg
    130   135   140
Ile Thr
145

<210> 798
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00398975_21-19F1

<400> 798
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
             20   25   30

agc gat tta ctg cgt ggt gca ttt cac cta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35   40   45

```
aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ctg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg cca cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 799
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00398975_21-19F1

<220>
<223> Synthetic Protein Sequence

<400> 799

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
```

```
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 800
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00398977_21-19F3

<400> 800
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

ata ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
```

```
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                    441
Ile Thr  *
145
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<210> 801
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00398977_21-19F3

<220>
<223> Synthetic Protein Sequence

<400> 801

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 802
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00399101_GAT21-21A7

<400> 802
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
1 5 10 15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
20 25 30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc 144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
35 40 45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt 192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
50 55 60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65 70 75 80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
85 90 95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
100 105 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag 384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg 432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140

atc aca taa 441
Ile Thr *
145

<210> 803
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00399101_GAT21-21A7

<220>
<223> Synthetic Protein Sequence

<400> 803
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg

```
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 804
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00399539_21-26C1

<400> 804

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45

aaa ctg att tcc gtt gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
```

```
tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ctg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 805
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00399539_21-26C1

<220>
<223> Synthetic Protein Sequence

<400> 805

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 806
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00399765_21-28H11

<400> 806

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag att cga ggt gtg gct acc tta gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Ile Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 807
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00399765_21-28H11

<220>
<223> Synthetic Protein Sequence

<400> 807
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20   25   30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Ile Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 808
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00400238_GAT22-19F1

<400> 808
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96

```
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc atc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

ata ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145


<210> 809
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00400238_GAT22-19F1

<220>
<223> Synthetic Protein Sequence

<400> 809
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
```

```
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 810
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00400319_GAT22-20D10

<400> 810

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt act agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
```

```
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 811
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> D_S00400319_GAT22-20D10

<220>
<223> Synthetic Protein Sequence

<400> 811

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 812
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> D_S00401090_GAT22-29G1

<400> 812

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atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggc   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgc aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 813
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> D_S00401090_GAT22-29G1

<220>
<223> Synthetic Protein Sequence

<400> 813
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 814
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> 18-28D9b

<400> 814
atg ata gag gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga ata ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20   25   30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc ttt tac agg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
         35   40   45

```
aaa ctg att tcc ata gct tca ttc cac cag gcc gag cac tcg gaa ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aaa gcg gga tca act cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Val Lys His Ala Glu Glu
                 85                  90                  95

atc ctt cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

ata ttt gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 815
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 18-28D9b

<220>
<223> Synthetic Protein Sequence

<400> 815

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
```

```
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 816
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> 20-8H12c

<400> 816
atg ata gag gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
```

```
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                    441
Ile Thr  *
145
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<210> 817
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 20-8H12c

<220>
<223> Synthetic Protein Sequence

<400> 817

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 818
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> 20-16A3c

<400> 818
atg ata gag gtg aaa ccg att aac gca gag gat acc tat gaa cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
20 25 30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc 144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
35 40 45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt 192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
50 55 60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65 70 75 80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
85 90 95

att cta cgt aag agg ggg gcg gac ctg ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag 384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg 432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140

atc aca taa 441
Ile Thr *
145

<210> 819
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 20-16A3c

<220>
<223> Synthetic Protein Sequence

<400> 819
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg

```
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 820
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> 20-30C6c

<400> 820

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atg ata gag gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
```

```
tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 821
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 20-30C6c

<220>
<223> Synthetic Protein Sequence

<400> 821

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 822
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> 11-3C3b

<400> 822
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atg ata gag gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aaa ata ctc aga cca aac cag ccg ata gaa gcg tgt atg tat gaa   96
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
             20                  25                  30

agc gat tta ctt cgt ggt gca ctt cac tta ggc ggc tat tac agg ggc   144
Ser Asp Leu Leu Arg Gly Ala Leu His Leu Gly Gly Tyr Tyr Arg Gly
         35                  40                  45

aaa ctg att tcc ata gcg tca ttc cac cag gcc gag cac tca gaa ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aaa gcg gga tcg agt cta att aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                 85                  90                  95

att ctt cgt aag agg ggg gcg gac ttg ctt tgg tgc aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttt gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 823
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 11-3C3b

<220>
<223> Synthetic Protein Sequence

<400> 823
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Lys Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Tyr Glu
            20   25   30
Ser Asp Leu Leu Arg Gly Ala Leu His Leu Gly Gly Tyr Tyr Arg Gly
        35   40   45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Ile Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 824
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<220>
<223> 18-28D9c

<400> 824
atg ata gag gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga ata ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96

```
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctt cgt ggt gca ttt cac tta ggc ggc ttt tac agg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
         35                  40                  45

aaa ctg att tcc ata gct tca ttc cac cag gcc gag cac tcg gaa ctc   192
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctc cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aaa gcg gga tca act cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Val Lys His Ala Glu Glu
                 85                  90                  95

atc ctt cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg agg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

ata ttt gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 825
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 18-28D9c

<220>
<223> Synthetic Protein Sequence

<400> 825

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Ile Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Arg Gly
        35                  40                  45
Lys Leu Ile Ser Ile Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
```

```
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Thr Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Ile Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 826
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<400> 826
atgattgaag tcaaa 15

<210> 827
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<400> 827
agtatcgagg tgaag 15

<210> 828
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<400> 828
Met Ile Glu Val Lys
 1   5

<210> 829
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<400> 829
Arg Pro Asn Gln Pro Leu Glu Ala Cys Met
 1   5   10

<210> 830
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<400> 830
Lys Pro Gln Gln Pro Val Glu Ser Cys Met
 1   5   10

<210> 831
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Protein Sequence

<400> 831
Lys Pro Asn Asn Pro Leu Asp Ala Cys Val
 1   5   10

<210> 832
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT23-1F7

<400> 832
atg ata gag gta aaa ccg att aac gca gaa gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20   25   30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly

```
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc cag aaa cag tat cag ctt cga ggt gtg gct acc ttg gag ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agc cta gtt aaa cgc gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys Arg Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgc aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcg gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 833
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 23-1F7

<400> 833

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Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys Arg Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
```

```
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 834
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT23-2H1


<400> 834
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

cag ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gag ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga ccc cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
```

```
atc aca taa                                                           441
Ile Thr  *
145


<210> 835
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 23-2H1

<400> 835
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 836
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT23-2H11

<400> 836
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
```

```
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

ggc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Gly Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cat gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgc aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
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<210> 837
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 23-2H11

<400> 837

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Gly Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
```

```
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 838
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT23-3H1

<400> 838

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta acg cgt ggt gca ttt cac cta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
```

```
gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145


<210> 839
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 23-3H1

<400> 839
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 840
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT23-5A3

<400> 840
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
```

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30

agt gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tat cag ctt cga ggc gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tcg ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145


<210> 841
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 23-5A3

<400> 841
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
```

```
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 842
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT23-6A3

<400> 842

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga ccg aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

cag ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
```

```
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 843
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 23-6A3

<400> 843

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 844
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS

<222> (1)...(441)
<223> GAT23-6H10

<400> 844
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20   25   30

agc gat tta acg cgt ggt gca ttt cac cta ggc ggc ttc tac ggg ggc 144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35   40   45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt 192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50   55   60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65   70   75   80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85   90   95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag ggg gag 384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg 432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140

atc aca taa 441
Ile Thr *
145

<210> 845
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 23-6H10

<400> 845
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

```
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 846
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT24-4D5

<400> 846

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta acg cgt ggt gcg ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cgg gcc gag cac acg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Arg Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc cag aaa cag tat cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
```

```
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag cta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 847
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 24-4D5

<400> 847

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Arg Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 848
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT24-5H5

<400> 848
```
atg ata gag gta aaa ccg att aac gca gaa gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

aac gat tta atg cgt agt gca ttt cac tta ggc ggc ttc cac ggg ggc   144
Asn Asp Leu Met Arg Ser Ala Phe His Leu Gly Gly Phe His Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tat cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag ttg ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg ccg gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 849
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> 24-5H5

<400> 849
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20   25   30
Asn Asp Leu Met Arg Ser Ala Phe His Leu Gly Gly Phe His Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 850
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT23-13D7

<400> 850
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45

aaa ctg att tcc gtc gct tca ttc cac agg gcc gag cac acg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Arg Ala Glu His Thr Glu Leu
    50   55   60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240

```
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt act agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag cta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 851
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 23-13D7

```
<400> 851
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Arg Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 852

<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT24-9G5

<400> 852
```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa tac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys Tyr Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gtg gac ctg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gtg gga ccc cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 853
<211> 146

<212> PRT
<213> Artificial Sequence

<220>
<223> 24-9G5

<400> 853
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys Tyr Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 854
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT24-9H9

<400> 854
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20   25   30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35   40   45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192

```
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcg gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg cct cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 855
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 24-9H9

<400> 855

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
```

145

<210> 856
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT24-12A5

<400> 856
```
atg ata gat gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Asp Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tat cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gcc gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 857
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 24-12A5

<400> 857
Met Ile Asp Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20   25   30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 858
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT24-14B7

<400> 858
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20   25   30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144

```
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

cag ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtc aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgc aag agg ggg gcg gac atg att tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110

tca gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145


<210> 859
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 24-14B7

<400> 859
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
```

```
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 860
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT24-15B10

<400> 860

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
```

```
atc aca taa                                                           441
Ile Thr  *
145


<210> 861
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 24-15B10

<400> 861
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 862
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT24-15C3

<400> 862
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
```

```
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

cag ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 863
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 24-15C3

```
<400> 863
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
```

```
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 864
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT24-16B1

<400> 864

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg gta gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Val Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
```

```
gta ttc gac acg ccg cca gtg gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 865
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 24-16B1

<400> 865

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Val Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 866
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT24-16H12

<400> 866

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
```

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg gtt tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt   192
Lys Leu Val Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 867
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 24-16H12

```
<400> 867
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Val Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
```

```
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 868
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT24-17A10

<400> 868

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tac cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ctg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
```

```
tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 869
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 24-17A10

<400> 869

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 870
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<223> GAT24-17G11

<400> 870

```
atg ata gag gta aaa ccg att aac gca gag gat act tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg gtt tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Val Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 871
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 24-17G11

<400> 871

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
```

```
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Val Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 872
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT24-19H3

<400> 872

```
atg ata gag gta aaa ccg att aac gca gaa gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gct gag cac acg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95
```

```
att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttt agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 873
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 24-19H3

<400> 873

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 874
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT23-14A3

<400> 874
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
1 5 10 15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
20 25 30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc 144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
35 40 45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt 192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
50 55 60

cag ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65 70 75 80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
85 90 95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
100 105 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag 384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg 432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140

atc aca taa 441
Ile Thr *
145

<210> 875
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 23-14A3

<400> 875
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 876
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT23-14B4

<400> 876
atg ata gag gta aaa ccg att aac gca gaa gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45

aaa ctg att tcc gtc gct tca ttc cac cgg gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Arg Ala Glu His Ser Glu Leu
    50   55   60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80

```
tat cgt gag cag aag gcg ggt tcc agt ctg gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 877
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 23-14B4

<400> 877

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Arg Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 878
<211> 441
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT23-15G3

<400> 878
```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac gtc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Val Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 879
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 23-15G3

<400> 879
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Val Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 880
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT23-18G4

<400> 880
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cgc tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu Arg Ser Glu Leu
    50   55   60

```
cag ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gca gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Ala Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 881
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 23-18G4

```
<400> 881
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu Arg Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Ala Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 882
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT23-18H5

<400> 882
```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tat cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 883
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 23-18H5

<400> 883
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 884
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT23-19C3

<400> 884
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20   25   30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tat ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35   40   45

```
aaa ctg atc tcc gtc gct tca ttc cac cag gcc ggg cac acg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Gly His Thr Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac ata ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcg gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 885
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 23-19C3

```
<400> 885
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Gly His Thr Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Ile Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
```

```
    130                 135                 140
Ile Thr
145


<210> 886
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT23-19F6

<400> 886
atg ata gag gta aaa ccg att aac gca gaa gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc cgg aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Arg Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
```

Ile Thr *
145

<210> 887
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 23-19F6

<400> 887
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20   25   30
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50   55   60
Gln Gly Arg Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 888
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT25-1D10

<400> 888
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30

```
agc gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

cag ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag cta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 889
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 25-1D10

```
<400> 889
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
```

```
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 890
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT26-2D9

<400> 890

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

cag ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg ccg gta gga cct cac atc ctg atg tac aaa agg   432
```

```
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                    441
Ile Thr  *
145


<210> 891
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 26-2D9

<400> 891
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 892
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT26-2H4

<400> 892
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
```

```
cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

aac gat tta acg cgt ggt gcg ttt cac tta ggc ggc ttc tac ggg ggc   144
Asn Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg atc tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tac cgt gag cag aag gcg ggt act agt cta gtc aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag cta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 893
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 26-2H4

```
<400> 893
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Asn Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
```

```
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 894
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT26-3B5

<400> 894

```
atg ata gag gta aaa ccg att aac gca gaa gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cac aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tat ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg atc tcc gtc gct tca ttc cac cag gct gag cac acg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtc aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag ttg ggc ttc agc gag cag gga gag   384
```

```
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 895
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 26-3B5

<400> 895

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 896
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT26-8F11

<400> 896
atg ata gag gta aaa ccg att aac gca gaa gat acc tat gaa cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
20 25 30

aac gat tta acg cgt ggc gca ttt cac tta ggc ggc ttc tac ggg ggc 144
Asn Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
35 40 45

aaa ctg att tcc gtc gct tca ttc cac cag gcc ggg cac tcg gaa ctt 192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Gly His Ser Glu Leu
50 55 60

cag ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65 70 75 80

tat cgt gag cag aag gcg gga acc agt cta gtc aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
85 90 95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
100 105 110

tcc gcc tca ggc tac tac aga aag ttg ggc ttc agc gag cag gga gag 384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg 432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140

atc aca taa 441
Ile Thr *
145

<210> 897
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 26-8F11

<400> 897
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
1 5 10 15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
20 25 30
Asn Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly

```
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Gly His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 898
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT26-9G5

<400> 898

```
atg ata gag gta aaa ccg att aac gca gaa gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gca gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Ala Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg gtt tcc gtc gct tcg ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Val Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
```

```
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag ttg ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 899
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 26-9G5

<400> 899

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Ala Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Val Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 900
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>

<221> CDS
<222> (1)...(441)
<223> GAT26-15D10

<400> 900

```
atg ata gag gtg aaa ccg att aac gca gag gat acc tac gaa cta aga   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

cag ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag ttg ggc ttt agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 901
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 26-15D10

<400> 901

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
```

```
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 902
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT26-20H11

<400> 902

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

cag ggc cag aaa cag tat cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgc gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
```

```
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac agg aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 903
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 26-20H11

<400> 903

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 904
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT26-20H12

<400> 904
```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

ggc gac tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Gly Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

cag ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtc aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

atc cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tca gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag ggg gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg ccg gtg gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 905
<211> 146
<212> PRT
<213> Artificial Sequence

<220>

<223> 26-20H12

<400> 905
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Gly Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 906
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT25-8H7

<400> 906
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30

agc gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35   40   45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50   55   60

caa ggc aag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240

```
Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gcg gac atg att tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110

tct gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 907
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 25-8H7

```
<400> 907
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 908

<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT25-14C12

<400> 908
```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg gtt tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Val Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att ctg cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 909
<211> 146

<212> PRT
<213> Artificial Sequence

<220>
<223> 25-14C12

<400> 909
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Val Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 910
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT25-17F3

<400> 910
atg ata gag gta aaa ccg att aac gca gaa gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20   25   30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35   40   45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192

```
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tat cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgc aag agg ggg gcg gac atg att tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcg gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac gtc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Val Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 911
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 25-17F3

<400> 911

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Val Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
```

145

<210> 912
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT25-19C8

<400> 912
atg ata gag gta aaa ccg att aac gca gaa gat acc tat gac cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20   25   30

agc gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc 144
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35   40   45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt 192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50   55   60

caa ggc cag aaa cag tat cag ctt cga ggc gtg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65   70   75   80

tat cgt gag cag aag gcg ggt tcc agt cta gtc aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85   90   95

att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag 384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125

gta ttc gac acg ccg cca gta ggt cct cac atc ctg atg tat aaa agg 432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140

atc aca taa 441
Ile Thr *
145

<210> 913
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 25-19C8

<400> 913
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 914
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> GAT25-23C1

<400> 914
atg ata gag gta aaa ccg att aac gca gaa gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20   25   30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144

```
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc cgg aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Arg Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tac cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg ccg gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 915
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> 25-23C1

```
<400> 915
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Arg Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
```

```
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 916
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> R12G1

<400> 916
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac act gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc aag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg att tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110

tct gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
```

```
atc aca taa                                                             441
Ile Thr  *
145


<210> 917
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> R12G1

<400> 917
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145


<210> 918
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> R12G2

<400> 918
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
```

```
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac act gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc aag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg att tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110

tct gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 919
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> R12G2

```
<400> 919
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
```

```
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 920
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> R12G3

<400> 920

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30

aac gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Asn Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60

caa ggc aag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gcg gac atg att tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110

tct gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
```

```
gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 921
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> R12G3

<400> 921

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Asn Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 922
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> R12G4

<400> 922

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
```

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30

agc gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc aag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gcg gac atg att tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110

tct gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145


<210> 923
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> R12G4

<400> 923
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
```

```
    50                  55                  60
Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 924
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> R12G5

<400> 924

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc aag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg att tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110
```

```
tct gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 925
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> R12G5

```
<400> 925
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 926
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)

<223> R12G6

<400> 926

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

aac gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Asn Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc aag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg att tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110

tct gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 927
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> R12G6

<400> 927

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
```

```
            20                  25                  30
Asn Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50                  55                  60
Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 928
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> R12G7

<400> 928

```
atg ata gag gta aaa ccg att aac gca gaa gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

aac gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc cac ggg ggc   144
Asn Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe His Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac act gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc cag aaa cag tat cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95
```

```
att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag ttg ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg ccg gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 929
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> R12G7

<400> 929

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20                  25                  30
Asn Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe His Gly Gly
        35                  40                  45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50                  55                  60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
```

<210> 930
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence

<220>
<221> CDS
<222> (1)...(441)
<223> R12G8

<400> 930
atg ata gag gta aaa ccg att aac gca gaa gat acc tat gac cta agg 48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
1 5 10 15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat 96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
20 25 30

aac gat tta atg cgt agt gca ttt cac tta ggc ggc ttc cac ggg ggc 144
Asn Asp Leu Met Arg Ser Ala Phe His Leu Gly Gly Phe His Gly Gly
35 40 45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac act gaa ctt 192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
50 55 60

caa ggc cag aaa cag tat cag ctt cga ggt gtg gct acc ttg gaa ggt 240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65 70 75 80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa 288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
85 90 95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg cgg aca 336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
100 105 110

tcc gcc tca ggc tac tac aga aag ttg ggc ttc agc gag cag gga gag 384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
115 120 125

gta ttc gac acg ccg ccg gta gga cct cac atc ctg atg tat aaa agg 432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
130 135 140

atc aca taa 441
Ile Thr *
145

<210> 931
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> R12G8

<400> 931
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20   25   30
Asn Asp Leu Met Arg Ser Ala Phe His Leu Gly Gly Phe His Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 932
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4604SR

<220>
<221> CDS
<222> (1)...(441)
<223> encodes 20-H812 (SEQ 739)

<400> 932
atg ata gag gtg aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atc ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Ile Phe Glu
            20   25   30

agc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45

aga ctg att tcc gtc gct tca ttc cac cag gcc gag cac tct gaa ctt   192
Arg Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60

caa ggc cag aaa cag tac cag ctt cga ggt atg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Met Ala Thr Leu Glu Gly
65   70   75   80

```
tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg agg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145


<210> 933
<211> 449
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4609SR

<220>
<221> CDS
<222> (1)...(441)
<223> encodes 22-18C5 (SEQ 795)

<400> 933
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta acg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tct gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tat cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80
```

```
tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg agg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa ggcgcgcc                                             449
Ile Thr  *
145
```

<210> 934
<211> 449
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4610R

<220>
<221> CDS
<222> (1)...(441)
<223> encodes 22-16D8 (SEQ 793)

<400> 934

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta ctg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Leu Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
```

```
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg agg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttt agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa ggcgcgcc                                           449
Ile Thr  *
145


<210> 935
<211> 449
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4611R

<220>
<221> CDS
<222> (1)...(441)
<223> encodes 22-15B4 (SEQ 789)

<400> 935
atg ata gag gta aaa ccg att aac gca gaa gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

agc gat tta atg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Met Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
```

```
                85                  90                  95

att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg agg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa ggcgcgcc                                          449
Ile Thr  *
145
```

<210> 936
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4614SR

<220>
<221> CDS
<222> (1)...(441)
<223> encodes 24-5H5 (SEQ 849)

<400> 936

```
atg ata gag gta aaa ccg att aac gca gaa gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

aac gat tta atg cgt agt gca ttt cac tta ggc ggc ttc cac ggg ggc   144
Asn Asp Leu Met Arg Ser Ala Phe His Leu Gly Gly Phe His Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tct gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tat cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
```

```
att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg agg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag ttg ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg ccg gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 937
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4614VSR

<220>
<221> CDS
<222> (1)...(441)
<223> encodes 24-5H5 (SEQ 849)

<400> 937

```
atg ata gag gtg aaa ccg att aac gca gaa gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gat   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
             20                  25                  30

aac gat tta atg cgt agt gca ttt cac tta ggc ggc ttc cac ggg ggc   144
Asn Asp Leu Met Arg Ser Ala Phe His Leu Gly Gly Phe His Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tct gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tat cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95
```

```
att cta cgt aag agg ggg gcg gac atg ctt tgg tgt aat gcg agg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag ttg ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg ccg gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                      441
Ile Thr  *
145
```

<210> 938
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4615R

<220>
<221> CDS
<222> (1)...(441)
<223> encodes 23-2H11 (SEQ 837)

<400> 938

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

ggc gat tta atg cgt ggt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Gly Asp Leu Met Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cat gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgc aag agg ggg gcg gac cta ctt tgg tgt aat gcg agg aca   336
```

```
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 939
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4616R

<220>
<221> CDS
<222> (1)...(441)
<223> encodes 24-15C3 (SEQ 863)

<400> 939

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

cag ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg gga acc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Thr Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg agg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
```

```
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 940
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4617R

<220>
<221> CDS
<222> (1)...(441)
<223> encodes 23-6H10 (SEQ 845)

<400> 940

```
atg ata gag gta aaa ccg att aac gca gag gat acc tat gaa cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta acg cgt ggt gca ttt cac cta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu Leu
     50                  55                  60

caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac cta ctt tgg tgt aat gcg agg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
```

```
tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag ggg gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 941
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4618SR

<220>
<221> CDS
<222> (1)...(441)
<223> encodes 25-8H7 (SEQ 907)

```
<400> 941
atg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tct gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc aag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg att tgg tgt aat gcg agg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110
```

```
tct gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 942
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4618VSR

<220>
<221> CDS
<222> (1)...(441)
<223> encodes 25-8H7 (SEQ 907)

```
<400> 942
atg ata gag gtg aaa ccg att aac gca gag gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
             20                  25                  30

agc gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tct gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc aag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa ggt   240
Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                 85                  90                  95

att cta cgt aag agg ggg gcg gac atg att tgg tgt aat gcg agg aca   336
Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg Thr
            100                 105                 110

tct gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
```

```
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125

gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 943
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4619SR

<220>
<221> CDS
<222> (1)...(441)
<223> encodes 25-19C8 (SEQ 913)

<400> 943

```
atg ata gag gta aaa ccg att aac gca gaa gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30

agc gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tct gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tat cag ctt cga ggc gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtc aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg agg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
```

```
        115                 120                 125

gta ttc gac acg ccg cca gta ggt cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145


<210> 944
<211> 441
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4619VSR

<220>
<221> CDS
<222> (1)...(441)
<223> encodes 25-19C8 (SEQ 913)

<400> 944
atg ata gag gtg aaa ccg att aac gca gaa gat acc tat gac cta agg   48
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1               5                  10                  15

cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt gaa   96
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20                  25                  30

agc gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg ggc   144
Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
         35                  40                  45

aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tct gaa ctt   192
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
     50                  55                  60

caa ggc cag aaa cag tat cag ctt cga ggc gtg gct acc ttg gaa ggt   240
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
 65                  70                  75                  80

tat cgt gag cag aag gcg ggt tcc agt cta gtc aaa cac gct gaa gaa   288
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95

att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg agg aca   336
Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110

tcc gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga gag   384
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
```

```
gta ttc gac acg ccg cca gta ggt cct cac atc ctg atg tat aaa agg   432
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140

atc aca taa                                                       441
Ile Thr  *
145
```

<210> 945
<211> 452
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4611A

<220>
<221> CDS
<222> (1)...(444)
<223> encodes 22-15B4 M1MA

<400> 945

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atg gcg ata gag gta aaa ccg att aac gca gaa gat acc tat gac cta   48
Met Ala Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu
 1               5                  10                  15

agg cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt   96
Arg His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe
            20                  25                  30

gat agc gat tta atg cgt agt gca ttt cac tta ggc ggc ttc tac ggg   144
Asp Ser Asp Leu Met Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly
        35                  40                  45

ggc aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg gaa   192
Gly Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu
    50                  55                  60

ctt caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa   240
Leu Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu
65                  70                  75                  80

ggt tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa   288
Gly Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu
                85                  90                  95

gaa att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg cgg   336
Glu Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg
            100                 105                 110

aca tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag gga   384
Thr Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly
        115                 120                 125
```

```
gag gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa   432
Glu Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys
    130                 135                 140

agg atc aca taa ggcgcgcc                                      452
Arg Ile Thr  *
145
```

<210> 946
<211> 147
<212> PRT
<213> Artificial Sequence

<220>
<223> 22-15B4 M1MA

<400> 946

```
Met Ala Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu
 1               5                  10                  15
Arg His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe
            20                  25                  30
Asp Ser Asp Leu Met Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly
        35                  40                  45
Gly Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr Glu
    50                  55                  60
Leu Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu
65                  70                  75                  80
Gly Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu
                85                  90                  95
Glu Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala Arg
            100                 105                 110
Thr Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln Gly
        115                 120                 125
Glu Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys
    130                 135                 140
Arg Ile Thr
145
```

<210> 947
<211> 455
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4611AA

<220>
<221> CDS
<222> (1)...(447)
<223> encodes 22-15B4 M1MAA

<400> 947

```
atg gcg gcc ata gag gta aaa ccg att aac gca gaa gat acc tat gac   48
Met Ala Ala Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp
```

```
 1               5                  10                  15

cta agg cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg   96
Leu Arg His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met
            20                  25                  30

ttt gat agc gat tta atg cgt agt gca ttt cac tta ggc ggc ttc tac   144
Phe Asp Ser Asp Leu Met Arg Ser Ala Phe His Leu Gly Gly Phe Tyr
        35                  40                  45

ggg ggc aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac acg   192
Gly Gly Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr
    50                  55                  60

gaa ctt caa ggc cag aaa cag tac cag ctt cga ggt gtg gct acc ttg   240
Glu Leu Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu
65                  70                  75                  80

gaa ggt tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct   288
Glu Gly Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala
                85                  90                  95

gaa gaa att cta cgt aag agg ggg gtg gac cta ctt tgg tgt aat gcg   336
Glu Glu Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala
            100                 105                 110

cgg aca tcc gcc tca ggc tac tac aaa aag tta ggc ttc agc gag cag   384
Arg Thr Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln
        115                 120                 125

gga gag gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat   432
Gly Glu Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr
    130                 135                 140

aaa agg atc aca taa ggcgcgcc                                     455
Lys Arg Ile Thr  *
145
```

<210> 948
<211> 148
<212> PRT
<213> Artificial Sequence

<220>
<223> 22-15B4 M1MAA

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<400> 948
Met Ala Ala Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp
 1               5                  10                  15
Leu Arg His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met
            20                  25                  30
Phe Asp Ser Asp Leu Met Arg Ser Ala Phe His Leu Gly Gly Phe Tyr
        35                  40                  45
Gly Gly Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Thr
    50                  55                  60
```

```
Glu Leu Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu
65                  70                  75                  80
Glu Gly Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala
                85                  90                  95
Glu Glu Ile Leu Arg Lys Arg Gly Val Asp Leu Leu Trp Cys Asn Ala
            100                 105                 110
Arg Thr Ser Ala Ser Gly Tyr Tyr Lys Lys Leu Gly Phe Ser Glu Gln
        115                 120                 125
Gly Glu Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr
    130                 135                 140
Lys Arg Ile Thr
145
```

<210> 949
<211> 444
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4618A

<220>
<221> CDS
<222> (1)...(444)
<223> encodes 25-8H7 M1MA

<400> 949

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atg gcg ata gag gta aaa ccg att aac gca gag gat acc tat gac cta   48
Met Ala Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu
 1               5                  10                  15

agg cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt   96
Arg His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe
             20                  25                  30

gaa agc gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg   144
Glu Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly
         35                  40                  45

ggc aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tcg gaa   192
Gly Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu
     50                  55                  60

ctt caa ggc aag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa   240
Leu Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu
 65                  70                  75                  80

ggt tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa   288
Gly Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu
                 85                  90                  95

gaa att cta cgt aag agg ggg gcg gac atg att tgg tgt aat gcg cgg   336
Glu Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg
            100                 105                 110
```

```
aca tct gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga   384
Thr Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly
        115                 120                 125

gag gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa   432
Glu Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys
    130                 135                 140

agg atc aca taa                                                   444
Arg Ile Thr  *
145
```

<210> 950
<211> 147
<212> PRT
<213> Artificial Sequence

<220>
<223> 25-8H7 M1MA

<400> 950

```
Met Ala Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu
 1               5                  10                  15
Arg His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe
            20                  25                  30
Glu Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly
        35                  40                  45
Gly Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu
    50                  55                  60
Leu Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu
65                  70                  75                  80
Gly Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu
                85                  90                  95
Glu Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg
            100                 105                 110
Thr Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly
        115                 120                 125
Glu Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys
    130                 135                 140
Arg Ile Thr
145
```

<210> 951
<211> 444
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4620

<220>
<221> CDS
<222> (1)...(444)
<223> encodes 25-8H7 M1MA (SEQ ID NO:950)

<400> 951
atg gct att gag gtt aaa cct att aac gca gag gat acc tat gac cta 48
Met Ala Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu
 1   5   10   15

agg cat aga gtc ctc aga cca aac cag ccg ata gaa gcg tgt atg ttt 96
Arg His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe
            20   25   30

gaa agc gat tta acg cgt agt gca ttt cac tta ggc ggc ttc tac ggg 144
Glu Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly
         35   40   45

ggc aaa ctg att tcc gtc gct tca ttc cac cag gcc gag cac tct gaa 192
Gly Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu
     50   55   60

ctt caa ggc aag aaa cag tac cag ctt cga ggt gtg gct acc ttg gaa 240
Leu Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu
 65   70   75   80

ggt tat cgt gag cag aag gcg ggt tcc agt cta gtt aaa cac gct gaa 288
Gly Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu
                85   90   95

gaa att cta cgt aag agg ggg gcg gac atg att tgg tgt aat gcg agg 336
Glu Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg
            100   105   110

aca tct gcc tca ggc tac tac aga aag tta ggc ttc agc gag cag gga 384
Thr Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly
        115   120   125

gag gta ttc gac acg ccg cca gta gga cct cac atc ctg atg tat aaa 432
Glu Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys
    130   135   140

agg atc aca taa 444
Arg Ile Thr *
145

<210> 952
<211> 444
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic nucleic acid sequence GAT4621

<220>
<221> CDS
<222> (1)...(444)
<223> encodes 25-8H7 M1MA (SEQ ID NO:950)

<400> 952
atg gct att gag gtt aag cct atc aac gca gag gat acc tat gac ctt 48
Met Ala Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu
1 5 10 15

agg cat aga gtg ctc aga cca aac cag cct atc gaa gcc tgc atg ttt 96
Arg His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe
20 25 30

gag tct gac ctt act agg agt gca ttt cac ctt ggt gga ttc tac gga 144
Glu Ser Asp Leu Thr Arg Ser Ala Phe His Leu Gly Gly Phe Tyr Gly
35 40 45

ggt aaa ctg att tcc gtg gct tca ttc cac caa gct gag cac tct gaa 192
Gly Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu
50 55 60

ctt caa ggt aag aag cag tac cag ctt aga ggt gtg gct acc ttg gaa 240
Leu Gln Gly Lys Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu
65 70 75 80

ggt tat aga gag cag aag gct ggt tcc agt ctc gtg aaa cac gct gaa 288
Gly Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu
85 90 95

gag att ctc aga aag aga ggt gct gac atg atc tgg tgt aat gcc agg 336
Glu Ile Leu Arg Lys Arg Gly Ala Asp Met Ile Trp Cys Asn Ala Arg
100 105 110

aca tct gct tca gga tac tac agg aag ttg gga ttc agt gag caa gga 384
Thr Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly
115 120 125

gag gtg ttc gat act cct cca gtt gga cct cac atc ctg atg tat aag 432
Glu Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys
130 135 140

agg atc aca taa 444
Arg Ile Thr *
145

<210> 953
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> fil 3 con

<221> VARIANT
<222> 4
<223> Val or Ile

<221> VARIANT
<222> 14

<223> Asp or Glu

<221> VARIANT
<222> 18
<223> Arg or Lys

<221> VARIANT
<222> 19
<223> Val or Ile

<221> VARIANT
<222> 26
<223> Ile or Leu or Val

<221> VARIANT
<222> 28
<223> Ala or Val

<221> VARIANT
<222> 30
<223> Met or Ile

<221> VARIANT
<222> 31
<223> Phe or Tyr

<221> VARIANT
<222> 32
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<221> VARIANT
<222> 33
<223> Ser or Asn

<221> VARIANT
<222> 36
<223> Thr or Met or Leu

<221> VARIANT
<222> 38
<223> Gly or Ser

<221> VARIANT
<222> 45
<223> Phe or Tyr

<221> VARIANT
<222> 47
<223> Gly or Arg

<221> VARIANT
<222> 49
<223> Lys or Arg

<221> VARIANT
<222> 51

<223> Ile or Val

<221> VARIANT
<222> 53
<223> Val or Ile

<221> VARIANT
<222> 58
<223> Gln or Arg

<221> VARIANT
<222> 60
<223> Glu or Gly

<221> VARIANT
<222> 62
<223> Ser or Thr

<221> VARIANT
<222> 63
<223> Glu or Asp

<221> VARIANT
<222> 64
<223> Leu or Ile

<221> VARIANT
<222> 67
<223> Gln or Lys or Arg

<221> VARIANT
<222> 72
<223> Leu or Ile

<221> VARIANT
<222> 75
<223> Val or Met

<221> VARIANT
<222> 83
<223> Asp or Glu

<221> VARIANT
<222> 88
<223> Ser or Thr

<221> VARIANT
<222> 89
<223> Ser or Thr

<221> VARIANT
<222> 91
<223> Val or Ile or Leu

<221> VARIANT
<222> 92

<223> Lys or Arg

<221> VARIANT
<222> 98
<223> Leu or Ile

<221> VARIANT
<222> 103
<223> Ala or Val

<221> VARIANT
<222> 105
<223> Met or Leu or Ile

<221> VARIANT
<222> 106
<223> Ile or Leu

<221> VARIANT
<222> 117
<223> Tyr or Phe

<221> VARIANT
<222> 119
<223> Arg or Lys

<221> VARIANT
<222> 128
<223> Glu or Asp

<221> VARIANT
<222> 129
<223> Val or Ile

<221> VARIANT
<222> 131
<223> Asp or Glu

<221> VARIANT
<222> 135
<223> Val or Ala

<221> VARIANT
<222> 139
<223> Ile or Val

<221> VARIANT
<222> 140
<223> Leu or Met

<221> VARIANT
<222> 145
<223> Ile or Leu

<400> 953
Met Ile Glu Xaa Lys Pro Ile Asn Ala Glu Asp Thr Tyr Xaa Leu Arg

```
 1               5                  10                  15
His Xaa Xaa Leu Arg Pro Asn Gln Pro Xaa Glu Xaa Cys Xaa Xaa Xaa
            20                  25                  30
Xaa Asp Leu Xaa Arg Xaa Ala Phe His Leu Gly Gly Xaa Tyr Xaa Gly
        35                  40                  45
Xaa Leu Xaa Ser Xaa Ala Ser Phe His Xaa Ala Xaa His Xaa Xaa Xaa
    50                  55                  60
Gln Gly Xaa Lys Gln Tyr Gln Xaa Arg Gly Xaa Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Xaa Gln Lys Ala Gly Xaa Xaa Leu Xaa Xaa His Ala Glu Glu
                85                  90                  95
Ile Xaa Arg Lys Arg Gly Xaa Asp Xaa Xaa Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Xaa Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Xaa
        115                 120                 125
Xaa Phe Xaa Thr Pro Pro Xaa Gly Pro His Xaa Xaa Met Tyr Lys Arg
    130                 135                 140
Xaa Thr
145
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<210> 954
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> con alt a

<221> VARIANT
<222> 14
<223> Asp or Glu

<221> VARIANT
<222> 32
<223> Glu or Asp

<221> VARIANT
<222> 33
<223> Ser or Asn

<221> VARIANT
<222> 38
<223> Gly or Ser

<221> VARIANT
<222> 46
<223> His or Tyr

<221> VARIANT
<222> 51
<223> Ile or Val

<221> VARIANT
<222> 58
<223> Gln or Arg

<221> VARIANT
<222> 60
<223> Glu or Gly

<221> VARIANT
<222> 62
<223> Ser or Thr

<221> VARIANT
<222> 67
<223> Gln or Lys

<221> VARIANT
<222> 88
<223> Ser or Thr

<221> VARIANT
<222> 103
<223> Ala or Val

<221> VARIANT
<222> 105
<223> Met or Leu

<221> VARIANT
<222> 106
<223> Ile or Leu

<221> VARIANT
<222> 119
<223> Arg or Lys

<221> VARIANT
<222> 139
<223> Ile or Val

<400> 954

```
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Xaa Leu Arg
 1               5                  10                  15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Xaa
            20                  25                  30
Xaa Asp Leu Met Arg Xaa Ala Phe His Leu Gly Gly Phe Xaa Gly Gly
        35                  40                  45
Lys Leu Xaa Ser Val Ala Ser Phe His Xaa Ala Xaa His Xaa Glu Leu
    50                  55                  60
Gln Gly Xaa Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Xaa Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Xaa Asp Xaa Xaa Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Xaa Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
```

145

<210> 955
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> con alt b

<221> VARIANT
<222> 14
<223> Asp or Glu

<221> VARIANT
<222> 32
<223> Glu or Asp

<221> VARIANT
<222> 33
<223> Ser or Asn

<221> VARIANT
<222> 38
<223> Gly or Ser

<221> VARIANT
<222> 46
<223> His or Tyr

<221> VARIANT
<222> 51
<223> Ile or Val

<221> VARIANT
<222> 58
<223> Gln or Arg

<221> VARIANT
<222> 60
<223> Glu or Gly

<221> VARIANT
<222> 62
<223> Ser or Thr

<221> VARIANT
<222> 67
<223> Gln or Lys

<221> VARIANT
<222> 88
<223> Ser or Thr

<221> VARIANT
<222> 103

<223> Ala or Val

<221> VARIANT
<222> 106
<223> Ile or Leu

<221> VARIANT
<222> 119
<223> Arg or Lys

<221> VARIANT
<222> 139
<223> Ile or Val

<400> 955
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Xaa Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Xaa
            20   25   30
Xaa Asp Leu Thr Arg Xaa Ala Phe His Leu Gly Gly Phe Xaa Gly Gly
        35   40   45
Lys Leu Xaa Ser Val Ala Ser Phe His Xaa Ala Xaa His Xaa Glu Leu
    50   55   60
Gln Gly Xaa Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Xaa Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Xaa Asp Met Xaa Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Xaa Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 956
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> con alt c

<400> 956
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Glu
            20   25   30
Ser Asp Leu Thr Arg Gly Ala Phe His Leu Gly Gly Phe Tyr Gly Gly
        35   40   45
Lys Leu Ile Ser Val Ala Ser Phe His Gln Ala Glu His Ser Glu Leu
    50   55   60
Gln Gly Gln Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu

```
                85                  90                  95
Ile Leu Arg Lys Arg Gly Ala Asp Met Leu Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Ile Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145

<210> 957
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> con alt e

<221> VARIANT
<222> 14
<223> Asp or Glu

<221> VARIANT
<222> 33
<223> Gly or Ser or Asn

<221> VARIANT
<222> 38
<223> Gly or Ser

<221> VARIANT
<222> 46
<223> His or Tyr

<221> VARIANT
<222> 51
<223> Ile or Val

<221> VARIANT
<222> 58
<223> Gln or Arg

<221> VARIANT
<222> 60
<223> Glu or Gly

<221> VARIANT
<222> 62
<223> Ser or Thr

<221> VARIANT
<222> 67
<223> Gln or Lys or Arg

<221> VARIANT
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<223> Ser or Thr

<221> VARIANT
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<221> VARIANT
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<223> Ile or Leu

<221> VARIANT
<222> 119
<223> Arg or Lys

<221> VARIANT
<222> 139
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<400> 957
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Xaa Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20   25   30
Xaa Asp Leu Thr Arg Xaa Ala Phe His Leu Gly Gly Phe Xaa Gly Gly
        35   40   45
Lys Leu Xaa Ser Val Ala Ser Phe His Xaa Ala Xaa His Xaa Glu Leu
    50   55   60
Gln Gly Xaa Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Xaa Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Xaa Asp Xaa Xaa Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Xaa Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 958
<211> 146
<212> PRT
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<220>
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<221> VARIANT
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<221> VARIANT
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<223> Gly or Ser

<221> VARIANT
<222> 46
<223> His or Tyr

<221> VARIANT
<222> 51
<223> Ile or Val

<221> VARIANT
<222> 58
<223> Gln or Arg

<221> VARIANT
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<223> Glu or Gly

<221> VARIANT
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<223> Ser or Thr

<221> VARIANT
<222> 67
<223> Gln or Lys or Arg

<221> VARIANT
<222> 88
<223> Ser or Thr

<221> VARIANT
<222> 103
<223> Ala or Val

<221> VARIANT
<222> 106
<223> Ile or Leu

<221> VARIANT
<222> 119
<223> Arg or Lys

<221> VARIANT
<222> 139
<223> Ile or Val

<400> 958
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Xaa
            20   25   30
Xaa Asp Leu Xaa Arg Xaa Ala Phe His Leu Gly Gly Phe Xaa Gly Gly
        35   40   45
Lys Leu Xaa Ser Val Ala Ser Phe His Xaa Ala Xaa His Xaa Glu Leu
    50   55   60
Gln Gly Xaa Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Xaa Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Xaa Asp Leu Xaa Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Xaa Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 959
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
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<221> VARIANT
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<221> VARIANT
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<223> His or Tyr

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<223> Gln or Lys or Arg

<221> VARIANT
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<221> VARIANT
<222> 103
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<221> VARIANT
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<223> Leu or Met

<221> VARIANT
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<223> Ile or Leu

<221> VARIANT
<222> 119
<223> Arg or Lys

<221> VARIANT
<222> 139
<223> Ile or Val

<400> 959
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Glu Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20   25   30
Xaa Asp Leu Met Arg Xaa Ala Phe His Leu Gly Gly Phe Xaa Gly Gly
        35   40   45
Lys Leu Xaa Ser Val Ala Ser Phe His Xaa Ala Xaa His Xaa Glu Leu
    50   55   60
Gln Gly Xaa Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Xaa Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Xaa Asp Xaa Xaa Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Xaa Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 960
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
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<221> VARIANT
<222> 32
<223> Glu or Asp

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<223> Gly or Ser or Asn

<221> VARIANT
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<223> Thr or Met

<221> VARIANT
<222> 46
<223> His or Tyr

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<223> Ser or Thr

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<223> Gln or Lys or Arg

<221> VARIANT
<222> 88
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<221> VARIANT
<222> 103
<223> Ala or Val

<221> VARIANT
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<223> Leu or Met

<221> VARIANT
<222> 106
<223> Ile or Leu

<221> VARIANT
<222> 119
<223> Arg or Lys

<221> VARIANT
<222> 139
<223> Ile or Val

<400> 960
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Xaa Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Xaa
            20   25   30
Xaa Asp Leu Xaa Arg Ser Ala Phe His Leu Gly Gly Phe Xaa Gly Gly
        35   40   45
Lys Leu Xaa Ser Val Ala Ser Phe His Xaa Ala Xaa His Xaa Glu Leu
    50   55   60
Gln Gly Xaa Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Xaa Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Xaa Asp Xaa Xaa Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Xaa Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 961
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> con alt i

<221> VARIANT
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<221> VARIANT
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<223> Thr or Met

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<223> His or Tyr

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<223> Gln or Lys or Arg

<221> VARIANT
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<223> Ser or Thr

<221> VARIANT
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<221> VARIANT
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<223> Leu or Met

<221> VARIANT
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<223> Ile or Leu

<221> VARIANT
<222> 119
<223> Arg or Lys

<221> VARIANT
<222> 139
<223> Ile or Val

<400> 961
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Xaa Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Asp
            20   25   30
Asn Asp Leu Xaa Arg Xaa Ala Phe His Leu Gly Gly Phe Xaa Gly Gly
        35   40   45
Lys Leu Xaa Ser Val Ala Ser Phe His Xaa Ala Xaa His Xaa Glu Leu
    50   55   60
Gln Gly Xaa Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly

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65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Xaa Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Xaa Asp Xaa Xaa Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Xaa Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145

<210> 962
<211> 146
<212> PRT
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<220>
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<222> 32
<223> Glu or Asp

<221> VARIANT
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<223> Gly or Ser or Asn

<221> VARIANT
<222> 36
<223> Thr or Met

<221> VARIANT
<222> 38
<223> Gly or Ser

<221> VARIANT
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<223> His or Tyr

<221> VARIANT
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<223> Ile or Val

<221> VARIANT
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<221> VARIANT
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<223> Gln or Lys or Arg

<221> VARIANT
<222> 88
<223> Ser or Thr

<221> VARIANT
<222> 103
<223> Ala or Val

<221> VARIANT
<222> 106
<223> Ile or Leu

<221> VARIANT
<222> 119
<223> Arg or Lys

<221> VARIANT
<222> 139
<223> Ile or Val

<400> 962
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Xaa Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Xaa
            20   25   30
Xaa Asp Leu Xaa Arg Xaa Ala Phe His Leu Gly Gly Phe Xaa Gly Gly
        35   40   45
Lys Leu Xaa Ser Val Ala Ser Phe His Xaa Ala Xaa His Xaa Glu Leu
    50   55   60
Gln Gly Xaa Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Glu Gln Lys Ala Gly Xaa Ser Leu Val Lys His Ala Glu Glu
                85   90   95
Ile Leu Arg Lys Arg Gly Xaa Asp Met Xaa Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Tyr Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115   120   125
Val Phe Asp Thr Pro Pro Val Gly Pro His Xaa Leu Met Tyr Lys Arg
    130   135   140
Ile Thr
145

<210> 963
<211> 146
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<223> Arg or Lys

<221> VARIANT
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<223> Ile or Leu or Val

<221> VARIANT
<222> 28
<223> Ala or Val

<221> VARIANT
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<223> Met or Ile

<221> VARIANT
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<221> VARIANT
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<221> VARIANT
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<223> Ser or Asn

<221> VARIANT
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<223> Gly or Ser

<221> VARIANT
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<223> Phe or Tyr

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<221> VARIANT
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<223> Lys or Arg

<221> VARIANT
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<221> VARIANT
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<221> VARIANT
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<223> Gln or Arg

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<221> VARIANT
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<223> Gln or Lys or Arg

<221> VARIANT
<222> 72
<223> Leu or Ile

<221> VARIANT
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<223> Val or Met

<221> VARIANT
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<221> VARIANT
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<223> Ser or Thr

<221> VARIANT
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<223> Ser or Thr

<221> VARIANT
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<223> Val or Ile or Leu

<221> VARIANT
<222> 92
<223> Lys or Arg

<221> VARIANT
<222> 98

<223> Leu or Ile

<221> VARIANT
<222> 103
<223> Ala or Val

<221> VARIANT
<222> 105
<223> Met or Leu or Ile

<221> VARIANT
<222> 106
<223> Ile or Leu

<221> VARIANT
<222> 117
<223> Tyr or Phe

<221> VARIANT
<222> 119
<223> Arg or Lys

<221> VARIANT
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<223> Glu or Asp

<221> VARIANT
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<223> Val or Ile

<221> VARIANT
<222> 131
<223> Asp or Glu

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<221> VARIANT
<222> 139
<223> Ile or Val

<221> VARIANT
<222> 140
<223> Leu or Met

<221> VARIANT
<222> 145
<223> Ile or Leu

<400> 963
Met Ile Glu Xaa Lys Pro Ile Asn Ala Glu Asp Thr Tyr Asp Leu Arg
 1   5   10   15
His Xaa Val Leu Arg Pro Asn Gln Pro Xaa Glu Xaa Cys Xaa Xaa Xaa
            20   25   30
Xaa Asp Leu Met Arg Xaa Ala Phe His Leu Gly Gly Xaa Tyr Xaa Gly

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        35                  40                  45
Xaa Leu Xaa Ser Xaa Ala Ser Phe His Xaa Ala Xaa His Xaa Xaa Xaa
    50                  55                  60
Gln Gly Xaa Lys Gln Tyr Gln Xaa Arg Gly Xaa Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Xaa Gln Lys Ala Gly Xaa Xaa Leu Xaa Xaa His Ala Glu Glu
                85                  90                  95
Ile Xaa Arg Lys Arg Gly Xaa Asp Xaa Xaa Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Xaa Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Xaa
        115                 120                 125
Xaa Phe Xaa Thr Pro Pro Xaa Gly Pro His Xaa Xaa Met Tyr Lys Arg
    130                 135                 140
Xaa Thr
145
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<210> 964
<211> 146
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<213> Artificial Sequence

<220>
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<221> VARIANT
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<223> Arg or Lys

<221> VARIANT
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<223> Ile or Leu or Val

<221> VARIANT
<222> 28
<223> Ala or Val

<221> VARIANT
<222> 30
<223> Met or Ile

<221> VARIANT
<222> 31
<223> Phe or Tyr

<221> VARIANT
<222> 32
<223> Glu or Asp

<221> VARIANT
<222> 33
<223> Ser or Asn

<221> VARIANT
<222> 38
<223> Gly or Ser

<221> VARIANT
<222> 45
<223> Phe or Tyr

<221> VARIANT
<222> 47
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<221> VARIANT
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<223> Lys or Arg

<221> VARIANT
<222> 51
<223> Ile or Val

<221> VARIANT
<222> 58
<223> Gln or Arg

<221> VARIANT
<222> 60
<223> Glu or Gly

<221> VARIANT
<222> 62
<223> Ser or Thr

<221> VARIANT
<222> 63
<223> Glu or Asp

<221> VARIANT
<222> 64
<223> Leu or Ile

<221> VARIANT
<222> 67
<223> Gln or Lys or Arg

<221> VARIANT
<222> 72
<223> Leu or Ile

<221> VARIANT
<222> 75
<223> Val or Met

<221> VARIANT
<222> 83
<223> Asp or Glu

<221> VARIANT
<222> 88
<223> Ser or Thr

<221> VARIANT
<222> 89
<223> Ser or Thr

<221> VARIANT
<222> 91
<223> Val or Ile or Leu

<221> VARIANT
<222> 92
<223> Lys or Arg

<221> VARIANT
<222> 98
<223> Leu or Ile

<221> VARIANT
<222> 103
<223> Ala or Val

<221> VARIANT
<222> 105
<223> Met or Leu or Ile

<221> VARIANT
<222> 106
<223> Ile or Leu

<221> VARIANT
<222> 117
<223> Tyr or Phe

<221> VARIANT
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<221> VARIANT
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<221> VARIANT
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<223> Val or Ile

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<221> VARIANT
<222> 139
<223> Ile or Val

<221> VARIANT
<222> 140
<223> Leu or Met

<221> VARIANT
<222> 145
<223> Ile or Leu

<400> 964
Met Ile Glu Xaa Lys Pro Ile Asn Ala Glu Asp Thr Tyr Xaa Leu Arg
 1   5   10   15
His Xaa Val Leu Arg Pro Asn Gln Pro Xaa Glu Xaa Cys Xaa Xaa Xaa
            20   25   30
Xaa Asp Leu Met Arg Xaa Ala Phe His Leu Gly Gly Xaa Tyr Xaa Gly
        35   40   45
Xaa Leu Xaa Ser Val Ala Ser Phe His Xaa Ala Xaa His Xaa Xaa Xaa
    50   55   60
Gln Gly Xaa Lys Gln Tyr Gln Xaa Arg Gly Xaa Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Xaa Gln Lys Ala Gly Xaa Xaa Leu Xaa Xaa His Ala Glu Glu
                85   90   95
Ile Xaa Arg Lys Arg Gly Xaa Asp Xaa Xaa Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Xaa Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Xaa
        115   120   125
Xaa Phe Xaa Thr Pro Pro Xaa Gly Pro His Xaa Xaa Met Tyr Lys Arg
    130   135   140
Xaa Thr
145

<210> 965
<211> 146
<212> PRT
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<220>
<223> con alt d

<221> VARIANT
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<221> VARIANT
<222> 32
<223> Glu or Asp

<221> VARIANT
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<223> Ser or Asn or Gly

<221> VARIANT
<222> 36
<223> Thr or Met

<221> VARIANT
<222> 46
<223> His or Tyr

<221> VARIANT
<222> 51
<223> Ile or Val

<221> VARIANT
<222> 58
<223> Gln or Arg

<221> VARIANT
<222> 60
<223> Glu or Gly

<221> VARIANT
<222> 67
<223> Gln or Lys or Arg

<221> VARIANT
<222> 103
<223> Ala or Val

<221> VARIANT
<222> 105
<223> Met or Leu

<221> VARIANT
<222> 106
<223> Ile or Leu

<221> VARIANT
<222> 119
<223> Arg or Lys

<221> VARIANT
<222> 139
<223> Ile or Val

<400> 965
Met Ile Glu Val Lys Pro Ile Asn Ala Glu Asp Thr Tyr Xaa Leu Arg
 1   5   10   15
His Arg Val Leu Arg Pro Asn Gln Pro Ile Glu Ala Cys Met Phe Xaa
            20   25   30
Xaa Asp Leu Xaa Arg Xaa Ala Phe His Leu Gly Gly Phe Xaa Gly Gly
        35   40   45
Lys Leu Xaa Ser Val Ala Ser Phe His Xaa Ala Xaa His Thr Glu Leu
    50   55   60
Gln Gly Xaa Lys Gln Tyr Gln Leu Arg Gly Val Ala Thr Leu Glu Gly

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65                  70                  75                  80
Tyr Arg Glu Gln Lys Ala Gly Ser Ser Leu Val Lys His Ala Glu Glu
                85                  90                  95
Ile Leu Arg Lys Arg Gly Xaa Asp Xaa Xaa Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Tyr Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Glu
        115                 120                 125
Val Phe Asp Thr Pro Pro Val Gly Pro His Xaa Leu Met Tyr Lys Arg
    130                 135                 140
Ile Thr
145
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<210> 966
<211> 146
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<220>
<223> con alt n

<221> VARIANT
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<223> Val or Ile

<221> VARIANT
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<223> Asp or Glu

<221> VARIANT
<222> 18
<223> Arg or Lys

<221> VARIANT
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<223> Val or Ile

<221> VARIANT
<222> 26
<223> Ile or Leu or Val

<221> VARIANT
<222> 28
<223> Ala or Val

<221> VARIANT
<222> 30
<223> Met or Ile

<221> VARIANT
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<221> VARIANT
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<223> Glu or Asp

<221> VARIANT
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<223> Ser or Asn

<221> VARIANT
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<223> Thr or Met or Leu

<221> VARIANT
<222> 38
<223> Gly or Ser

<221> VARIANT
<222> 45
<223> Phe or Tyr

<221> VARIANT
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<223> Gly or Arg

<221> VARIANT
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<221> VARIANT
<222> 51
<223> Ile or Val

<221> VARIANT
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<223> Val or Ile

<221> VARIANT
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<221> VARIANT
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<221> VARIANT
<222> 64
<223> Leu or Ile

<221> VARIANT
<222> 67
<223> Gln or Lys or Arg

<221> VARIANT
<222> 72
<223> Leu or Ile

<221> VARIANT
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<223> Val or Met

<221> VARIANT
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<223> Asp or Glu

<221> VARIANT
<222> 89
<223> Ser or Thr

<221> VARIANT
<222> 91
<223> Val or Ile or Leu

<221> VARIANT
<222> 92
<223> Lys or Arg

<221> VARIANT
<222> 98
<223> Leu or Ile

<221> VARIANT
<222> 103
<223> Ala or Val

<221> VARIANT
<222> 105
<223> Met or Leu or Ile

<221> VARIANT
<222> 106
<223> Ile or Leu

<221> VARIANT
<222> 117
<223> Tyr or Phe

<221> VARIANT
<222> 119
<223> Arg or Lys

<221> VARIANT
<222> 128
<223> Glu or Asp

<221> VARIANT
<222> 129
<223> Val or Ile

<221> VARIANT
<222> 131
<223> Asp or Glu

<221> VARIANT
<222> 135
<223> Val or Ala

<221> VARIANT
<222> 139
<223> Ile or Val

<221> VARIANT
<222> 140
<223> Leu or Met

<221> VARIANT
<222> 145
<223> Ile or Leu

<400> 966
Met Ile Glu Xaa Lys Pro Ile Asn Ala Glu Asp Thr Tyr Xaa Leu Arg
 1   5   10   15
His Xaa Xaa Leu Arg Pro Asn Gln Pro Xaa Glu Xaa Cys Xaa Xaa Xaa
            20   25   30
Xaa Asp Leu Xaa Arg Xaa Ala Phe His Leu Gly Gly Xaa Tyr Xaa Gly
        35   40   45
Xaa Leu Xaa Ser Xaa Ala Ser Phe His Xaa Ala Xaa His Xaa Xaa Xaa
    50   55   60
Gln Gly Xaa Lys Gln Tyr Gln Xaa Arg Gly Xaa Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Xaa Gln Lys Ala Gly Thr Xaa Leu Xaa Xaa His Ala Glu Glu
                85   90   95
Ile Xaa Arg Lys Arg Gly Xaa Asp Xaa Xaa Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Xaa Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Xaa
        115   120   125
Xaa Phe Xaa Thr Pro Pro Xaa Gly Pro His Xaa Xaa Met Tyr Lys Arg
    130   135   140
Xaa Thr
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His Xaa Xaa Leu Arg Pro Asn Gln Pro Xaa Glu Xaa Cys Xaa Xaa Xaa
            20   25   30
Xaa Asp Leu Xaa Arg Xaa Ala Phe His Leu Gly Gly Xaa Tyr Xaa Gly
        35   40   45
Xaa Leu Xaa Ser Xaa Ala Ser Phe His Xaa Ala Xaa His Xaa Xaa Xaa
    50   55   60
Gln Gly Xaa Lys Gln Tyr Gln Xaa Arg Gly Xaa Ala Thr Leu Glu Gly

65 70 75 80
Tyr Arg Xaa Gln Lys Ala Gly Xaa Xaa Leu Xaa Xaa His Ala Glu Glu
85 90 95
Ile Xaa Arg Lys Arg Gly Xaa Asp Xaa Xaa Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Xaa Tyr Arg Lys Leu Gly Phe Ser Glu Gln Gly Xaa
115 120 125
Xaa Phe Asp Thr Pro Pro Xaa Gly Pro His Xaa Xaa Met Tyr Lys Arg
130 135 140
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His Xaa Val Leu Arg Pro Asn Gln Pro Xaa Glu Xaa Cys Xaa Xaa Xaa
            20   25   30
Xaa Asp Leu Xaa Arg Xaa Ala Phe His Leu Gly Gly Xaa Tyr Xaa Gly
        35   40   45
Xaa Leu Xaa Ser Xaa Ala Ser Phe His Xaa Ala Xaa His Xaa Xaa Xaa
    50   55   60
Gln Gly Xaa Lys Gln Tyr Gln Xaa Arg Gly Val Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Xaa Gln Lys Ala Gly Xaa Xaa Leu Xaa Xaa His Ala Glu Glu
                85   90   95
Ile Xaa Arg Lys Arg Gly Xaa Asp Xaa Xaa Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Xaa Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Xaa
        115   120   125
Xaa Phe Xaa Thr Pro Pro Xaa Gly Pro His Xaa Xaa Met Tyr Lys Arg
    130   135   140
Xaa Thr
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 1   5   10   15
His Xaa Xaa Leu Arg Pro Asn Gln Pro Xaa Glu Xaa Cys Xaa Xaa Xaa
            20   25   30
Xaa Asp Leu Xaa Arg Xaa Ala Phe His Leu Gly Gly Xaa Tyr Xaa Gly
        35   40   45
Arg Leu Xaa Ser Xaa Ala Ser Phe His Xaa Ala Xaa His Xaa Xaa Xaa
    50   55   60
Gln Gly Xaa Lys Gln Tyr Gln Xaa Arg Gly Xaa Ala Thr Leu Glu Gly

65 70 75 80
Tyr Arg Xaa Gln Lys Ala Gly Xaa Xaa Leu Xaa Xaa His Ala Glu Glu
85 90 95
Ile Xaa Arg Lys Arg Gly Xaa Asp Xaa Xaa Trp Cys Asn Ala Arg Thr
100 105 110
Ser Ala Ser Gly Xaa Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Xaa
115 120 125
Xaa Phe Xaa Thr Pro Pro Xaa Gly Pro His Xaa Xaa Met Tyr Lys Arg
130 135 140
Xaa Thr
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 1   5   10   15
His Xaa Xaa Leu Arg Pro Asn Gln Pro Xaa Glu Xaa Cys Xaa Xaa Xaa
            20   25   30
Xaa Asp Leu Xaa Arg Xaa Ala Phe His Leu Gly Gly Xaa Tyr Xaa Gly
        35   40   45
Xaa Leu Xaa Ser Val Ala Ser Phe His Xaa Ala Xaa His Xaa Xaa Xaa
    50   55   60
Gln Gly Xaa Lys Gln Tyr Gln Xaa Arg Gly Xaa Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Xaa Gln Lys Ala Gly Xaa Xaa Leu Xaa Xaa His Ala Glu Glu
                85   90   95
Ile Xaa Arg Lys Arg Gly Xaa Asp Xaa Xaa Trp Cys Asn Ala Arg Thr
            100   105   110
Ser Ala Ser Gly Xaa Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Xaa
        115   120   125
Xaa Phe Xaa Thr Pro Pro Xaa Gly Pro His Xaa Xaa Met Tyr Lys Arg
    130   135   140
Xaa Thr
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His Xaa Xaa Leu Arg Pro Asn Gln Pro Xaa Glu Xaa Cys Xaa Xaa Xaa
            20   25   30
Xaa Asp Leu Met Arg Xaa Ala Phe His Leu Gly Gly Xaa Tyr Xaa Gly
        35   40   45
Xaa Leu Xaa Ser Val Ala Ser Phe His Xaa Ala Xaa His Xaa Xaa Xaa
    50   55   60
Gln Gly Xaa Lys Gln Tyr Gln Xaa Arg Gly Xaa Ala Thr Leu Glu Gly
65   70   75   80
Tyr Arg Xaa Gln Lys Ala Gly Xaa Xaa Leu Xaa Xaa His Ala Glu Glu
                85   90   95
Ile Xaa Arg Lys Arg Gly Xaa Asp Xaa Xaa Trp Cys Asn Ala Arg Thr

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            100                 105                 110
Ser Ala Ser Gly Xaa Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Xaa
        115                 120                 125
Xaa Phe Xaa Thr Pro Pro Xaa Gly Pro His Xaa Xaa Met Tyr Lys Arg
    130                 135                 140
Xaa Thr
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His Xaa Xaa Leu Arg Pro Asn Gln Pro Xaa Glu Xaa Cys Xaa Xaa Xaa
            20                  25                  30
Xaa Asp Leu Xaa Arg Xaa Ala Phe His Leu Gly Gly Xaa Tyr Xaa Gly
        35                  40                  45
Xaa Leu Xaa Ser Xaa Ala Ser Phe His Xaa Ala Xaa His Xaa Xaa Xaa
    50                  55                  60
Gln Gly Xaa Lys Gln Tyr Gln Xaa Arg Gly Xaa Ala Thr Leu Glu Gly
65                  70                  75                  80
Tyr Arg Xaa Gln Lys Ala Gly Xaa Xaa Leu Xaa Xaa His Ala Glu Glu
                85                  90                  95
Ile Xaa Arg Lys Arg Gly Xaa Asp Xaa Xaa Trp Cys Asn Ala Arg Thr
            100                 105                 110
Ser Ala Ser Gly Xaa Tyr Xaa Lys Leu Gly Phe Ser Glu Gln Gly Xaa
        115                 120                 125
Xaa Phe Xaa Thr Pro Pro Xaa Gly Pro His Xaa Xaa Met Tyr Lys Arg
    130                 135                 140
Xaa Thr
145
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