FIG. 1

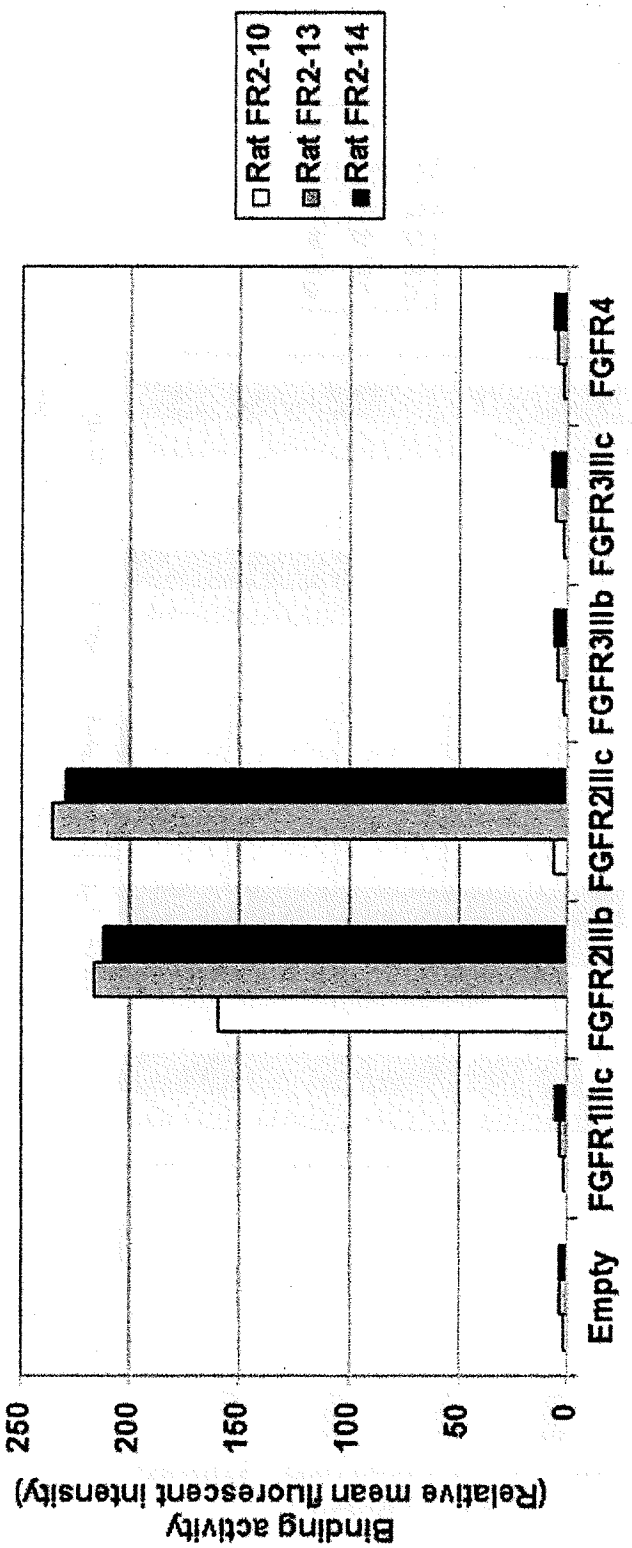

Rat FR2-10
Rat FR2-13
Rat FR2-14
Binding activity
(Relative mean fluorescent intensity)
250
200
150
100
50
0
Empty
FGFR1IIIc
FGFR2IIIb
FGFR2IIIc
FGFR3IIIb
FGFR3IIIc
FGFR4

FIG. 2

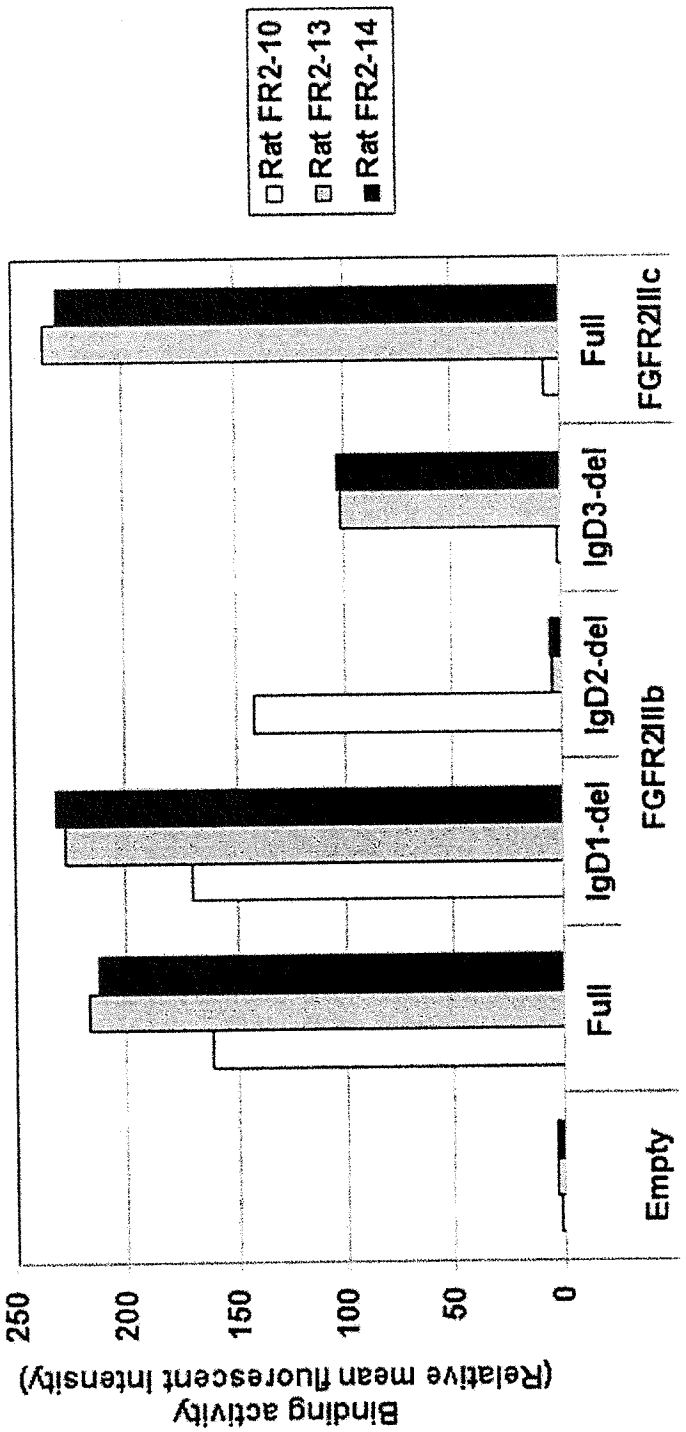

Rat FR2-10
Rat FR2-13
Rat FR2-14
Binding activity
(Relative mean fluorescent Intensity)
250
200
150
100
50
0
Empty
Full
IgD1-del
IgD2-del
IgD3-del
Full
FGFR2IIIb
FGFR2IIIc

FIG. 3A

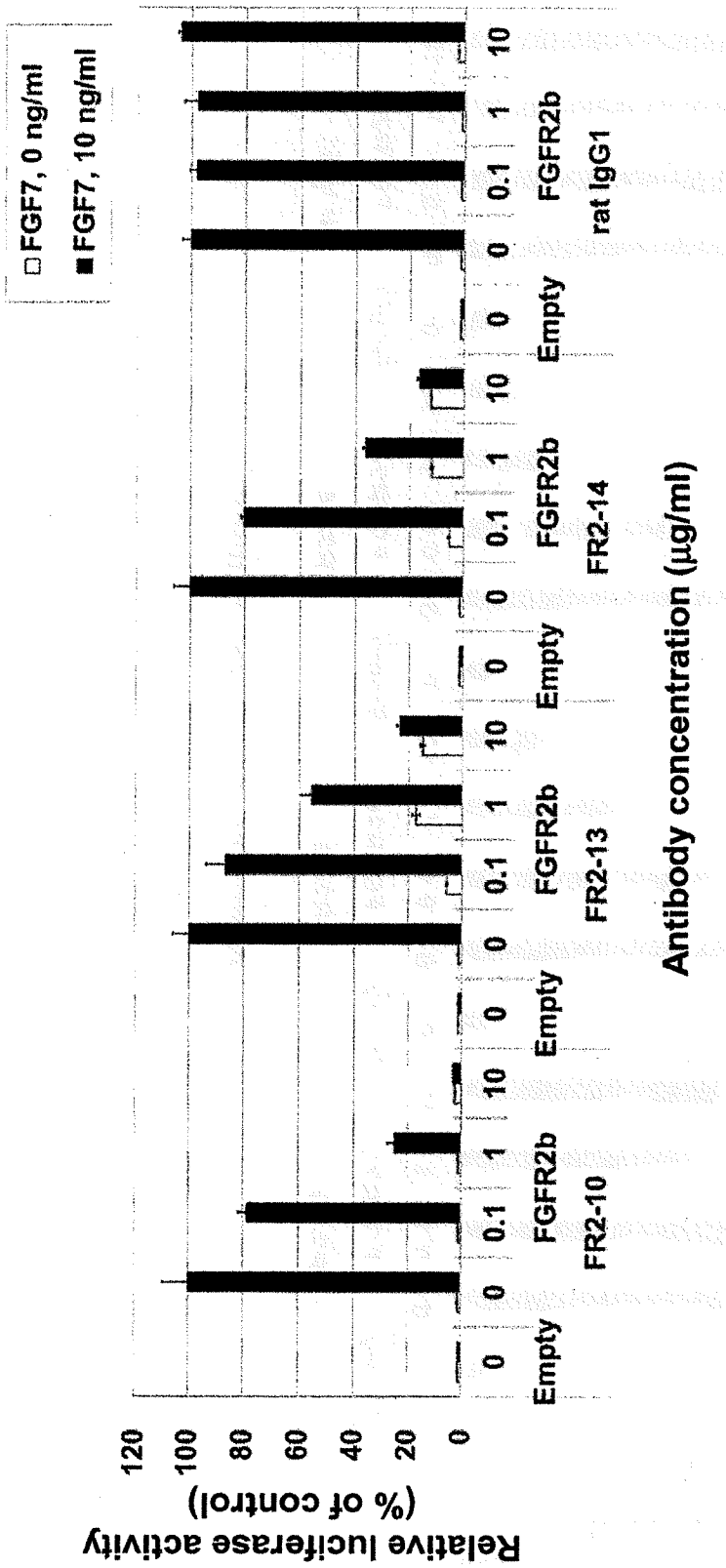

FGF7, 0 ng/ml
FGF7, 10 ng/ml
Relative luciferase activity
(% of control)
120
100
80
60
40
20
0
Empty
FGFR2b
FR2-10
FR2-13
FR2-14
rat IgG1
0
0.1
1
10
Antibody concentration (μg/ml)

FIG. 3B

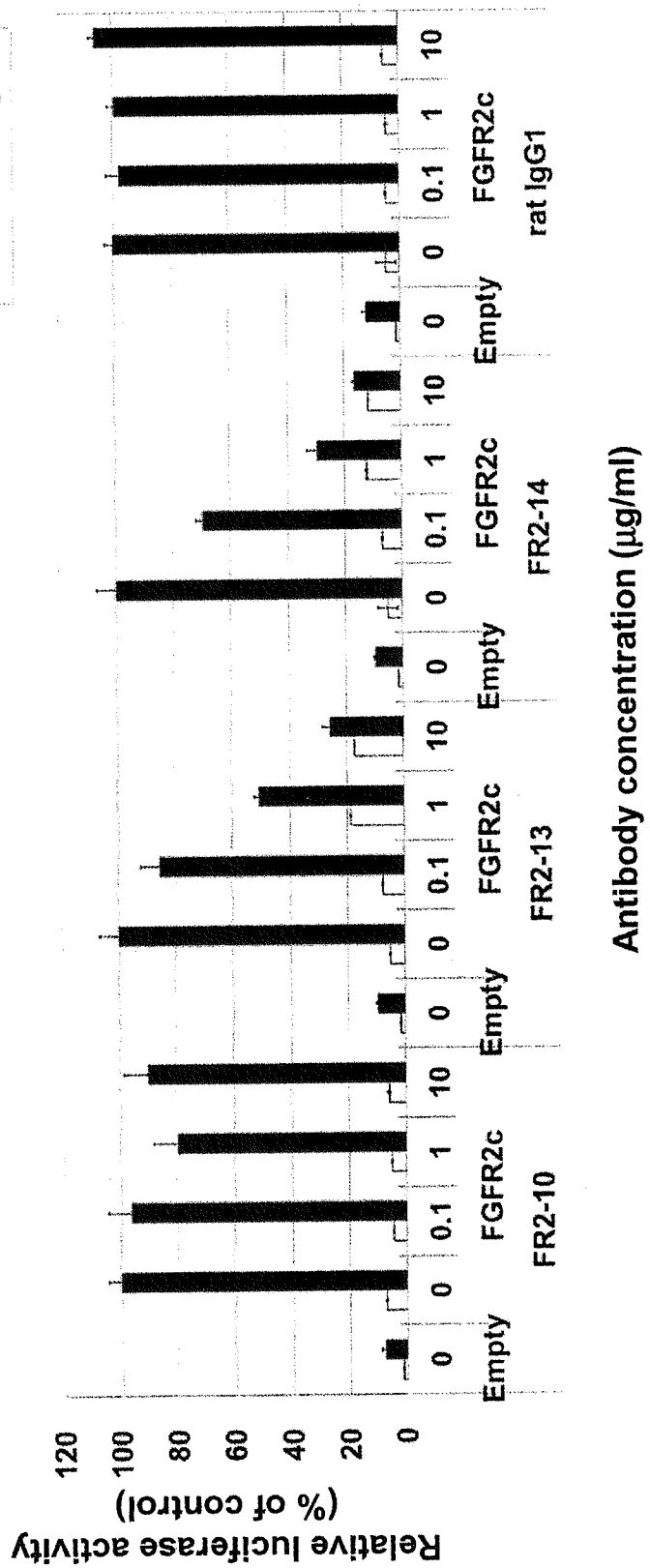

FGF9, 0 ng/ml
FGF9, 10 ng/ml
Relative luciferase activity
(% of control)
120
100
80
60
40
20
0
Empty
FGFR2c
FR2-10
FR2-13
FR2-14
rat IgG1
0
0.1
1
10
Antibody concentration (μg/ml)

FIG. 4

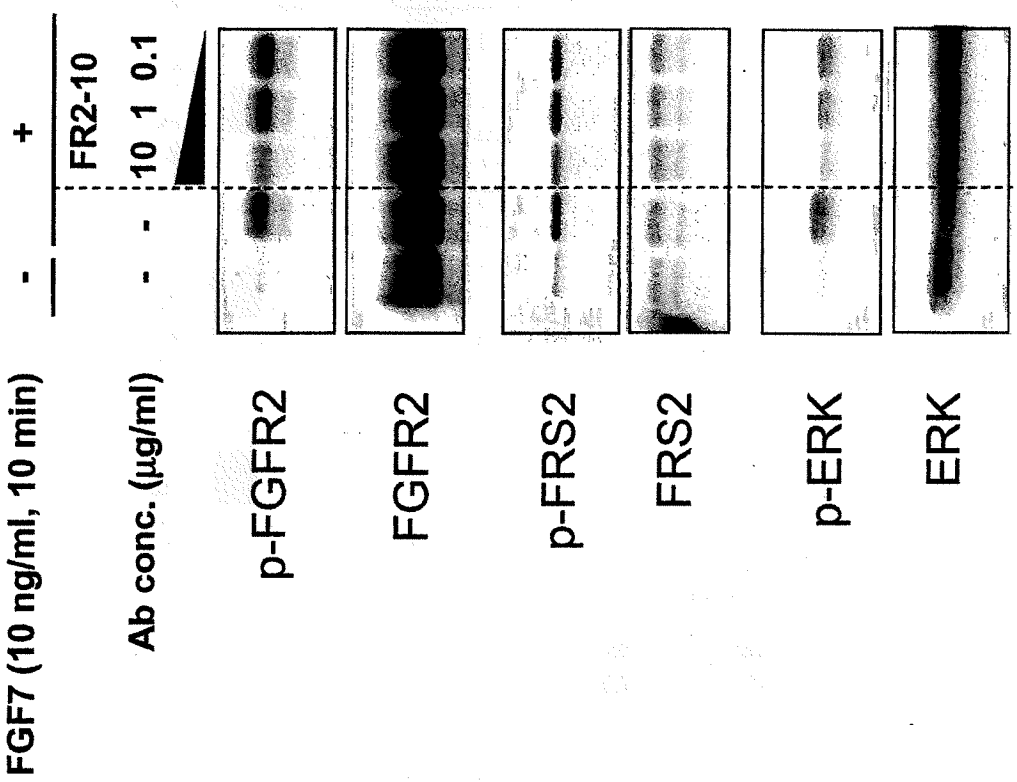

FGF7 (10 ng/ml, 10 min)
- +
Ab conc. (μg/ml)
- - FR2-10
10 1 0.1
p-FGFR2
FGFR2
p-FRS2
FRS2
p-ERK
ERK

FIG. 5

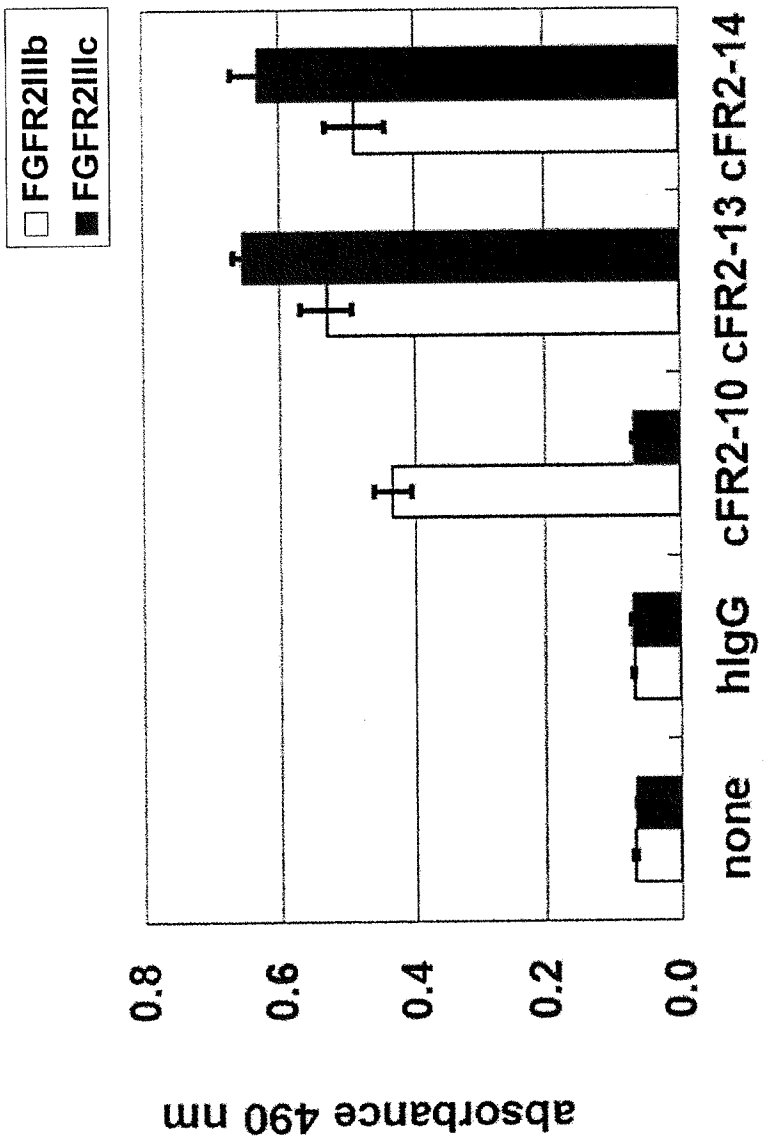

FGFR2IIIb
FGFR2IIIc
absorbance 490 nm
0.0
0.2
0.4
0.6
0.8
none
hIgG
cFR2-10
cFR2-13
cFR2-14

FIG. 6A

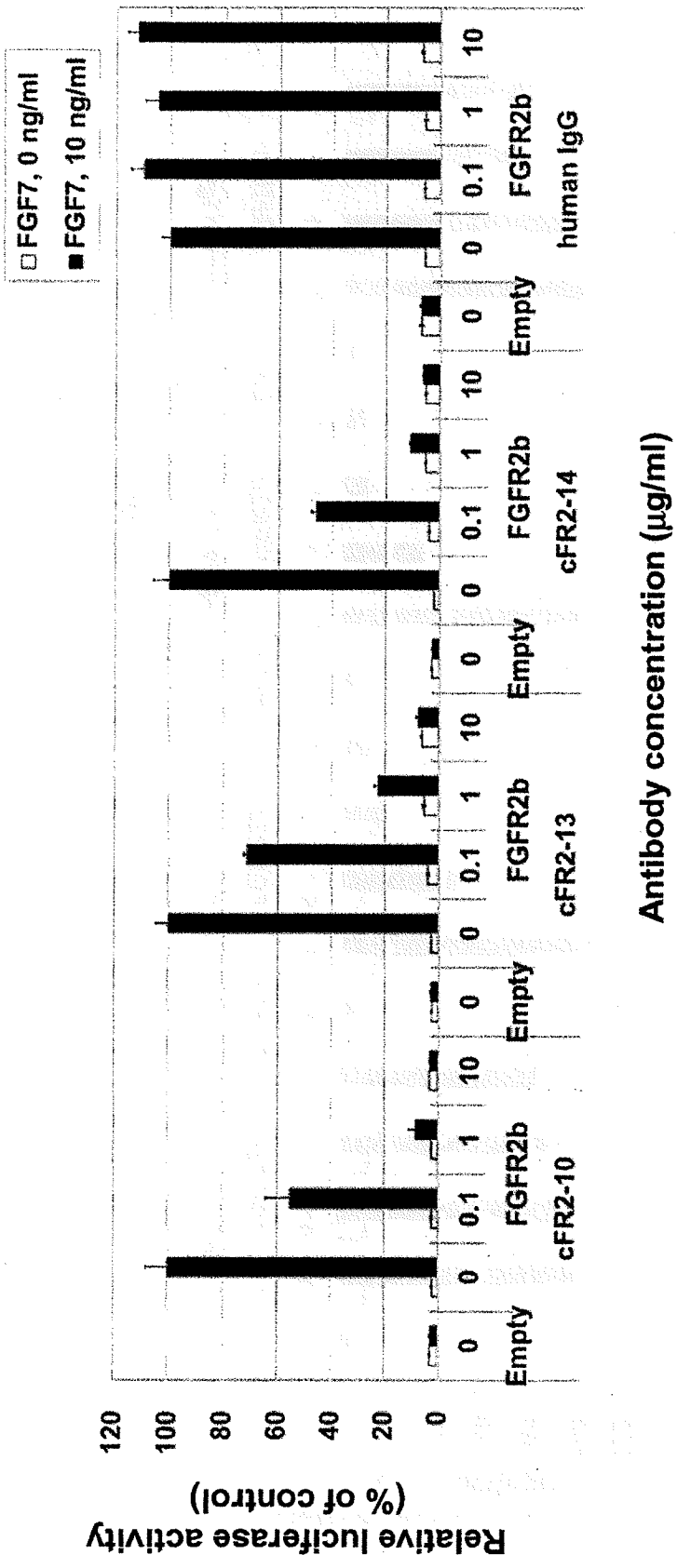

FGF7, 0 ng/ml
FGF7, 10 ng/ml
Relative luciferase activity (% of control)
120
100
80
60
40
20
0
Empty
cFR2-10
FGFR2b
cFR2-13
cFR2-14
human IgG
0
0.1
1
10
Antibody concentration (µg/ml)

FIG. 6B

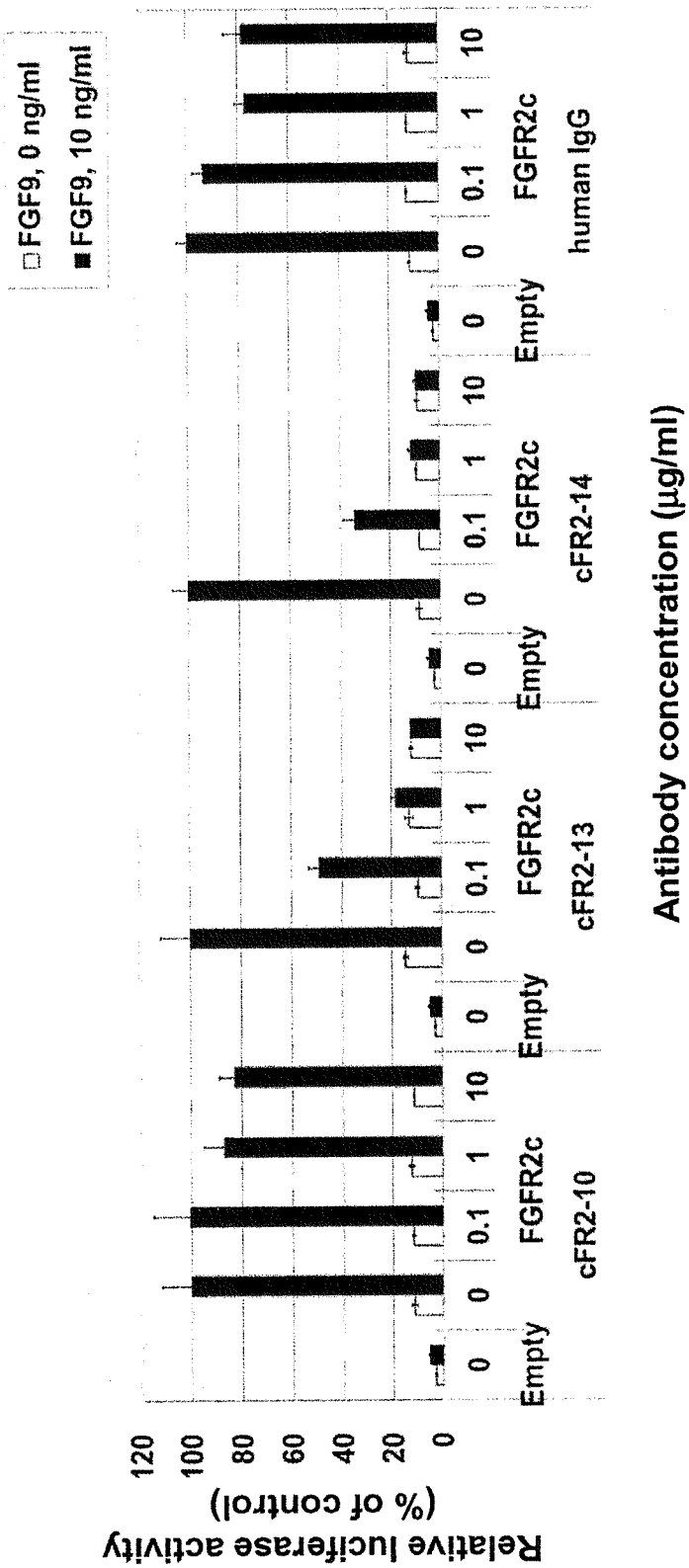

FGF9, 0 ng/ml
FGF9, 10 ng/ml
Relative luciferase activity
(% of control)
120
100
80
60
40
20
0
Empty
cFR2-10
FGFR2c
cFR2-13
cFR2-14
human IgG
0
0.1
1
10
Antibody concentration (μg/ml)

FIG. 7

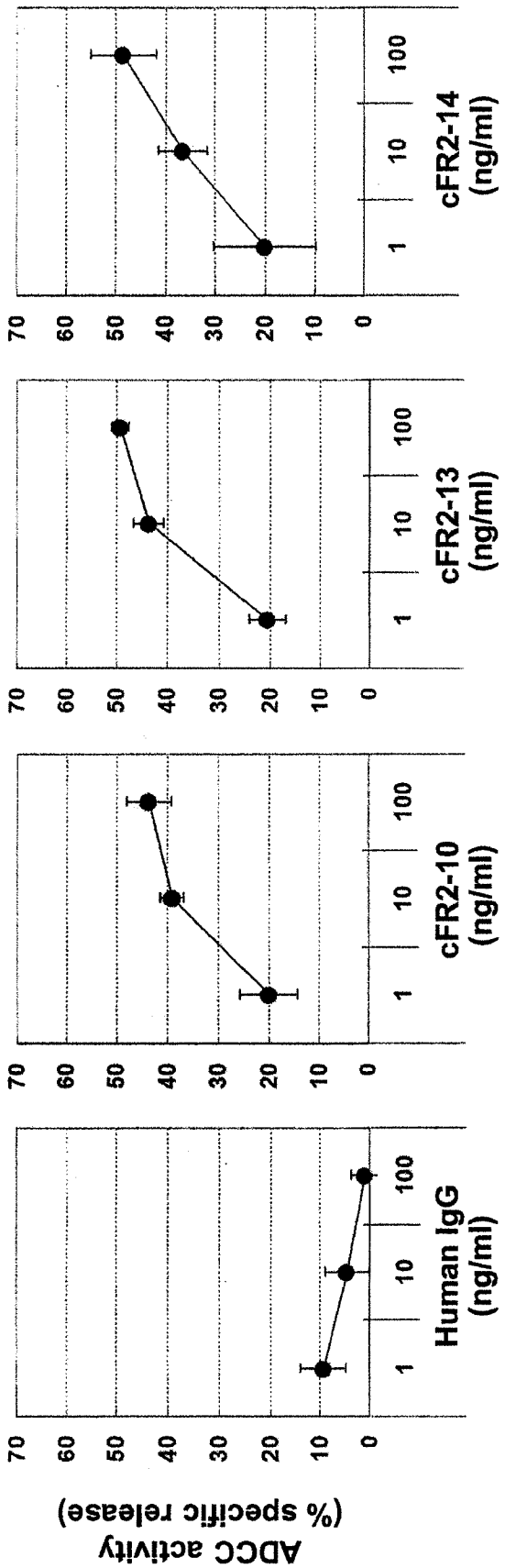

ADCC activity
(% specific release)
0
10
20
30
40
50
60
70
1
10
100
Human IgG
(ng/ml)
cFR2-10
(ng/ml)
cFR2-13
(ng/ml)
cFR2-14
(ng/ml)

FIG. 8

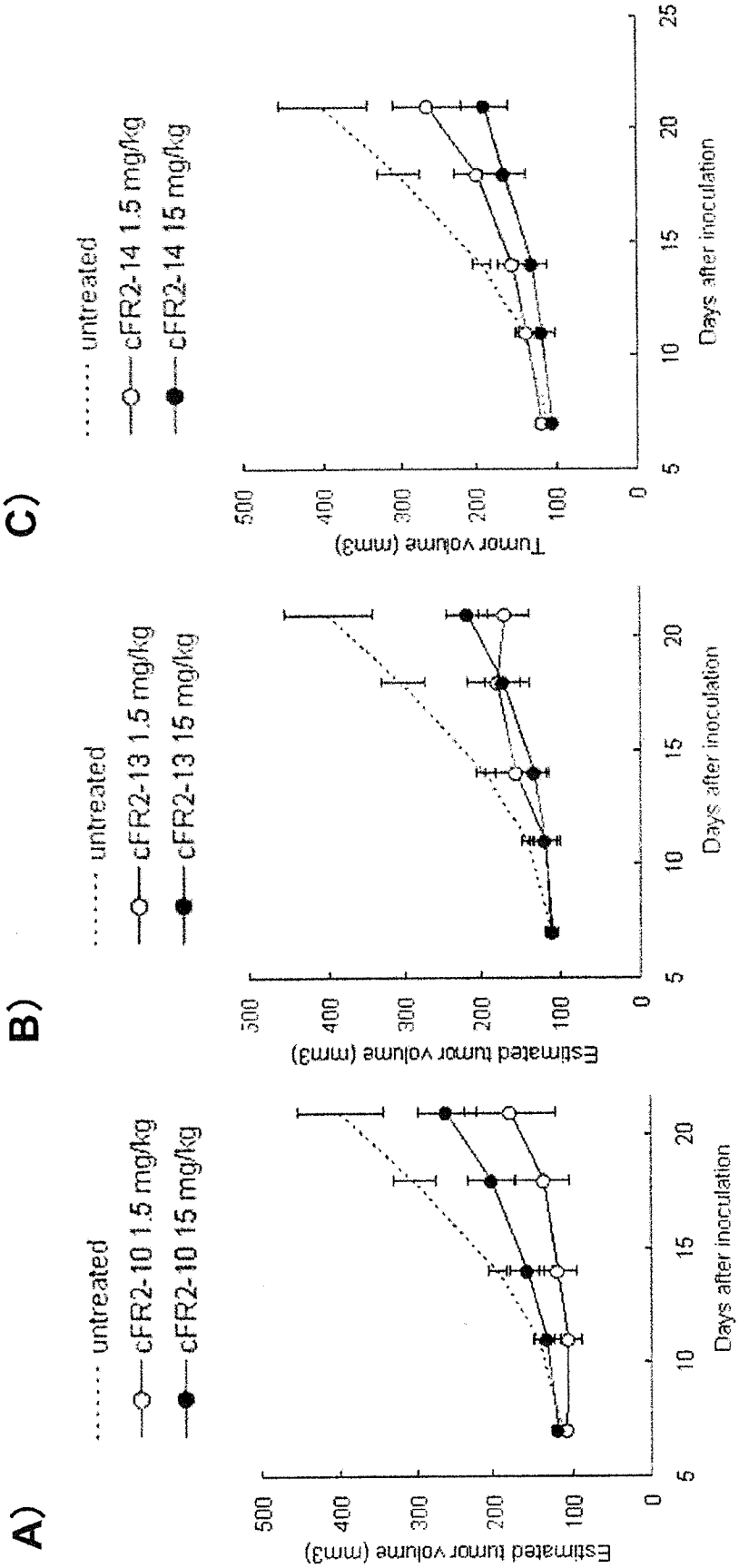

A)
untreated
cFR2-10 1.5 mg/kg
cFR2-10 15 mg/kg
Estimated tumor volume (mm3)
Days after inoculation
B)
untreated
cFR2-13 1.5 mg/kg
cFR2-13 15 mg/kg
Estimated tumor volume (mm3)
Days after inoculation
C)
untreated
cFR2-14 1.5 mg/kg
cFR2-14 15 mg/kg
Tumor volume (mm3)
Days after inoculation

Figure 9

EVQLVESGGGLV
(SEQ ID NO: 1 of Sequence Listing)

Figure 10

DIQMTQSPSSLSA
(SEQ ID NO: 2 of Sequence Listing)

Figure 11

QVKLL
(SEQ ID NO: 3 of Sequence Listing)

Figure 12

DIQMTQSPASLSASLGE
(SEQ ID NO: 4 of Sequence Listing)

Figure 13

QVKLL
(SEQ ID NO: 5 of Sequence Listing)

Figure 14

DIQMTQSPASLSASLGE
(SEQ ID NO: 6 of Sequence Listing)

Figure 15

GAGTTACTTTTGAGAGCAGTTCCAGGAG
(SEQ ID NO: 7 of Sequence Listing)

Figure 16

GGTTCTCCCACTCAGTAATC
(SEQ ID NO: 8 of Sequence Listing)

Figure 17

CATATGATCAGTGTCCTCTC
(SEQ ID NO: 9 of Sequence Listing)

Figure 18

ATATGATCAGTGTCCTCTCC
(SEQ ID NO: 10 of Sequence Listing)

Figure 19

gaggtgcagctggtggagtctgggggaggcctggtgcagcctggaaggtctctgaaactatcctgtgtagcctctggatt
cagattcaatgacttttggatgacctggatccgccaggctccagggaaggggctggagtgggttgcatccattacttata
ctggtgataacacttactatgcaggctctgtgaagggccgaatcactatctccagagataatgcgaagagcaccctatac
ctgcaaatgaacagtctgaggtctgaggacacggccacttattactgtacaagagatgactacggaggatatagccccta
ctatatggatgcctggggtcaaggaacttcagtcactgtctcctca
Variable region (1-366)
(SEQ ID NO: 11 of Sequence Listing)

Figure 20

EVQLVESGGGLVQPGRSLKLSCVASGFRFNDFWMTWIRQAPGKGLEWVASITYTGDNTYYAGSVKGRITISRDNAKSTLY
LQMNSLRSEDTATYYCTRDDYGGYSPYYMDAWGQGTSVTVSS
Variable region (1-122)
(SEQ ID NO: 12 of Sequence Listing)

Figure 21

caggttaagctgctgcagtctggggctgagctggtaaaacctggtgcttcagtgaagttgtcctgcaagacttctggttt
taccttcagcactagctatatgagttggttgaagcaggtgcctggaccgagtattgagtggattggatggatttatgctg
gagatggtggtactaagtataatcagaagttcaagggcaaggccacactgacagtagacaaatcttctagcacagcatac
atggatctcagcagcctgacatctgaggacgctgcagtctatttttgtgcaacggatggttatggggattggtttgctta
ctggggccaaggcactctggtcactgtctcttca
Variable region (1-354)
(SEQ ID NO: 13 of Sequence Listing)

Figure 22

QVKLLQSGAELVKPGASVKLSCKTSGFTFSTSYMSWLKQVPGPSIEWIGWIYAGDGGTKYNQKFKGKATLTVDKSSSTAY
MDLSSLTSEDAAVYFCATDGYGDWFAYWGQGTLVTVSS
Variable region (1-118)
(SEQ ID NO: 14 of Sequence Listing)

Figure 23

caggttaagctgctgcagtctggggctgagctggtaaaacctggtgcttcagtgaagttgtcctgcaagacttctggttt
tacattcagcactagttatatgagttggttgaagcaggtgcctggaccgagtactgagtggattggatggatttatgctg
gagatggtggtactaagtataatcagaagttcaagggcaaggccacactgacagtagacaaatttttctagcacagcatac
atggatctcagcagcctgacatctgaggacgctgcagtctatttctgtgcaacggatggttatggggattggtttacttа
ctggggccaaggcactctggtcactgtctcttca
Variable region (1-354)
SEQ ID NO: 15 of Sequence Listing

Figure 24

QVKLLQSGAELVKPGASVKLSCKTSGFTFSTSYMSWLKQVPGPSTEWIGWIYAGDGGTKYNQKFKGKATLTVDKFSSTAY
MDLSSLTSEDAAVYFCATDGYGDWFTYWGQGTLVTVSS

Variable region (1-118)

(SEQ ID NO: 16 of Sequence Listing)

Figure 25

TTCATGAGGCACACGACTGAGGCACCTCC

(SEQ ID NO: 17 of Sequence Listing)

Figure 26

TCCAGTTGCTAACTGTTCCG

(SEQ ID NO: 18 of Sequence Listing)

Figure 27

CAGTGGTATCAACGCAGAG

(SEQ ID NO: 19 of Sequence Listing)

Figure 28

gacatccagatgacccagtctccatcttccctgtctgcatttctgggagacagagtcactattacttgccgggcaagtca
agacattggaaattatttaagatggttccagcagaaaccggggaaatctcctaggcttatgatttatggtgcaaccaact
tggcaaatggggtcccatcaaggttcagtggcagtaggtctgggtcagattattctctgaccatcaacaacttggagtct
gaagacatggctatttattactgtctgaagcataatgagtatccattcacgttcggctcagggacgaagttggaaataaa
acgggct

Variable region (1-327)

(SEQ ID NO: 20 of Sequence Listing)

Figure 29

DIQMTQSPSSLSAFLGDRVTITCRASQDIGNYLRWFQQKPGKSPRLMIYGATNLANGVPSRFSGSRSGSDYSLTINNLES
EDMAIYYCLKHNEYPFTFGSGTKLEIKRA

Variable region (1-109)

(SEQ ID NO: 21 of Sequence Listing)

Figure 30

TACGTGCTGTCTTTGCTGTCCTGATCAG

(SEQ ID NO: 22 of Sequence Listing)

Figure 31

gacatccagatgacacagtctccagcttccctgtctgcatctctgggagaaactgtcaccatcgaatgtcgagcaagtga
ggacatttacagtaatttagcgtggtatcagcagaaaccagggaactctcctcagctcctgatctatgatgcaaatatct
tggcagatggggtcccatcacggttcagtggcagtgggtctggcacacagtattctctaaagataaacagcctgcaatct
gaagatgtcgcaagttatttctgtcaacagtataacaattatcctccgttcacgtttggagttgggaccaagctggaact
gaaacgggct

Variable region (1-330)

(SEQ ID NO: 23 of Sequence Listing)

Figure 32

DIQMTQSPASLSASLGETVTIECRASEDIYSNLAWYQQKPGNSPQLLIYDANILADGVPSRFSGSGSGTQYSLKINSLQS
EDVASYFCQQYNNYPPFTFGVGTKLELKRA

Variable region (1-110)

(SEQ ID NO: 24 of Sequence Listing)

Figure 33

gacatccagatgacacagtctccagcttccctgtctgcatctctgggagaaactgtcaccatcgaatgtcgagcaagtga
ggacatatacagtaatttagcgtggtatcagcagaaaccagggaactctcctcagctcctgatctatgatgcaaatatcc
tggcagatggggtcccatcacggttcagtggcagtgggtctggcacacagtattctctaaagataaacagcctgcaatct
gaagatgtcgcaagttatttctgtcaacagtataacaattatcctccgttcacgtttggagctgggaccaagctggaact
gaaacgggct

Variable region (1-330)

(SEQ ID NO: 25 of Sequence Listing)

Figure 34

DIQMTQSPASLSASLGETVTIECRASEDIYSNLAWYQQKPGNSPQLLIYDANILADGVPSRFSGSGSGTQYSLKINSLQS
EDVASYFCQQYNNYPPFTFGAGTKLELKRA

Variable region (1-110)

(SEQ ID NO: 26 of Sequence Listing)

Figure 35

gcctccggactctagagccaccATGGTGCTGCAGACCCAGGTGTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACG
GCGATATCGTGATGATTAAACGTACGGTGGCCGCCCCCTCCGTGTTCATCTTCCCCCCCTCCGACGAGCAGCTGAAGTCC
GGCACCGCCTCCGTGGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGGAAGGTGGACAACGCCCT
GCAGTCCGGGAACTCCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACAGCACCTACAGCCTGAGCAGCACCCTGACCC
TGAGCAAAGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGAGCTCCCCCGTCACCAAG
AGCTTCAACAGGGGGGAGTGTTAGgggcccgtttaaacgggggaggcta

(SEQ ID NO: 27 of Sequence Listing)

Figure 36

TATACCGTCGACCTCTAGCTAGAGCTTGGC

(SEQ ID NO: 28 of Sequence Listing)

Figure 37

GCTATGGCAGGGCCTGCCGCCCCGACGTTG
(SEQ ID NO: 29 of Sequence Listing)

Figure 38

gcctccggactctagagccaccATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCC
AGGTGCAATTGTGCAGGCGGTTAGCTCAGCCTCCACCAAGGGCCCAAGCGTCTTCCCCCTGGCACCCTCCTCCAAGAGCA
CCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGAGCTGGAACTCAGGC
GCCCTGACCAGCGGCGTGCACACCTTCCCCGCTGTCCTGCAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
GCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAG
TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCCTGCCCAGCACCTGAACTCCTGGGGGGACCCTCAGTCTTC
CTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
CGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGC
AGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC
AAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
GCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAACTACAAGACCACCCCTCCCGTGCTGGACTCCGAC
GGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGAT
GCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAATGAgatatcgggcccgtttaaa
cgggggaggcta
(SEQ ID NO: 30 of Sequence Listing)

Figure 39

atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcgtacggcgacatccagatgacccagtc
tccatcttccctgtctgcatttctgggagacagagtcactattacttgccgggcaagtcaagacattggaaattatttaa
gatggttccagcagaaaccggggaaatctcctaggcttatgatttatggtgcaaccaacttggcaaatggggtcccatca
aggttcagtggcagtaggtctgggtcagattatctctgaccatcaacaacttggagtctgaagacatggctatttatta
ctgtctgaagcataatgagtatccattcacgttcggctcagggacgaagttggaaataaaacgggctgtggccgcccctt
ccgtgttcatcttcccccctccgacgagcagctgaagtccggcaccgcctccgtggtgtgcctgctgaataacttctac
cccagagaggccaaggtgcagtggaaggtggacaacgccctgcagtccgggaactcccaggagagcgtgaccgagcagga
cagcaaggacagcacctacagcctgagcagcaccctgaccctgagcaaagccgactacgagaagcacaaggtgtacgcct
gcgaggtgacccaccagggcctgagctcccccgtcaccaagagcttcaacaggggggagtgt
Signal sequence (1-60), Variable region (61-387), Constant region (389-702)
(SEQ ID NO: 31 of Sequence Listing)

Figure 40

MVLQTQVFISLLLWISGAYGDIQMTQSPSSLSAFLGDRVTITCRASQDIGNYLRWFQQKPGKSPRLMIYGATNLANGVPS
RFSGSRSGSDYSLTINNLESEDMAIYYCLKHNEYPFTFGSGTKLEIKRAVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY
PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Signal sequence (1-20), Variable region (21-129), Constant region (130-234)
(SEQ ID NO: 32 of Sequence Listing)

Figure 41

ATCTCCGGCGCGTACGGCGACATCCAGATGACCCAGTCTCCATCTTCC
(SEQ ID NO: 33 of Sequence Listing)

Figure 42

GGAGGGGGCGGCCACAGCCCGTTTTATTTCCAACTTCGTCCCTG
(SEQ ID NO: 34 of Sequence Listing)

Figure 43

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagcgaggtgcagctggtggagtctgg
gggaggcctggtgcagcctggaaggtctctgaaactatcctgtgtagcctctggattcagattcaatgactttggatga
cctggatccgccaggctccagggaaggggctggagtgggttgcatccattacttatactggtgataacacttactatgca
ggctctgtgaagggccgaatcactatctccagagataatgcgaagagcaccctataccttgcaaatgaacagtctgaggtc
tgaggacacggccacttattactgtacaagagatgactacggaggatatagccccttactatatggatgcctggggtcaag
gaacttcagtcactgtcagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctct
ggcggcacagccgccctgggctgcctggtcaaggactacttccccgaaccctgtaccgtgagctggaactcaggcgccct
gaccagcggcgtgcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccct
ccagcagcttgggcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgag
cccaaatcttgtgacaaaactcacacatgcccaccctgcccagcacctgaactcctgggggggaccctcagtcttcctctt
ccccccaaaacccaaggacaccctcatgatctcccggaccctgaggtcacatgcgtggtggtggacgtgagccacgaag
accctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtac
aacagcacgtaccgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggt
ctccaacaaagccctcccagcccccatcgagaaaaccatctccaaagccaaagggcagccccgggaaccacaggtgtaca
ccctgcccccatcccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgac
atcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacccctcccgtgctggactccgacggctc
cttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatg
aggctctgcacaaccactacacccagaagagcctctccctgtctccggcaaa
Signal sequence (1-57), Variable region (58-423), Constant region(424-1413)
(SEQ ID NO: 35 of Sequence Listing)

Figure 44

MKHLWFFLLLVAAPRWVLSEVQLVESGGGLVQPGRSLKLSCVASGFRFNDFWMTWIRQAPGKGLEWVASITYTGDNTYYA
GSVKGRITISRDNAKSTLYLQMNSLRSEDTATYYCTRDDYGGYSPYYMDAWGQGTSVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVE
PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD
IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
Signal sequence (1-19), Variable region (20-141), Constant region(142-471)
(SEQ ID NO: 36 of Sequence Listing)

Figure 45

CCAGATGGGTGCTGAGCGAGGTGCAGCTGGTGGAGTCTGGGGGAGGC
(SEQ ID NO: 37 of Sequence Listing)

Figure 46

CTTGGTGGAGGCTGAGCTGACAGTGACTGAAGTTCCTTGACCCCAGGC
(SEQ ID NO: 38 of Sequence Listing)

Figure 47

atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcgtacggcgacatccagatgacacagtc
tccagcttccctgtctgcatctctgggagaaactgtcaccatcgaatgtcgagcaagtgaggacatttacagtaatttag
cgtggtatcagcagaaaccagggaactctcctcagctcctgatctatgatgcaaatatcttggcagatggggtcccatca
cggttcagtggcagtgggtctggcacacagtattctctaaagataaacagcctgcaatctgaagatgtcgcaagttattt
ctgtcaacagtataacaattatcctccgttcacgtttggagttgggaccaagctggaactgaaacgggctgtggccgccc
cctccgtgttcatcttcccccctccgacgagcagctgaagtccggcaccgcctccgtggtgtgcctgctgaataacttc
taccccagagaggccaaggtgcagtggaaggtggacaacgccctgcagtccgggaactcccaggagagcgtgaccgagca
ggacagcaaggacagcacctacagcctgagcagcaccctgaccctgagcaaagccgactacgagaagcacaaggtgtacg
cctgcgaggtgacccaccagggcctgagctcccccgtcaccaagagcttcaacaggggggagtgt
Signal sequence (1-60), Variable region (61-390), Constant region (391-705)
(SEQ ID NO: 39 of Sequence Listing)

Figure 48

MVLQTQVFISLLLWISGAYGDIQMTQSPASLSASLGETVTIECRASEDIYSNLAWYQQKPGNSPQLLIYDANILADGVPS
RFSGSGSGTQYSLKINSLQSEDVASYFCQQYNNYPPFTFGVGTKLELKRAVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Signal sequence (1-20), Variable region (21-130), Constant region (131-235)
(SEQ ID NO: 40 of Sequence Listing)

Figure 49

ATCTCCGGCGCGTACGGCGACATCCAGATGACACAGTCTCCAGCTTCC
(SEQ ID NO: 41 of Sequence Listing)

Figure 50

GGAGGGGGCGGCCACAGCCCGTTTCAGTTCCAGCTTGGTCCCAAC
(SEQ ID NO: 42 of Sequence Listing)

Figure 51

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggttaagctgctgcagtctgg
ggctgagctggtaaaacctggtgcttcagtgaagttgtcctgcaagacttctggttttaccttcagcactagctatatga
gttggttgaagcaggtgcctggaccgagtattgagtggattggatggatttatgctggagatggtggtactaagtataat
cagaagttcaagggcaaggccacactgacagtagacaaatcttctagcacagcatacatggatctcagcagcctgacatc
tgaggacgctgcagtctatttttgtgcaacggatggttatggggattggtttgcttactggggccaaggcactctggtca
ctgtcagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccaccctgcccagcacctgaactcctgggggacccctcagtcttcctcttcccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctcccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region (412-1401)

(SEQ ID NO: 43 of Sequence Listing)

Figure 52

MKHLWFFLLLVAAPRWVLSQVKLLQSGAELVKPGASVKLSCKTSGFTFSTSYMSWLKQVPGPSIEWIGWIYAGDGGTKYN
QKFKGKATLTVDKSSSTAYMDLSSLTSEDAAVYFCATDGYGDWFAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region (138-467)

(SEQ ID NO: 44 of Sequence Listing)

Figure 53

CCAGATGGGTGCTGAGCCAGGTTAAGCTGCTGCAGTCTGGGGCTGAG

(SEQ ID NO: 45 of Sequence Listing)

Figure 54

CTTGGTGGAGGCTGAGCTGACAGTGACCAGAGTGCCTTGGCCCCAG

(SEQ ID NO: 46 of Sequence Listing)

Figure 55

atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcgtacggcgacatccagatgacacagtc
tccagcttccctgtctgcatctctgggagaaactgtcaccatcgaatgtcgagcaagtgaggacatatacagtaatttag
cgtggtatcagcagaaaccagggaactctcctcagctcctgatctatgatgcaaatatcctggcagatggggtcccatca
cggttcagtggcagtgggtctggcacacagtattctctaaagataaacagcctgcaatctgaagatgtcgcaagttattt
ctgtcaacagtataacaattatcctccgttcacgtttggagctgggaccaagctggaactgaaacgggctgtggccgccc
cctccgtgttcatcttcccccctccgacgagcagctgaagtccggcaccgcctccgtggtgtgcctgctgaataacttc
taccccagagaggccaaggtgcagtggaaggtggacaacgccctgcagtccgggaactcccaggagagcgtgaccgagca
ggacagcaaggacagcacctacagcctgagcagcaccctgaccctgagcaaagccgactacgagaagcacaaggtgtacg
cctgcgaggtgacccaccagggcctgagctcccccgtcaccaagagcttcaacaggggggagtgt

Signal sequence (1-60), Variable region (61-390), Constant region (391-705)

(SEQ ID NO: 47 of Sequence Listing)

Figure 56

MVLQTQVFISLLLWISGAYGDIQMTQSPASLSASLGETVTIECRASEDIYSNLAWYQQKPGNSPQLLIYDANILADGVPS
RFSGSGSGTQYSLKINSLQSEDVASYFCQQYNNYPPFTFGAGTKLELKRAVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Signal sequence (1-20), Variable region (21-130), Constant region (131-235)

(SEQ ID NO: 48 of Sequence Listing)

Figure 57

GGAGGGGCGGCCACAGCCCGTTTCAGTTCCAGCTTGGTCCCAGC

(SEQ ID NO: 49 of Sequence Listing)

Figure 58

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggttaagctgctgcagtctgg
ggctgagctggtaaaacctggtgcttcagtgaagttgtcctgcaagacttctggttttacattcagcactagttatatga
gttggttgaagcaggtgcctggaccgagtactgagtggattggatggatttatgctggagatggtggtactaagtataat
cagaagttcaagggcaaggccacactgacagtagacaaatttttctagcacagcatacatggatctcagcagcctgacatc
tgaggacgctgcagtctatttctgtgcaacggatggttatggggattggtttacttactggggccaaggcactctggtca
ctgtcagctcagcctccaccaagggcccaagcgtcttcccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccctgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccaccctgcccagcacctgaactcctgggggaccctcagtcttcctcttcccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctcccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region (412-1401)

(SEQ ID NO: 50 of Sequence Listing)

Figure 59

MKHLWFFLLLVAAPRWVLSQVKLLQSGAELVKPGASVKLSCKTSGFTFSTSYMSWLKQVPGPSTEWIGWIYAGDGGTKYN
QKFKGKATLTVDKFSSTAYMDLSSLTSEDAAVYFCATDGYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region (138-467)

(SEQ ID NO: 51 of Sequence Listing)

Figure 60

DFWMT

(SEQ ID NO: 52 of Sequence Listing)

Figure 61

SITYTGDNTYYAGSVKG

(SEQ ID NO: 53 of Sequence Listing)

Figure 62

DDYGGYSPYYMDA

(SEQ ID NO: 54 of Sequence Listing)

Figure 63

TSYMS
(SEQ ID NO: 55 of Sequence Listing)

Figure 64

WIYAGDGGTKYNQKFKG
(SEQ ID NO: 56 of Sequence Listing)

Figure 65

DGYGDWFAY
(SEQ ID NO: 57 of Sequence Listing)

Figure 66

TSYMS
(SEQ ID NO: 58 of Sequence Listing)

Figure 67

WIYAGDGGTKYNQKFKG
(SEQ ID NO: 59 of Sequence Listing)

Figure 68

DGYGDWFTY
(SEQ ID NO: 60 of Sequence Listing)

Figure 69

RASQDIGNYLR
(SEQ ID NO: 61 of Sequence Listing)

Figure 70

GATNLAN
(SEQ ID NO: 62 of Sequence Listing)

Figure 71

LKHNEYPFT
(SEQ ID NO: 63 of Sequence Listing)

Figure 72

RASEDIYSNLA
(SEQ ID NO: 64 of Sequence Listing)

Figure 73

DANILAD
(SEQ ID NO: 65 of Sequence Listing)

Figure 74

QQYNNYPPFT
(SEQ ID NO: 66 of Sequence Listing)

Figure 75

RASEDIYSNLA
(SEQ ID NO: 67 of Sequence Listing)

Figure 76

DANILAD
(SEQ ID NO: 68 of Sequence Listing)

Figure 77

QQYNNYPPFT
(SEQ ID NO: 69 of Sequence Listing)

Figure 78

MVSWGRFICLVVVTMATLSLARPSFSLVEDTTLEPEEPPTKYQISQPEVYVAAPGESLEVRCLLKDAAVISWTKDGVHLG
PNNRTVLIGEYLQIKGATPRDSGLYACTASRTVDSETWYFMVNVTDAISSGDDEDDTDGAEDFVSENSNNKRAPYWTNTE
KMEKRLHAVPAANTVKFRCPAGGNPMPTMRWLKNGKEFKQEHRIGGYKVRNQHWSLIMESVVPSDKGNYTCVVENEYGSI
NHTYHLDVVERSPHRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYGPDGLPYLKVLKHSGINSS
NAEVLALFNVTEADAGEYICKVSNYIGQANQSAWLTVLPKQQAPGREKEITASPDYLEIAIYCIGVFLIACMVVTVILCR
MKNTTKKPDFSSQPAVHKLTKRIPLRRQVTVSAESSSSMNSNTPLVRITTRLSSTADTPMLAGVSEYELPEDPKWEFPRD
KLTLGKPLGEGCFGQVVMAEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKMIGKHKNIINLLGACTQDGP
LYVIVEYASKGNLREYLRARRPPGMEYSYDINRVPEEQMTFKDLVSCTYQLARGMEYLASQKCIHRDLAARNVLVTENNV
MKIADFGLARDINNIDYYKKTTNGRLPVKWMAPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKEG
HRMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTTNEEYLDLSQPLEQYSPSYPDTRSSCSSGDDSVFS
PDPMPYEPCLPQYPHINGSVKT
(SEQ ID NO: 70 of Sequence Listing)

Figure 79

MVSWGRFICLVVVTMATLSLARPSFSLVEDTTLEPEEPPTKYQISQPEVYVAAPGESLEVRCLLKDAAVISWTKDGVHLG
PNNRTVLIGEYLQIKGATPRDSGLYACTASRTVDSETWYFMVNVTDAISSGDDEDDTDGAEDFVSENSNNKRAPYWTNTE
KMEKRLHAVPAANTVKFRCPAGGNPMPTMRWLKNGKEFKQEHRIGGYKVRNQHWSLIMESVVPSDKGNYTCVVENEYGSI
NHTYHLDVVERSPHRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYGPDGLPYLKVLKAAGVNTT
DKEIEVLYIRNVTFEDAGEYTCLAGNSIGISFHSAWLTVLPAPGREKEITASPDYLEIAIYCIGVFLIACMVVTVILCRM
KNTTKKPDFSSQPAVHKLTKRIPLRRQVTVSAESSSSMNSNTPLVRITTRLSSTADTPMLAGVSEYELPEDPKWEFPRDK
LTLGKPLGEGCFGQVVMAEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKMIGKHKNIINLLGACTQDGPL
YVIVEYASKGNLREYLRARRPPGMEYSYDINRVPEEQMTFKDLVSCTYQLARGMEYLASQKCIHRDLAARNVLVTENNVM
KIADFGLARDINNIDYYKKTTNGRLPVKWMAPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKEGH
RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTTNEEYLDLSQPLEQYSPSYPDTRSSCSSGDDSVFSP
DPMPYEPCLPQYPHINGSVKT
(SEQ ID NO: 71 of Sequence Listing)

Figure 80

atggtgctgcagacccaggtgttcatctccctgctgctgtggatctccggcgcgtacggcgacatccagatgacccagag
ccccagcagcctgagcgccagcgtgggcgacagagtgaccatcacctgtcgggccagcgaggacatctacagcaacctgg
cctggtatcagcagaagccccggcaagagccccccagctgctgatctacgacgccaacatcctggccgacggcgtgccccagc
agattcagcggcagcggctccggcaccgactacaccctgaccatctccagcctgcagccccgaggacttcgccacctacta
ctgccagcagtacaacaactacccccccattcaccttcggccagggcaccaaggtggaaatcaagcgtacggtggccgccc
cctccgtgttcatcttcccccccctccgacgagcagctgaagtccggcaccgcctccgtggtgtgcctgctgaataacttc
taccccagagaggccaaggtgcagtggaaggtggacaacgccctgcagtccgggaactcccaggagagcgtgaccgagca
ggacagcaaggacagcacctacagcctgagcagcaccctgaccctgagcaaagccgactacgagaagcacaaggtgtacg
cctgcgaggtgacccaccagggcctgagctcccccgtcaccaagagcttcaacaggggggagtgt
Signal sequence (1-60), Variable region (61-390), Constant region (391-705)
(SEQ ID NO: 72 of Sequence Listing)

Figure 81

MVLQTQVFISLLLWISGAYGDIQMTQSPSSLSASVGDRVTITCRASEDIYSNLAWYQQKPGKSPQLLIYDANILADGVPS
RFSGSGSGTDYTLTISSLQPEDFATYYCQQYNNYPPFTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Signal sequence (1-20), Variable region (21-130), Constant region (131-235)
(SEQ ID NO: 73 of Sequence Listing)

Figure 82

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccagggactggaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgacggctacggcgactggttcacatactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccacccctgcccagcacctgaactcctgggggacccctcagtcttcctcttcccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttctttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctcccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region (412-1401)

(SEQ ID NO: 74 of Sequence Listing)

Figure 83

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGQGLEWMGWIYAGDGGTKYN
QKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCATDGYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region (138-467)

(SEQ ID NO: 75 of Sequence Listing)

Figure 84

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccagggactggaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgccgacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgacggctacggcgactggttcacatactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccacccctgcccagcacctgaactcctgggggacccctcagtcttcctcttcccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatgggcagccccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctcccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region(412-1401)

(SEQ ID NO: 76 of Sequence Listing)

Figure 85

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGQGLEWMGWIYAGDGGTKYN
QKFKGRVTLTADKSTSTAYMELSSLRSEDTAVYYCATDGYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region (138-467)

(SEQ ID NO: 77 of Sequence Listing)

Figure 86

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccccagcaccgaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgacggctacggcgactggttcacatactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccacccctgcccagcacctgaactcctgggggacccctcagtcttcctcttccccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctcccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region (412-1401)

(SEQ ID NO: 78 of Sequence Listing)

Figure 87

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGPSTEWMGWIYAGDGGTKYN
QKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCATDGYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region (138-467)

(SEQ ID NO: 79 of Sequence Listing)

Figure 88

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccccagcatcgaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgacggctacggcgactggttcgcctactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccaccctgcccagcacctgaactcctgggggacccctcagtcttcctcttcccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctcccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region(412-1401)

(SEQ ID NO: 80 of Sequence Listing)

Figure 89

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGPSIEWMGWIYAGDGGTKYN
QKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCATDGYGDWFAYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region (138-467)

(SEQ ID NO: 81 of Sequence Listing)

Figure 90

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccccagcaccgaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgagggctacggcgactggttcacatactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccaccctgcccagcacctgaactcctgggggacccctcagtcttcctcttccccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctcccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region(412-1401)

(SEQ ID NO: 82 of Sequence Listing)

Figure 91

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGPSTEWMGWIYAGDGGTKYN
QKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCATEGYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region(138-467)

(SEQ ID NO: 83 of Sequence Listing)

Figure 92

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccccagcaccgaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgacgcctacggcgactggttcacatactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccacccctgcccagcacctgaactcctgggggacccctcagtcttcctcttcccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctcccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region(412-1401)

(SEQ ID NO: 84 of Sequence Listing)

Figure 93

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGPSTEWMGWIYAGDGGTKYN
QKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCATDAYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region(138-467)

(SEQ ID NO: 85 of Sequence Listing)

Figure 94

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccccagcaccgaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgacgagtacggcgactggttcacatactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccacccctgcccagcacctgaactcctgggggacccctcagtcttcctcttcccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctcccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region (412-1401)

(SEQ ID NO: 86 of Sequence Listing)

Figure 95

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGPSTEWMGWIYAGDGGTKYN
QKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCATDEYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region (138-467)

(SEQ ID NO: 87 of Sequence Listing)

Figure 96

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccccagcaccgaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgacttctacggcgactggttcacatactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccacccctgcccagcacctgaactcctgggggacccctcagtcttcctcttccccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctcccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region (412-1401)

(SEQ ID NO: 88 of Sequence Listing)

Figure 97

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGPSTEWMGWIYAGDGGTKYN
QKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCATDFYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region(138-467)

(SEQ ID NO: 89 of Sequence Listing)

Figure 98

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccccagcaccgaaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgaccactacggcgactggttcacatactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccacccctgcccagcacctgaactcctgggggacccctcagtcttcctcttcccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctcccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region(412-1401)

(SEQ ID NO: 90 of Sequence Listing)

Figure 99

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGPSTEWMGWIYAGDGGTKYN
QKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCATDHYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region (138-467)

(SEQ ID NO: 91 of Sequence Listing)

Figure 100

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccccagcaccgaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgacatctacggcgactggttcacatactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccaccctgcccagcacctgaactcctgggggacccctcagtcttcctcttcccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttctttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctcccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region(412-1401)

(SEQ ID NO: 92 of Sequence Listing)

Figure 101

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGPSTEWMGWIYAGDGGTKYN
QKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCATDIYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region (138-467)

(SEQ ID NO: 93 of Sequence Listing)

Figure 102

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccccagcaccgaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgacaagtacggcgactggttcacatactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccacccctgcccagcacctgaacctcctgggggacccctcagtcttcctcttccccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region(412-1401)

(SEQ ID NO: 94 of Sequence Listing)

Figure 103

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGPSTEWMGWIYAGDGGTKYN
QKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCATDKYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region (138-467)

(SEQ ID NO: 95 of Sequence Listing)

Figure 104

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccccagcaccgaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgacctgtacggcgactggttcacatactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccacccctgcccagcacctgaactcctgggggacccctcagtcttcctcttcccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatgggcagccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region (412-1401)

(SEQ ID NO: 96 of Sequence Listing)

Figure 105

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGPSTEWMGWIYAGDGGTKYN
QKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCATDLYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region (138-467)

(SEQ ID NO: 97 of Sequence Listing)

Figure 106

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccccagcaccgaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgacatgtacggcgactggttcacatactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccaccctgcccagcacctgaactcctgggggacccctcagtcttcctcttcccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region(412-1401)

(SEQ ID NO: 98 of Sequence Listing)

Figure 107

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGPSTEWMGWIYAGDGGTKYN
QKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCATDMYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region (138-467)

(SEQ ID NO: 99 of Sequence Listing)

Figure 108

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccccagcaccgaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgaccagtacggcgactggttcacatactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccaccctgcccagcacctgaactcctgggggacccctcagtcttcctcttcccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctcccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region(412-1401)

(SEQ ID NO: 100 of Sequence Listing)

Figure 109

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGPSTEWMGWIYAGDGGTKYN
QKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCATDQYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region(138-467)

(SEQ ID NO: 101 of Sequence Listing)

Figure 110

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccccagcaccgaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgaccggtacggcgactggttcacatactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaacccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccaccctgcccagcacctgaactcctggggggaccctcagtcttcctcttccccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctcccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region(412-1401)

(SEQ ID NO: 102 of Sequence Listing)

Figure 111

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGPSTEWMGWIYAGDGGTKYN
QKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCATDRYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region(138-467)

(SEQ ID NO: 103 of Sequence Listing)

Figure 112

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccccagcaccgaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgacgtgtacggcgactggttcacatactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccacccctgcccagcacctgaactcctgggggacccctcagtcttcctcttcccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctcccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region(412-1401)

(SEQ ID NO: 104 of Sequence Listing)

Figure 113

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGPSTEWMGWIYAGDGGTKYN
QKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCATDVYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region (138-467)

(SEQ ID NO: 105 of Sequence Listing)

Figure 114

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccccagcaccgaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgactggtacggcgactggttcacatactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccaccctgcccagcacctgaactcctgggggacccctcagtcttcctcttccccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctcccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region (412-1401)

(SEQ ID NO: 106 of Sequence Listing)

Figure 115

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGPSTEWMGWIYAGDGGTKYN
QKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCATDWYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region (138-467)

(SEQ ID NO: 107 of Sequence Listing)

Figure 116

atgaaacacctgtggttcttcctcctgctggtggcagctcccagatgggtgctgagccaggtgcagctggtgcagtctgg
cgccgaagtgaagaaacctggggctagcgtgaaggtgtcctgcaaggccagcggcttcaccttcagcaccagctatatga
gctgggtccgccaggctccaggccccagcaccgaatggatgggctggatctatgccggcgacggcggcaccaagtacaac
cagaaattcaagggcagagtgaccctgaccgtggacaagagcaccagcaccgcctacatggaactgagcagcctgcggag
cgaggacaccgccgtgtactactgcgccaccgactactacggcgactggttcacatactggggccagggcaccctggtga
ccgtgagctcagcctccaccaagggcccaagcgtcttccccctggcaccctcctccaagagcacctctggcggcacagcc
gccctgggctgcctggtcaaggactacttccccgaaccgtgaccgtgagctggaactcaggcgccctgaccagcggcgt
gcacaccttccccgctgtcctgcagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgg
gcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagttgagcccaaatcttgt
gacaaaactcacacatgcccaccctgcccagcacctgaactcctgggggacccctcagtcttcctcttccccccaaaacc
caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtca
agttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccccgggaggagcagtacaacagcacgtac
cgggtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagc
cctcccagcccccatcgagaaaaccatctccaaagccaaaggccagccccgggaaccacaggtgtacaccctgcccccat
cccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggag
tgggagagcaatggccagcccgagaacaactacaagaccacccctcccgtgctggactccgacggctccttcttcctcta
cagcaagctcaccgtggacaagagcaggtggcagcagggcaacgtcttctcatgctccgtgatgcatgaggctctgcaca
accactacacccagaagagcctctccctgtctcccggcaaa

Signal sequence (1-57), Variable region (58-411), Constant region (412-1401)

(SEQ ID NO: 108 of Sequence Listing)

Figure 117

MKHLWFFLLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGFTFSTSYMSWVRQAPGPSTEWMGWIYAGDGGTKYN
QKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCATDYYGDWFTYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Signal sequence (1-19), Variable region (20-137), Constant region (138-467)

(SEQ ID NO: 109 of Sequence Listing)

Figure 118

GGCAGAGTGACCCTGACCGCCGACAAGAGCACCAGCACC

(SEQ ID NO: 110 of Sequence Listing)

Figure 119

GGTGCTGGTGCTCTTGTCGGCGGTCAGGGTCACTCTGCC

(SEQ ID NO: 111 of Sequence Listing)

Figure 120

CTGTTTCAAGGTCCGAGCAATAACAAACGTGCACCGTATTGG
(SEQ ID NO: 112 of Sequence Listing)

Figure 121

CGCAAGCTTGTCGACTCAAACAACATCCAGATGATAGGTATG
(SEQ ID NO: 113 of Sequence Listing)

FIG. 122

	Name	KD (M)	Analyte (Antigen variant)
1	hFR2-14_H1/L1	1.2E-08	III b
2	hFR2-14_H2/L1	8.7E-09	III b
3	hFR2-14_H3/L1	7.4E-09	III b
4	hFR2-14_H4/L1	5.4E-09	III b
5	cFR2-14	6.3E-08	III b
6	hFR2-14_H1/L1	3.0E-09	III c
7	hFR2-14_H2/L1	6.4E-09	III c
8	hFR2-14_H3/L1	3.3E-09	III c
9	hFR2-14_H4/L1	2.8E-09	III c

FIG. 123

	Name	KD (M)	Analyte (Antigen variant)
1	hFR2-14_H5/L1	9.5E-10	IIIc
2	hFR2-14_H6/L1	1.5E-09	IIIc
3	hFR2-14_H7/L1	1.2E-09	IIIc
4	hFR2-14_H8/L1	1.5E-09	IIIc
5	hFR2-14_H9/L1	5.1E-10	IIIc
6	hFR2-14_H10/L1	6.9E-10	IIIc
7	hFR2-14_H11/L1	2.1E-09	IIIc
8	hFR2-14_H12/L1	7.6E-10	IIIc
9	hFR2-14_H13/L1	6.7E-10	IIIc
10	hFR2-14_H14/L1	2.3E-09	IIIc
11	hFR2-14_H15/L1	3.4E-09	IIIc
12	hFR2-14_H16/L1	9.1E-10	IIIc
13	hFR2-14_H17/L1	1.5E-09	IIIc
14	hFR2-14_H18/L1	1.2E-09	IIIc
15	hFR2-14_H3/L1	6.4E-09	IIIc

FIG. 124

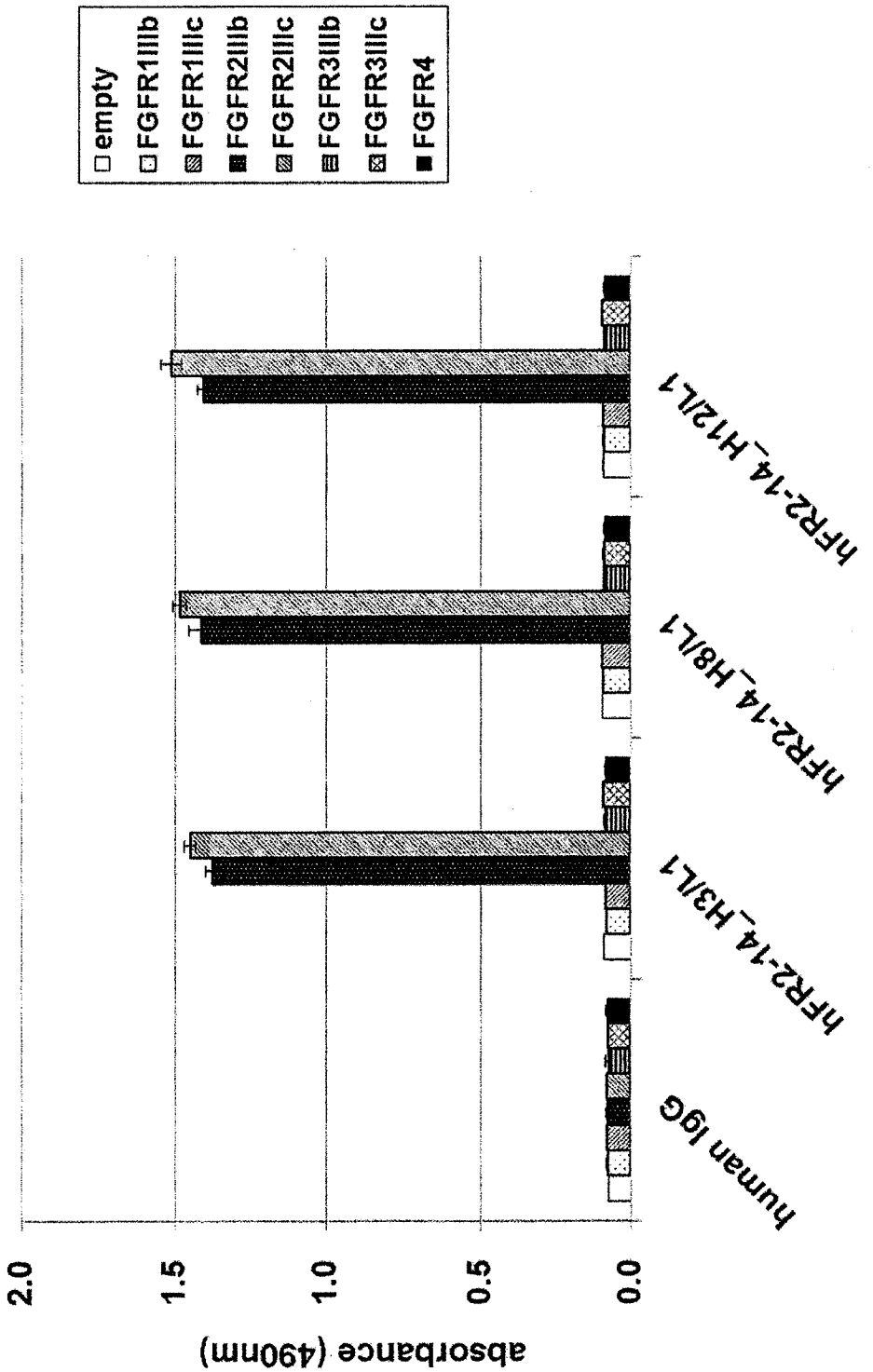

empty
FGFR1IIIb
FGFR1IIIc
FGFR2IIIb
FGFR2IIIc
FGFR3IIIb
FGFR3IIIc
FGFR4
human IgG
hFR2-14_H3/L1
hFR2-14_H8/L1
hFR2-14_H12/L1
0.0
0.5
1.0
1.5
2.0
absorbance (490nm)

FIG. 125A

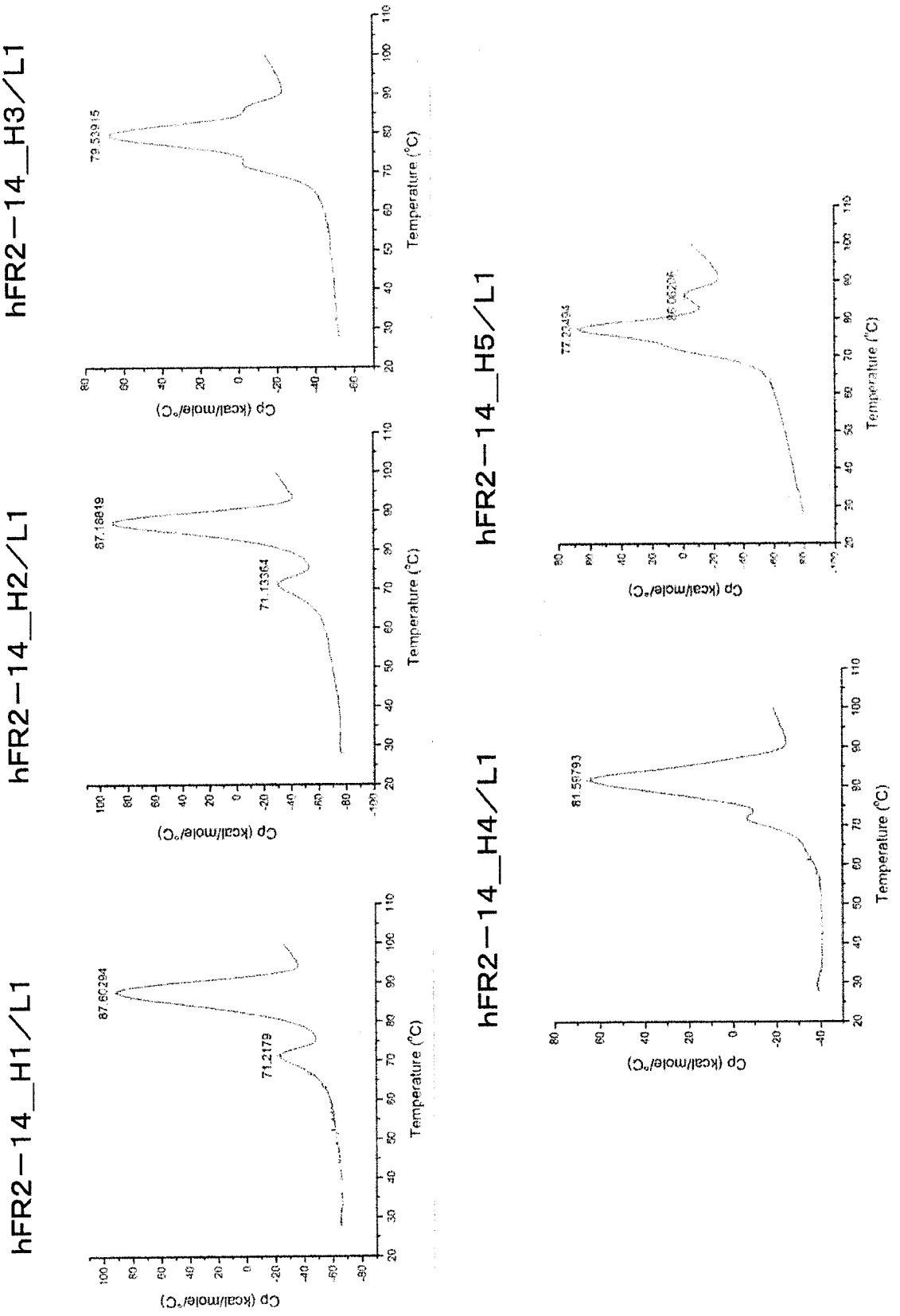

hFR2−14_H1/L1
87.60284
71.2179
hFR2−14_H2/L1
87.16819
71.13364
hFR2−14_H3/L1
79.53915
hFR2−14_H4/L1
81.58793
hFR2−14_H5/L1
77.23494
Cp (kcal/mole/°C)
Temperature (°C)

FIG. 125B

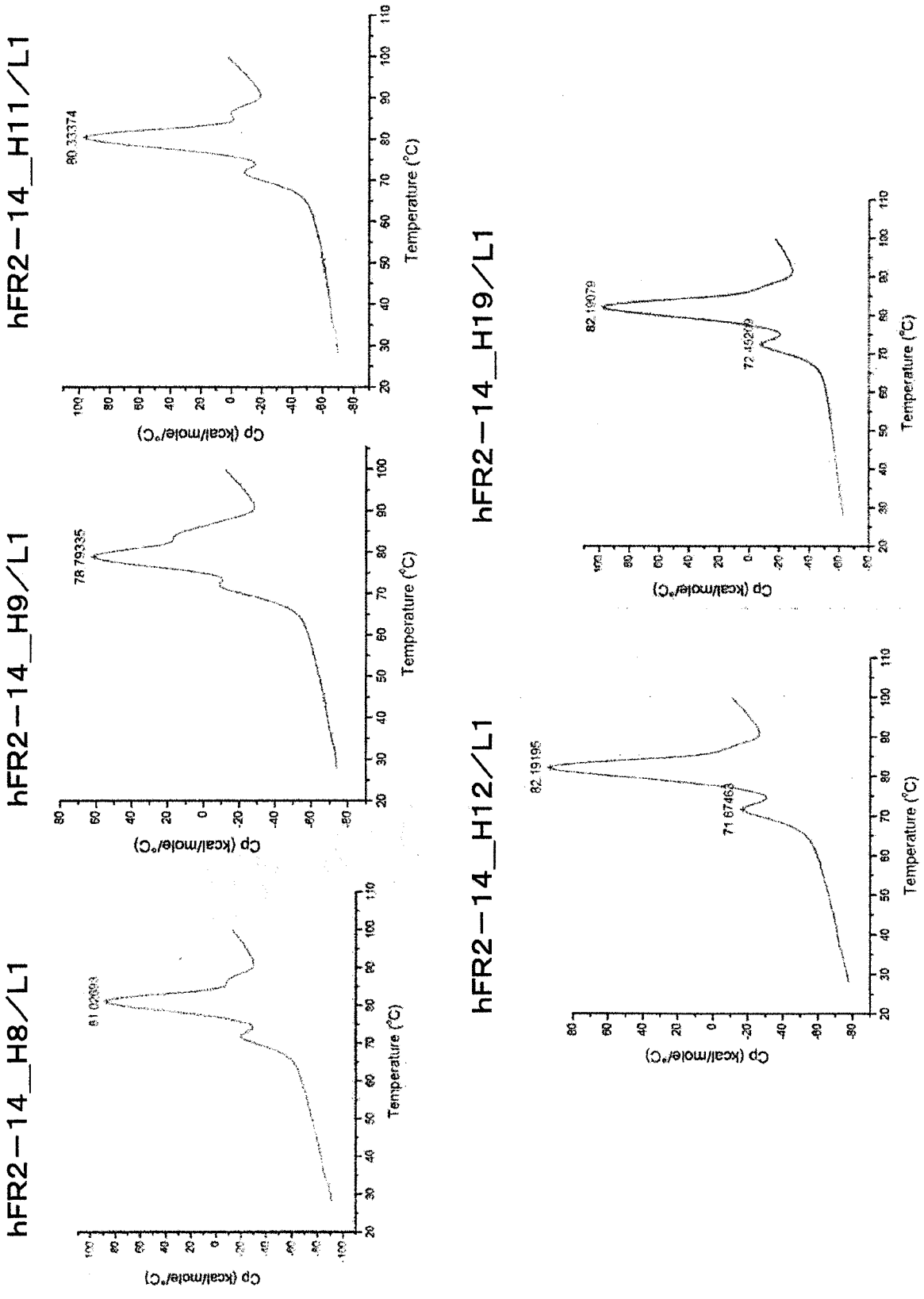

hFR2−14_H11/L1
80.33374
hFR2−14_H9/L1
78.79335
hFR2−14_H8/L1
hFR2−14_H19/L1
82.19079
hFR2−14_H12/L1
82.19195
71.67463
Cp (kcal/mole/°C)
Temperature (°C)

FIG. 125C

Name	Tm (°C)
hFR2−14_H1/L1	87.6
hFR2−14_H2/L1	87.2
hFR2−14_H3/L1	79.5
hFR2−14_H4/L1	81.6
hFR2−14_H5/L1	77.2
hFR2−14_H8/L1	81.0
hFR2−14_H9/L1	78.8
hFR2−14_H11/L1	80.3
hFR2−14_H12/L1	82.2
hFR2−14_H19/L1	82.2

FIG. 126

Experiment No.	Antibody name	Antibody-producing cell	KD (M)
1	hFR2-14_H1/L1	293F	3.4E-09
	hFR2-14_H1/L1 degraded analyte	293F	1.5E-07
	hFR2-14_H2/L1	293F	3.7E-09
	hFR2-14_H2/L1 degraded analyte	293F	4.0E-08
	hFR2-14_H3/L1	293F	1.2E-08
	hFR2-14_H3/L1 degraded analyte	293F	1.7E-07
	hFR2-14_H4/L1	293F	1.9E-09
	hFR2-14_H4/L1 degraded analyte	293F	8.3E-08
2	hFR2-14_H3/L1	293F	9.0E-09
	hFR2-14_H3/L1 degraded analyte	293F	1.1E-07
	hFR2-14_H5/L1	293F	1.5E-09
	hFR2-14_H5/L1 degraded analyte	293F	2.2E-09
	hFR2-14_H8/L1	293F	9.0E-10
	hFR2-14_H8/L1 degraded analyte	293F	1.6E-09
	hFR2-14_H9/L1	293F	1.9E-09
	hFR2-14_H9/L1 degraded analyte	293F	3.5E-08
	hFR2-14_H11/L1	293F	1.4E-09
	hFR2-14_H11/L1 degraded analyte	293F	4.7E-09
	hFR2-14_H12/L1	293F	9.5E-10
	hFR2-14_H12/L1 degraded analyte	293F	1.3E-09
3	hFR2-14_H12/L1	CHO	5.0E-09
	hFR2-14_H12/L1 degraded analyte	CHO	6.0E-09
	hFR2-14_H19/L1	CHO	5.5E-09
	hFR2-14_H19/L1 degraded analyte	CHO	4.7E-09

FIG. 127A

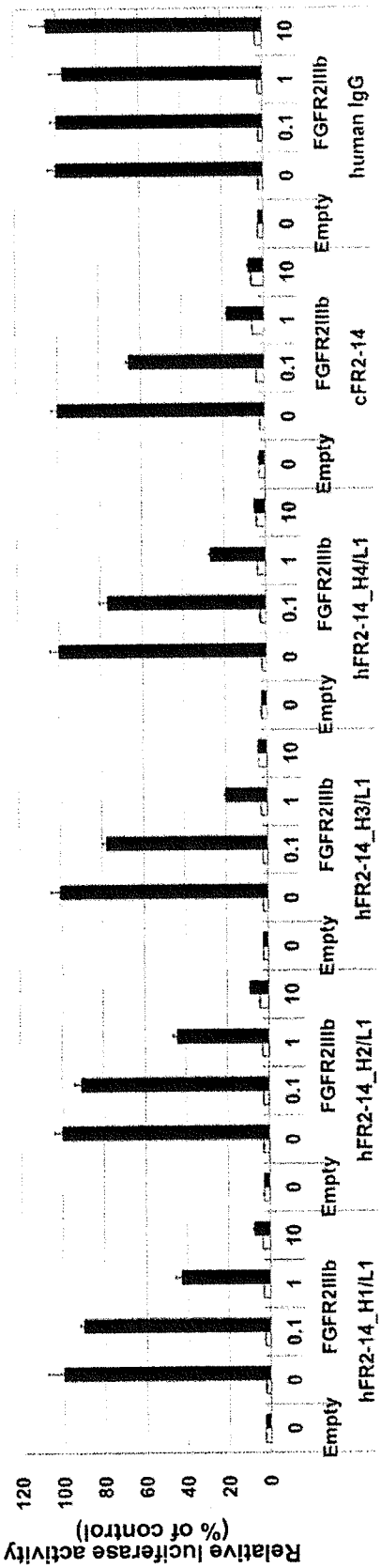

FGF7, 0 ng/ml
FGF7, 10 ng/ml
Relative luciferase activity (% of control)
120
100
80
60
40
20
0
Empty
FGFR2IIIb
hFR2-14_H1/L1
hFR2-14_H2/L1
hFR2-14_H3/L1
hFR2-14_H4/L1
cFR2-14
human IgG
0
0.1
1
10
Antibody concentration (μg/ml)

FIG. 127B

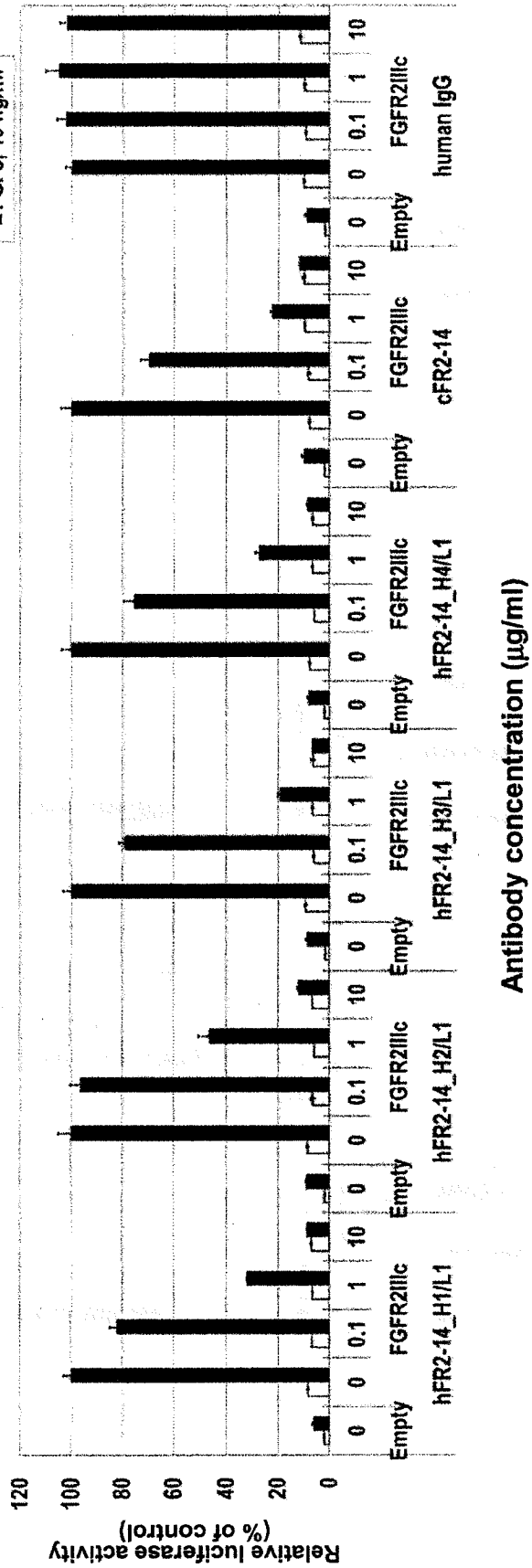

FGF9, 0 ng/ml
FGF9, 10 ng/ml
Relative luciferase activity (% of control)
120
100
80
60
40
20
0
Empty
hFR2-14_H1/L1
hFR2-14_H2/L1
hFR2-14_H3/L1
hFR2-14_H4/L1
cFR2-14
human IgG
FGFR2IIIc
Empty
0
0.1
1
10
Antibody concentration (µg/ml)

FIG. 128A

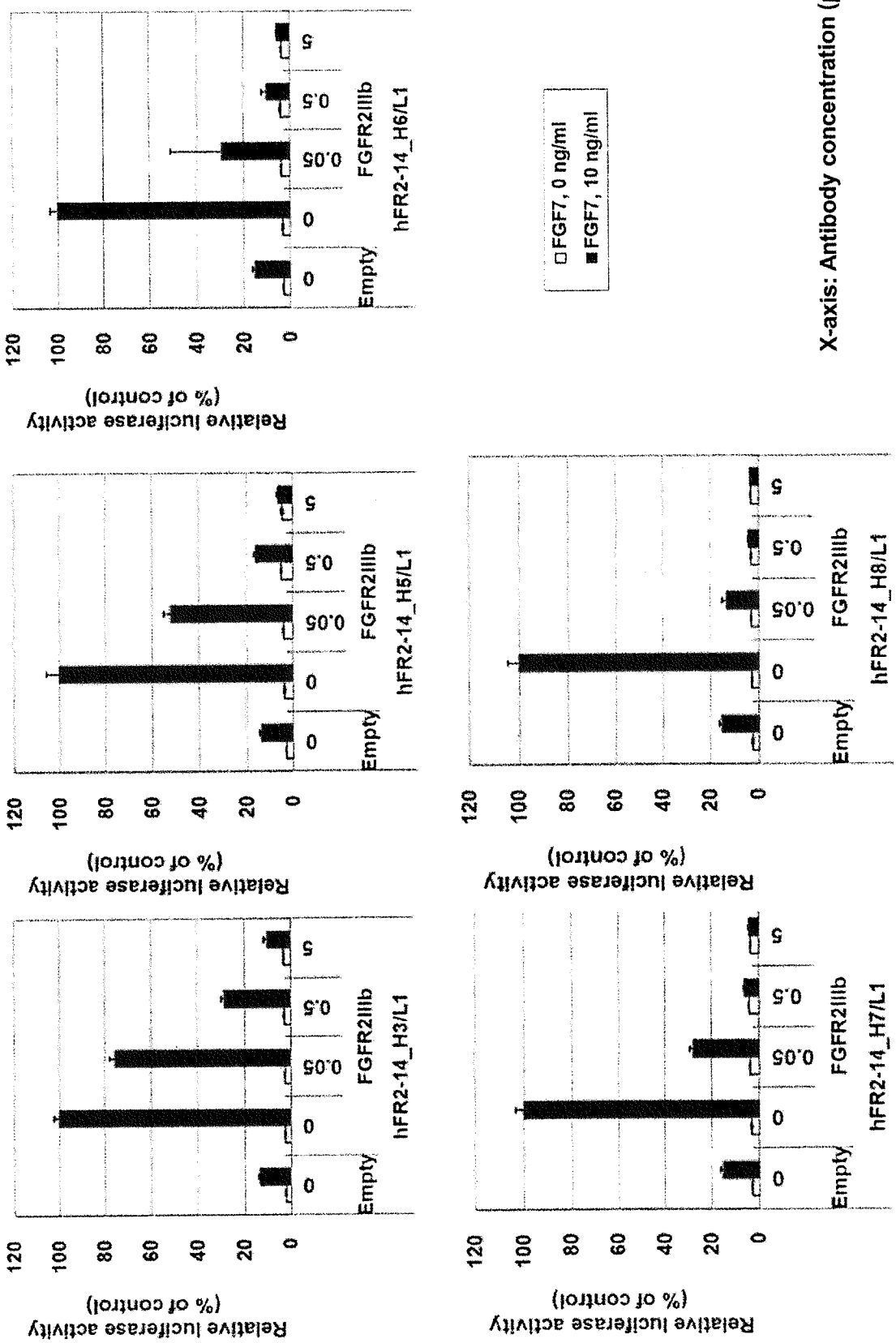

Relative luciferase activity (% of control)
120
100
80
60
40
20
0
Empty
0
0
0.05
0.5
5
FGFR2IIIb
hFR2-14_H6/L1
hFR2-14_H5/L1
hFR2-14_H8/L1
hFR2-14_H3/L1
hFR2-14_H7/L1
FGF7, 0 ng/ml
FGF7, 10 ng/ml
X-axis: Antibody concentration (μg/ml)

FIG. 128B

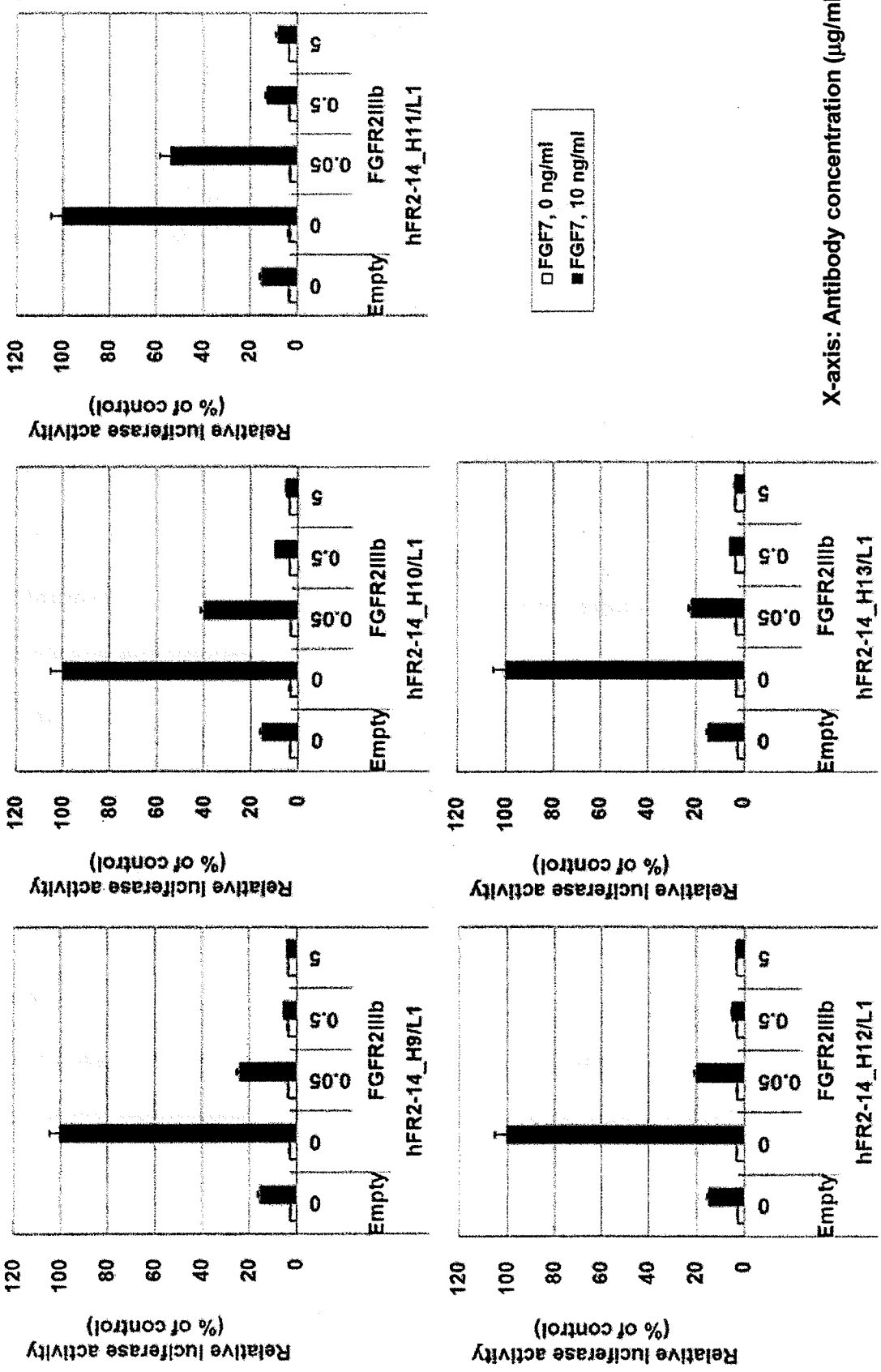

hFR2-14_H11/L1
hFR2-14_H10/L1
hFR2-14_H13/L1
hFR2-14_H9/L1
hFR2-14_H12/L1
FGFR2IIIb
Empty
0
0.05
0.5
5
120
100
80
60
40
20
0
Relative luciferase activity
(% of control)
FGF7, 0 ng/ml
FGF7, 10 ng/ml
X-axis: Antibody concentration (μg/ml)

FIG. 128C

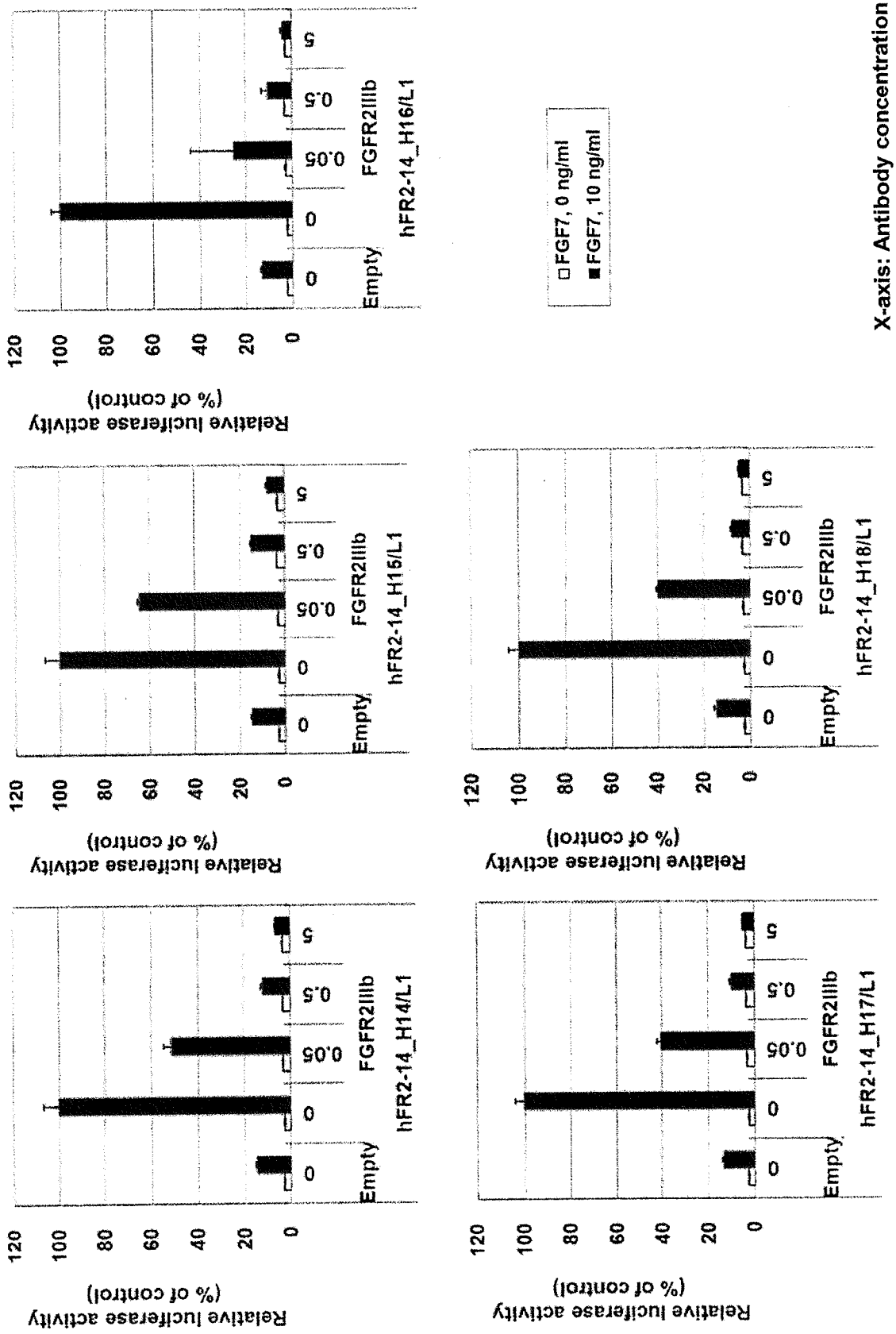

hFR2-14_H16/L1
hFR2-14_H15/L1
hFR2-14_H18/L1
hFR2-14_H14/L1
hFR2-14_H17/L1
FGFR2IIIb
Empty
0
0.05
0.5
5
Relative luciferase activity
(% of control)
120
100
80
60
40
20
0
FGF7, 0 ng/ml
FGF7, 10 ng/ml
X-axis: Antibody concentration (μg/ml)

FIG. 129A

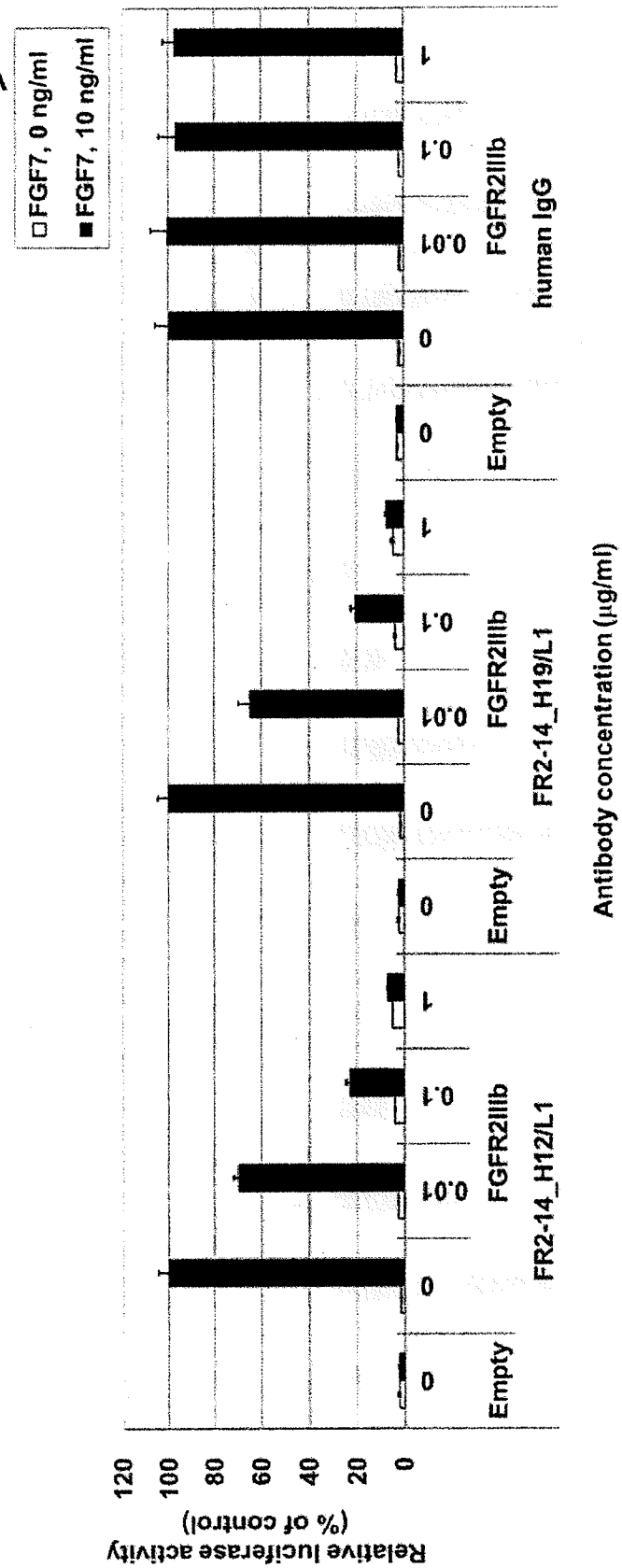

FGF7, 0 ng/ml
FGF7, 10 ng/ml
Relative luciferase activity
(% of control)
120
100
80
60
40
20
0
Empty
FGFR2IIIb
FR2-14_H12/L1
Empty
FGFR2IIIb
FR2-14_H19/L1
FGFR2IIIb
human IgG
0
0.01
0.1
1
Antibody concentration (μg/ml)

FIG. 129B

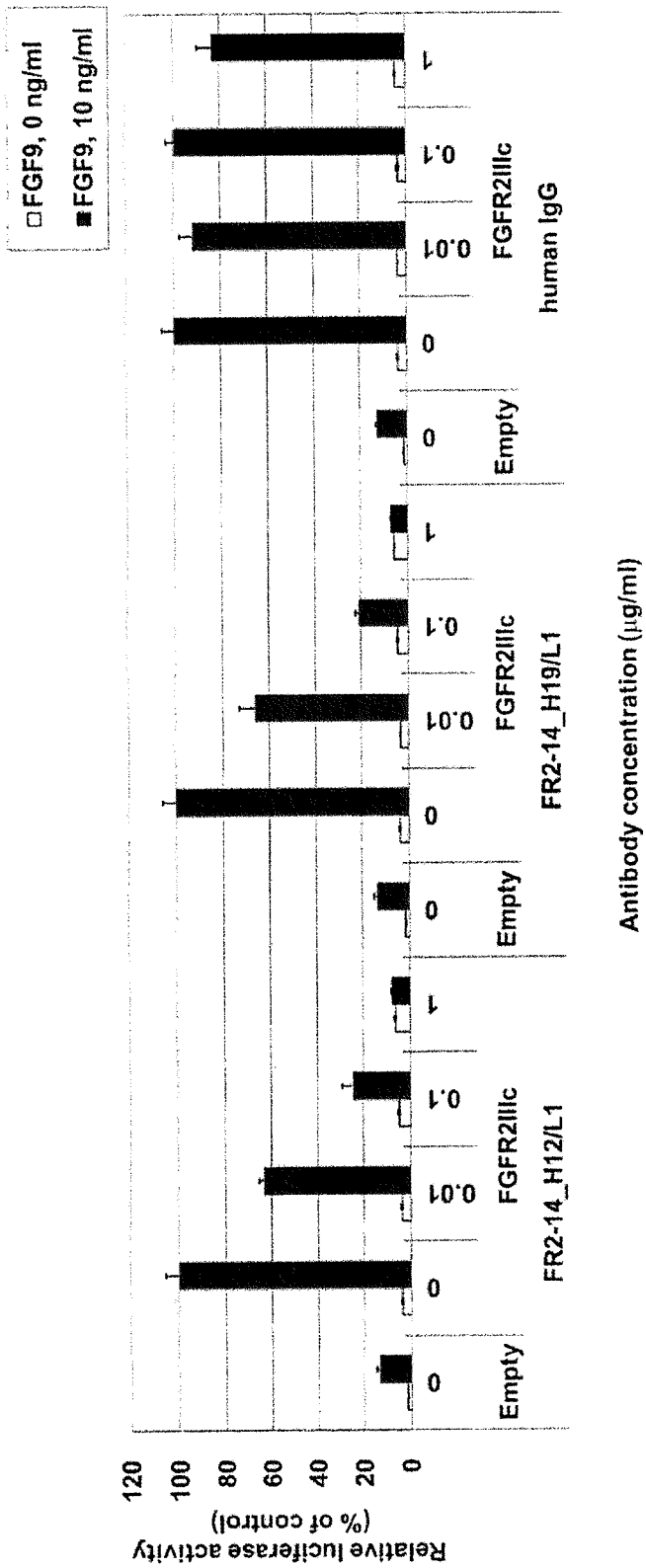

□FGF9, 0 ng/ml
■FGF9, 10 ng/ml
Relative luciferase activity (% of control)
120
100
80
60
40
20
0
Empty
FGFR2IIIc
FR2-14_H12/L1
FGFR2IIIc
FR2-14_H19/L1
human IgG
Antibody concentration (μg/ml)

FIG. 130A

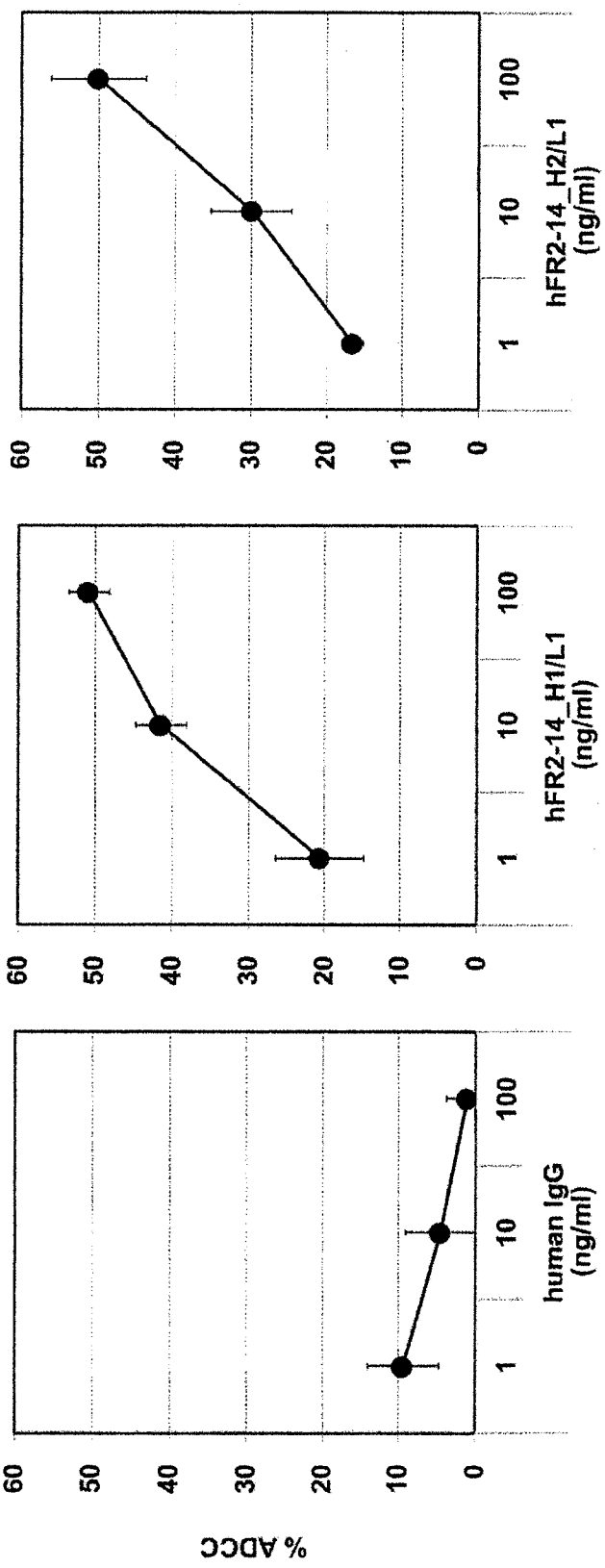

% ADCC
0
10
20
30
40
50
60
human IgG (ng/ml)
1
10
100
hFR2-14_H1/L1 (ng/ml)
hFR2-14_H2/L1 (ng/ml)

FIG. 130B

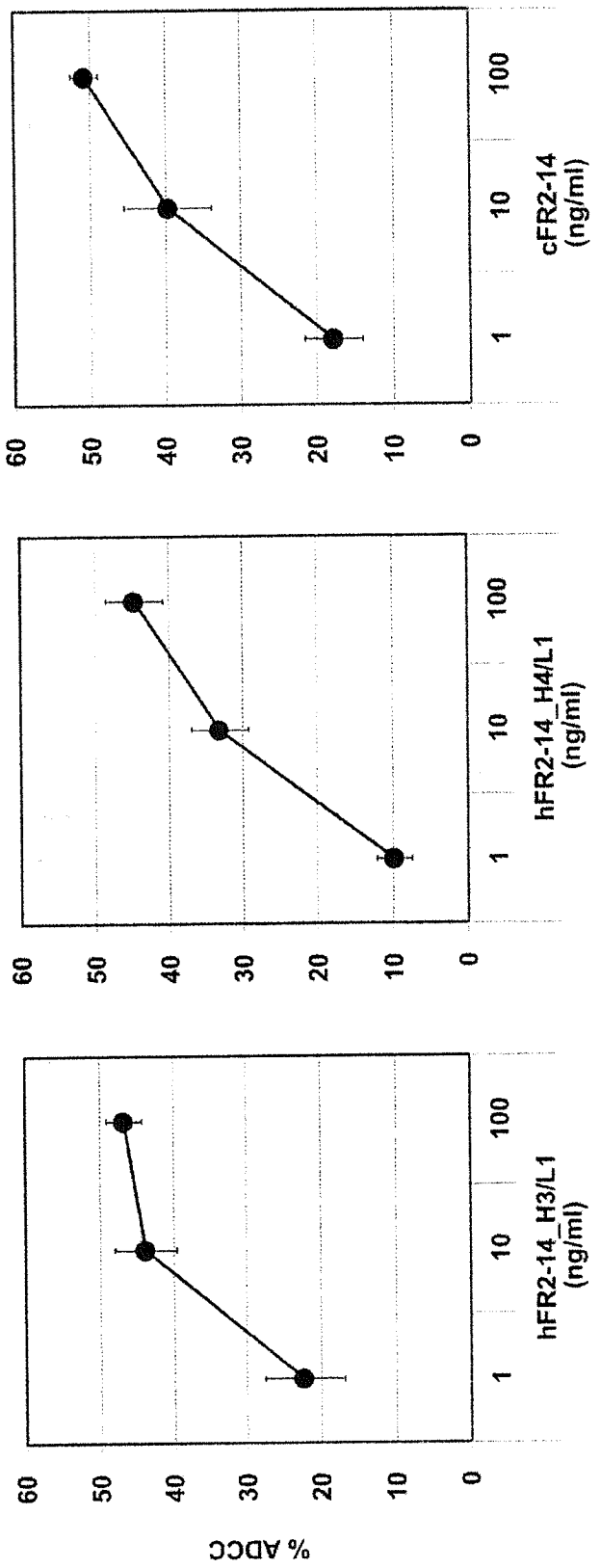

% ADCC
0
10
20
30
40
50
60
1
10
100
hFR2-14_H3/L1 (ng/ml)
hFR2-14_H4/L1 (ng/ml)
cFR2-14 (ng/ml)

FIG. 131

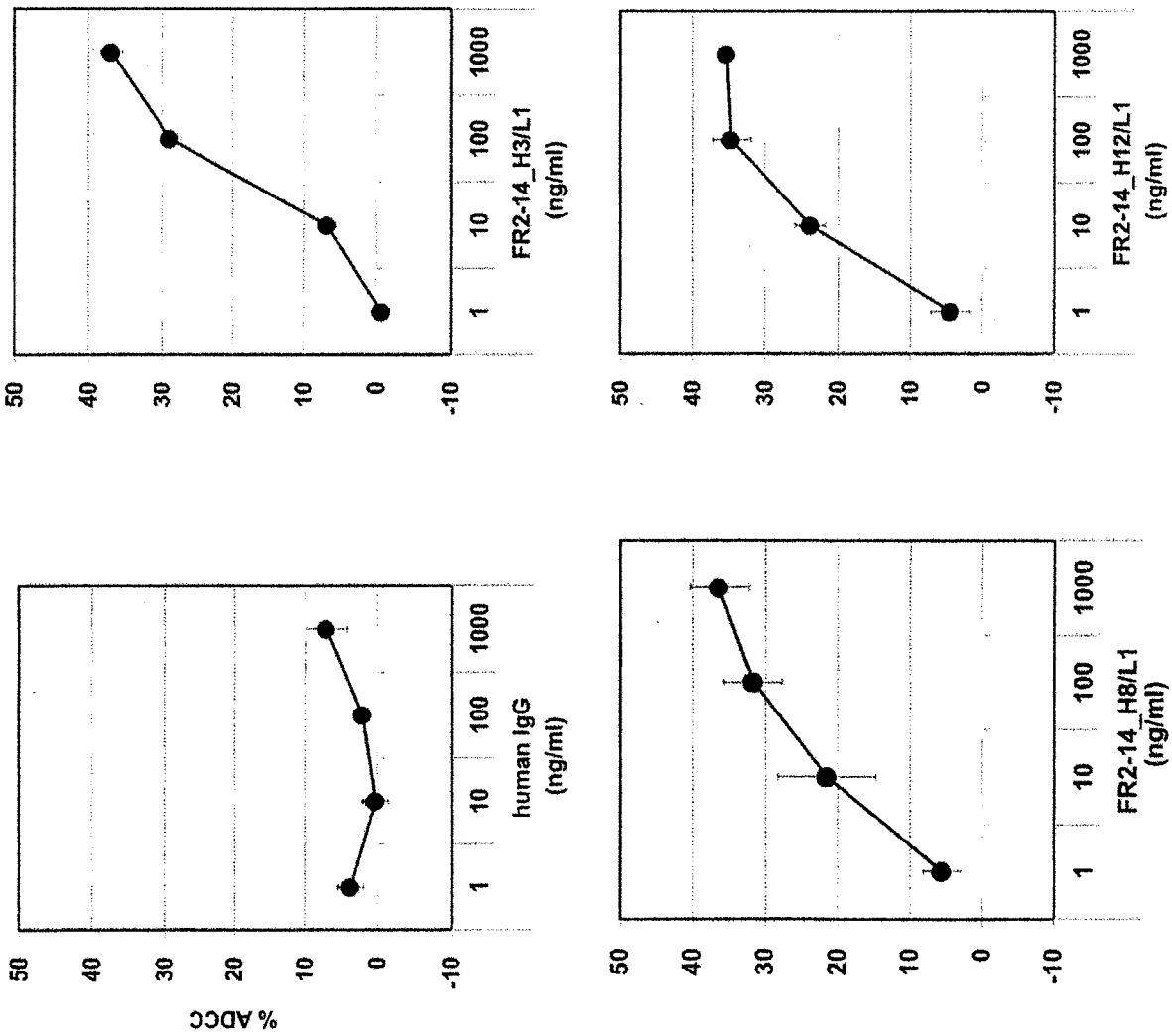

% ADCC
50
40
30
20
10
0
-10
1
10
100
1000
human IgG (ng/ml)
FR2-14_H3/L1 (ng/ml)
FR2-14_H12/L1 (ng/ml)
FR2-14_H8/L1 (ng/ml)

FIG. 132

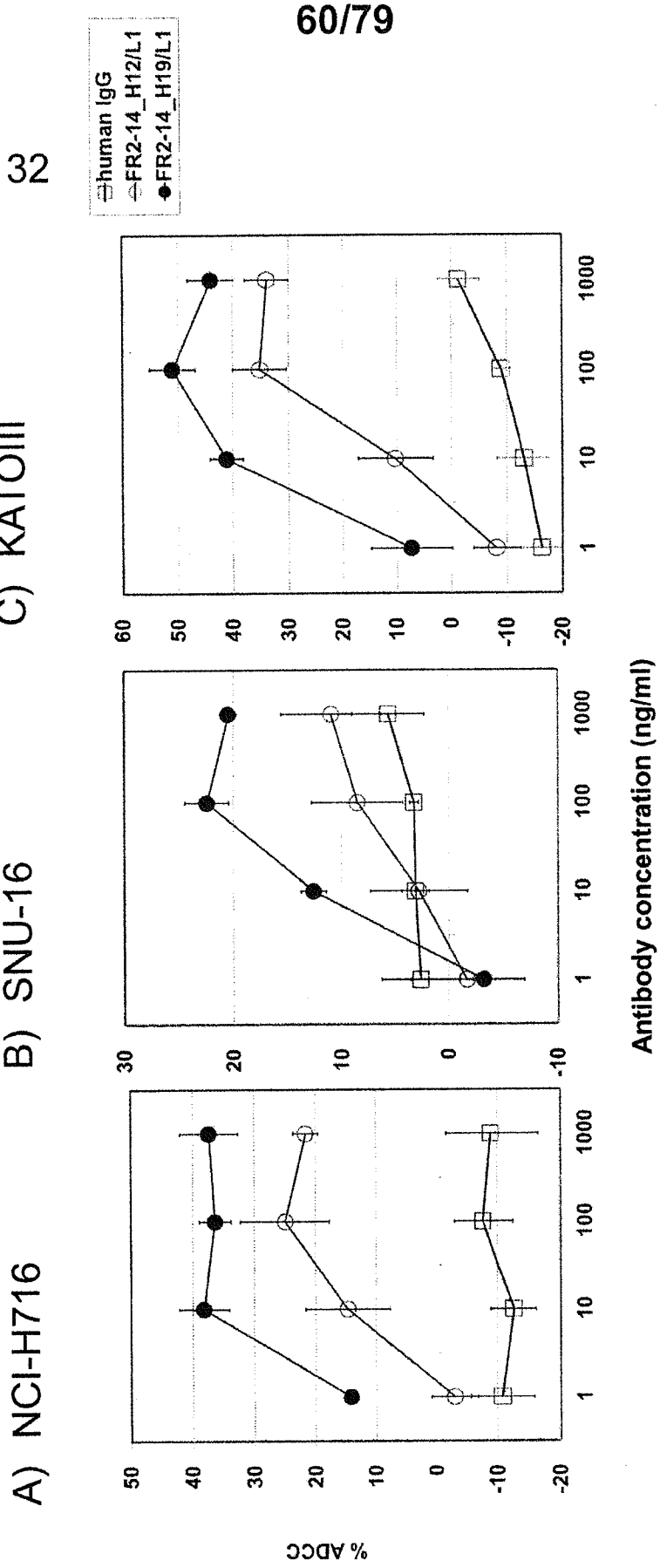

human IgG
FR2-14_H12/L1
FR2-14_H19/L1
A) NCI-H716
B) SNU-16
C) KATOIII
% ADCC
Antibody concentration (ng/ml)
50
40
30
20
10
0
-10
-20
60
1
10
100
1000

FIG. 133

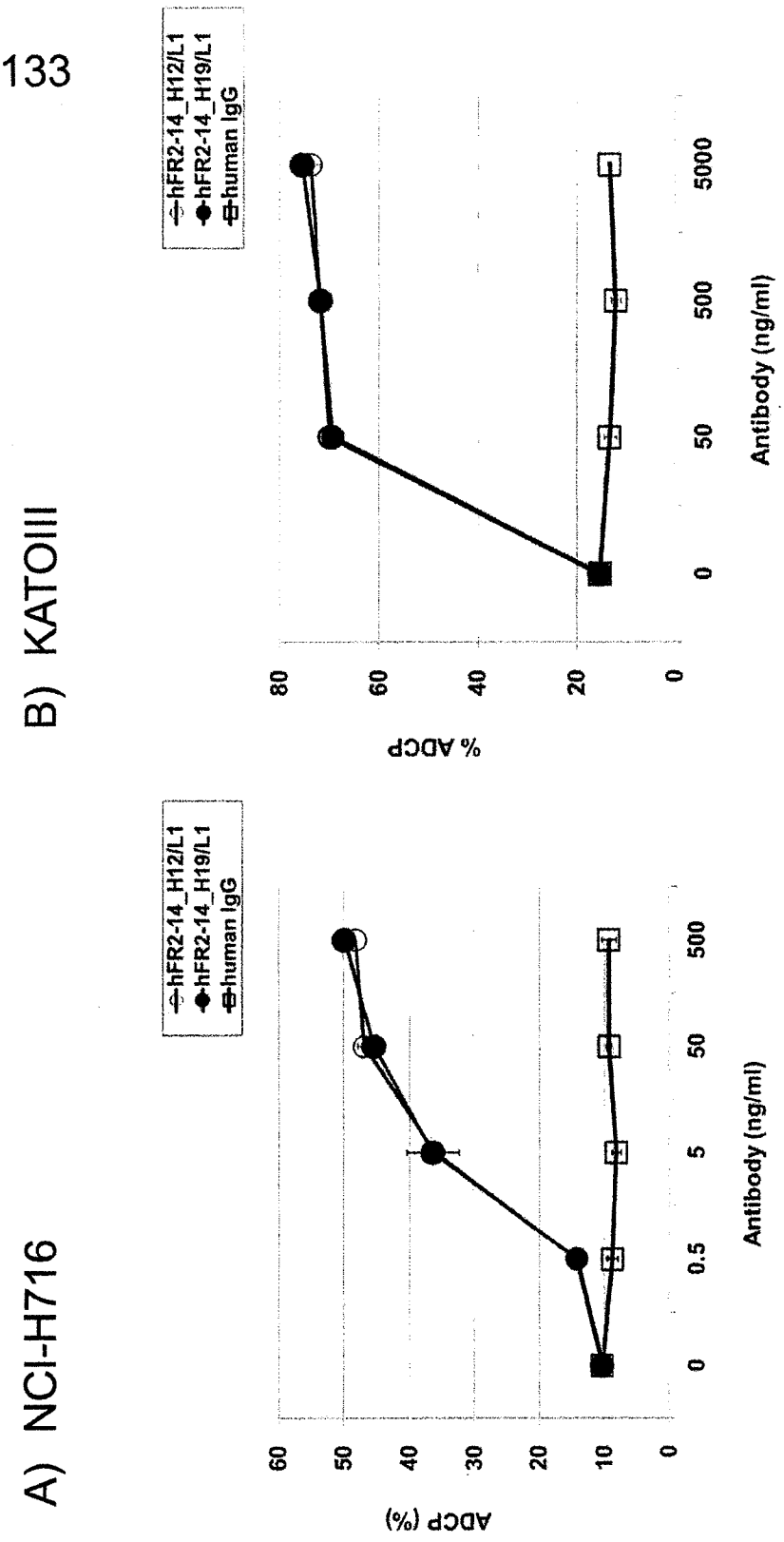

B) KATOIII
hFR2-14_H12/L1
hFR2-14_H19/L1
human IgG
% ADCP
80
60
40
20
0
0
50
500
5000
Antibody (ng/ml)
A) NCI-H716
hFR2-14_H12/L1
hFR2-14_H19/L1
human IgG
ADCP (%)
60
50
40
30
20
10
0
0
0.5
5
50
500
Antibody (ng/ml)

FIG. 134A

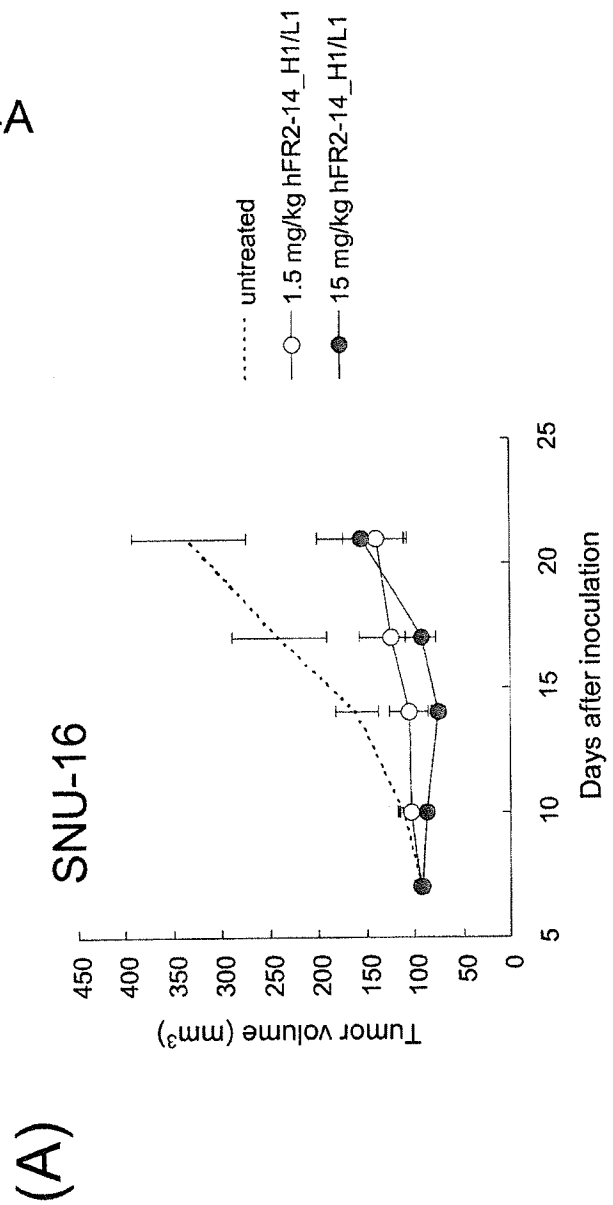

(A)
SNU-16
Tumor volume (mm3)
450
400
350
300
250
200
150
100
50
0
5
10
15
20
25
Days after inoculation
untreated
1.5 mg/kg hFR2-14_H1/L1
15 mg/kg hFR2-14_H1/L1

FIG. 134B

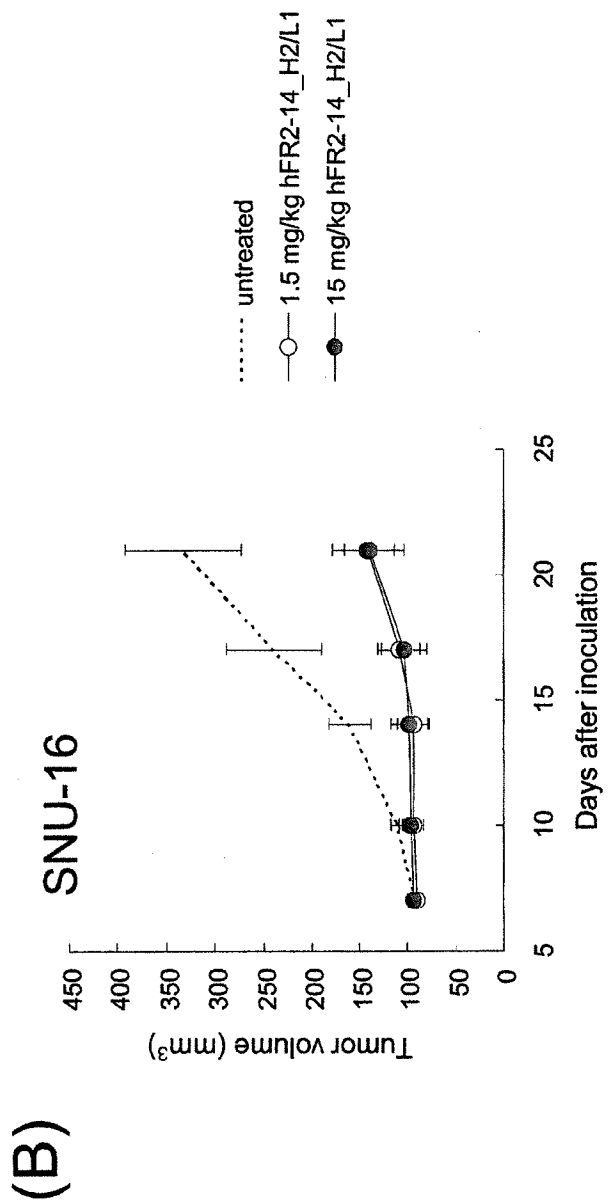

(B)
SNU-16
Tumor volume (mm3)
450
400
350
300
250
200
150
100
50
0
5
10
15
20
25
Days after inoculation
untreated
1.5 mg/kg hFR2-14_H2/L1
15 mg/kg hFR2-14_H2/L1

FIG. 134C

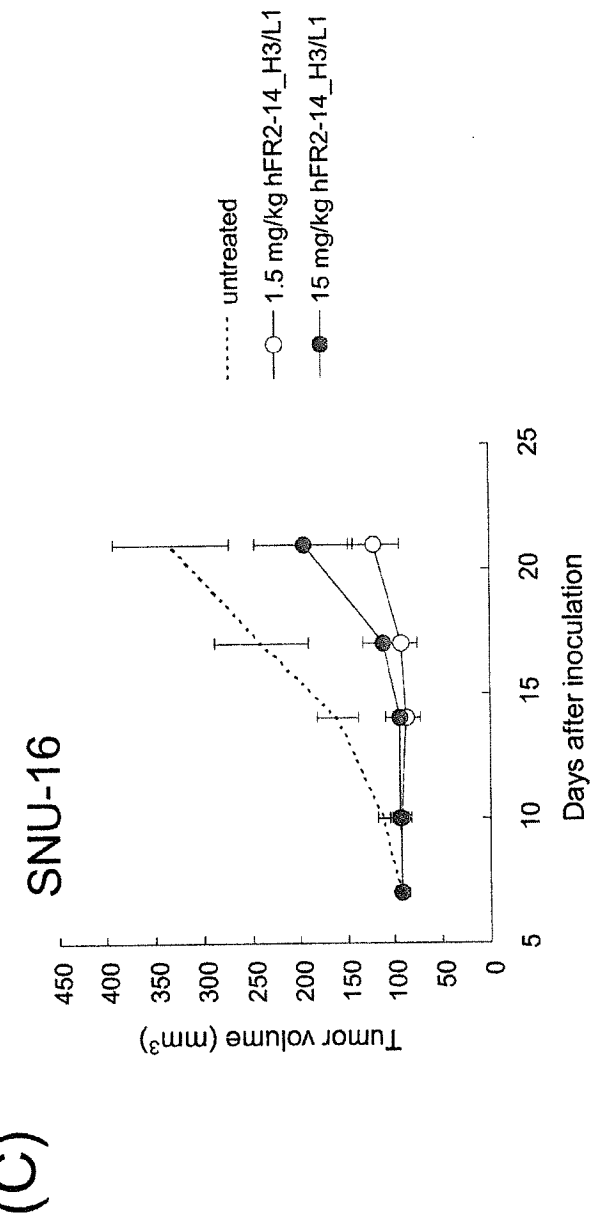

(C)
SNU-16
Tumor volume (mm³)
450
400
350
300
250
200
150
100
50
0
5
10
15
20
25
Days after inoculation
untreated
1.5 mg/kg hFR2-14_H3/L1
15 mg/kg hFR2-14_H3/L1

FIG. 134D

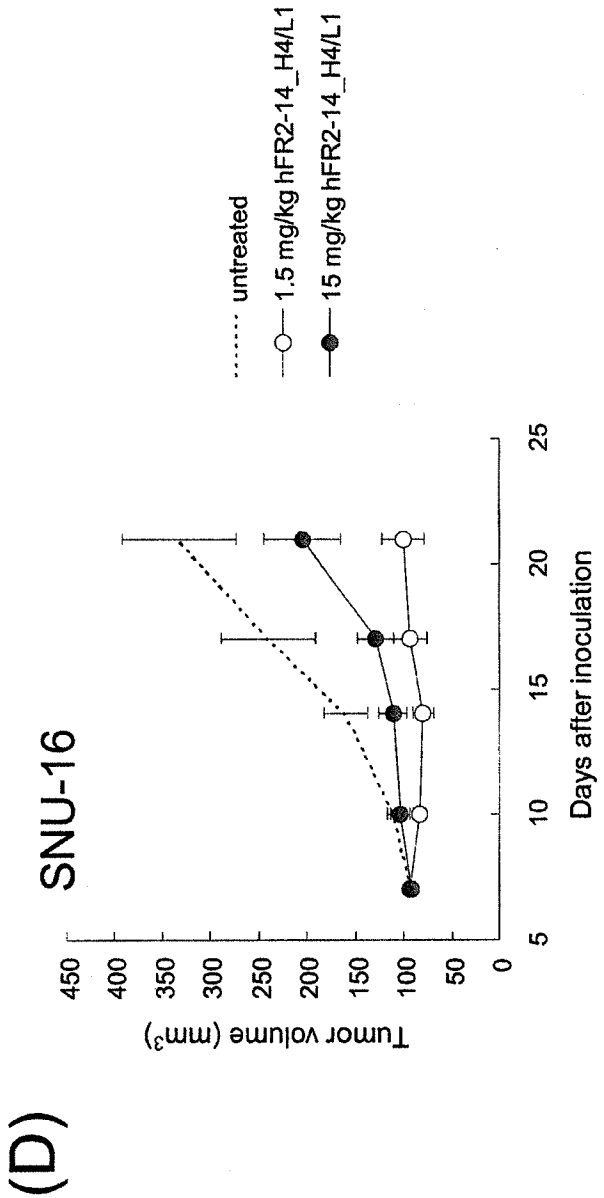

(D)
SNU-16
Tumor volume (mm3)
450
400
350
300
250
200
150
100
50
0
5
10
15
20
25
Days after inoculation
untreated
1.5 mg/kg hFR2-14_H4/L1
15 mg/kg hFR2-14_H4/L1

FIG. 135A

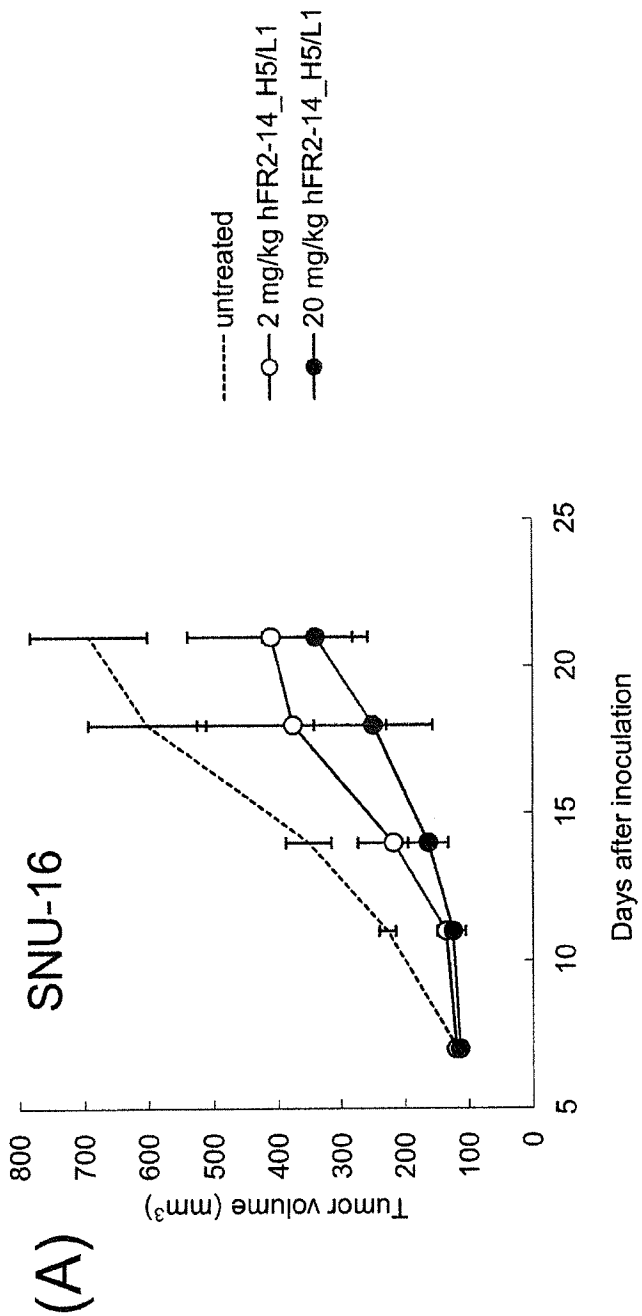

(A)
SNU-16
Tumor volume (mm3)
800
700
600
500
400
300
200
100
0
5
10
15
20
25
Days after inoculation
untreated
2 mg/kg hFR2-14_H5/L1
20 mg/kg hFR2-14_H5/L1

FIG. 135B

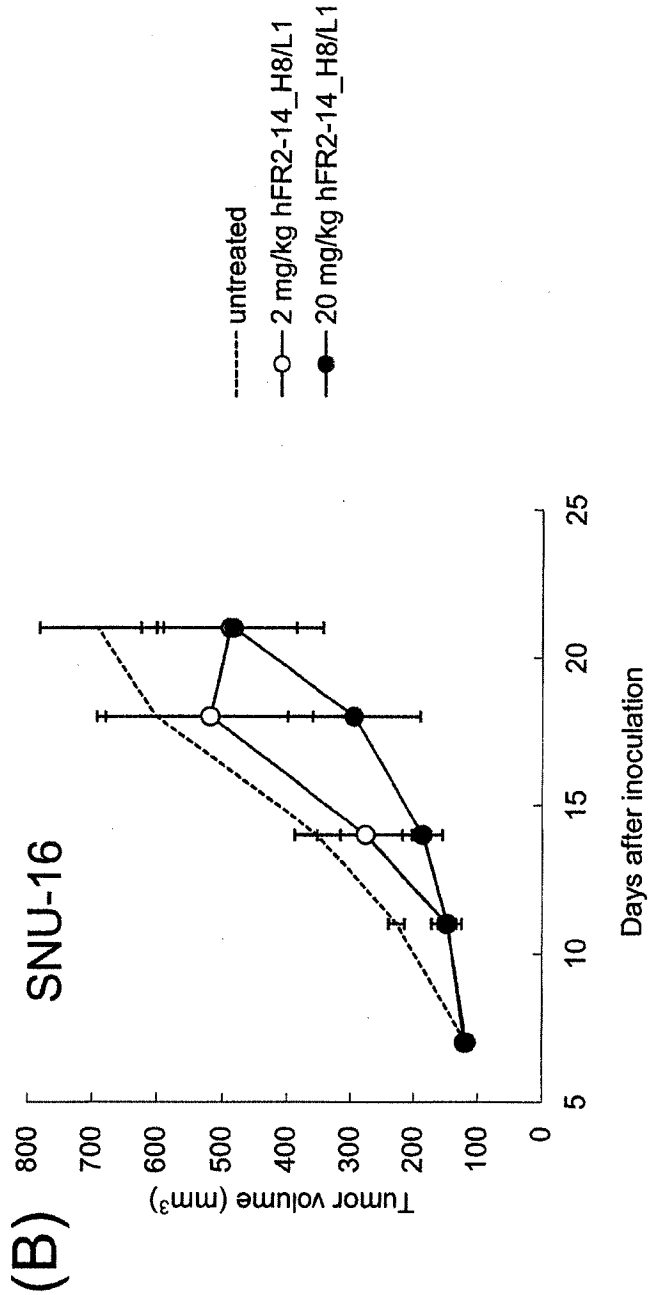

(B)
SNU-16
Tumor volume (mm3)
800
700
600
500
400
300
200
100
0
5
10
15
20
25
Days after inoculation
untreated
2 mg/kg hFR2-14_H8/L1
20 mg/kg hFR2-14_H8/L1

FIG. 135C

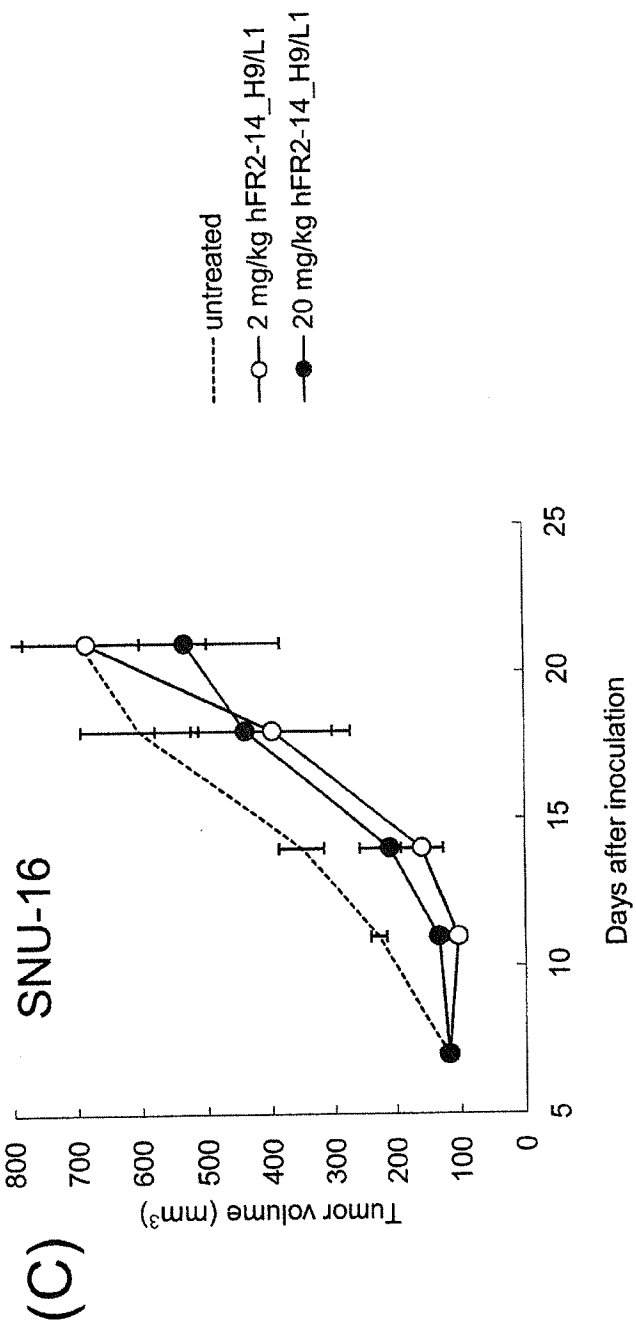

(C)
SNU-16
Tumor volume (mm³)
800
700
600
500
400
300
200
100
0
5
10
15
20
25
Days after inoculation
untreated
2 mg/kg hFR2-14_H9/L1
20 mg/kg hFR2-14_H9/L1

FIG. 135D

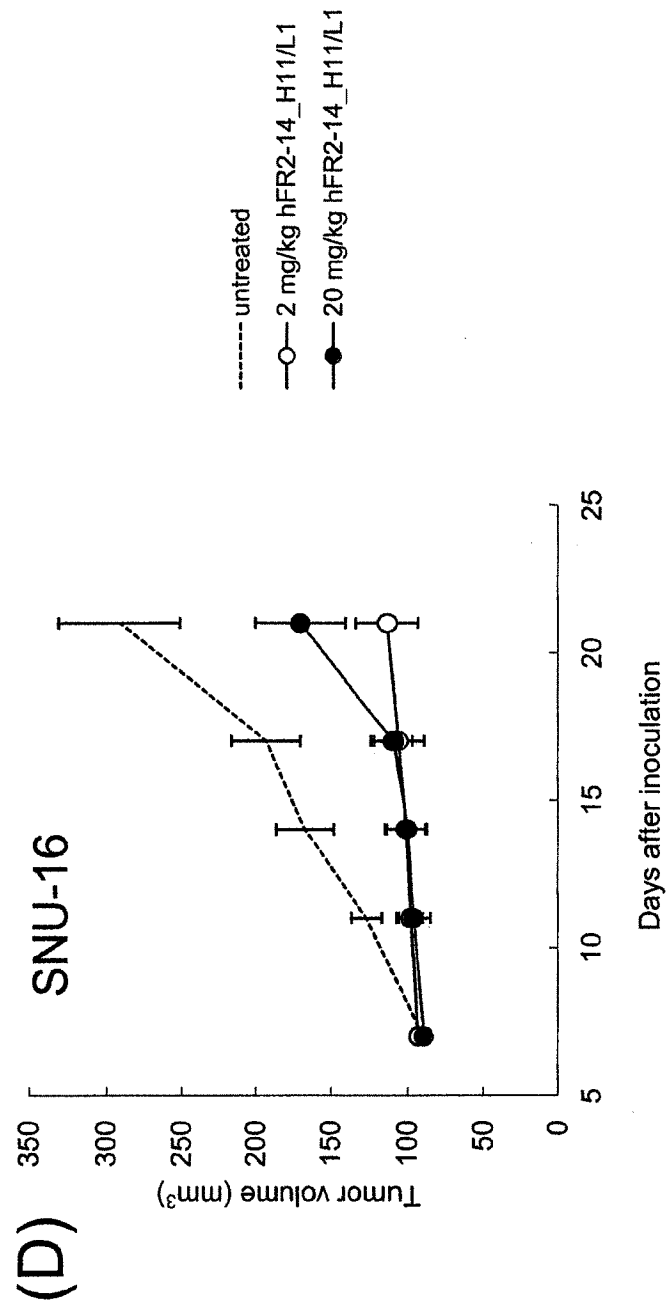

(D)
SNU-16
Tumor volume (mm3)
350
300
250
200
150
100
50
0
5
10
15
20
25
Days after inoculation
untreated
2 mg/kg hFR2-14_H11/L1
20 mg/kg hFR2-14_H11/L1

FIG. 135E

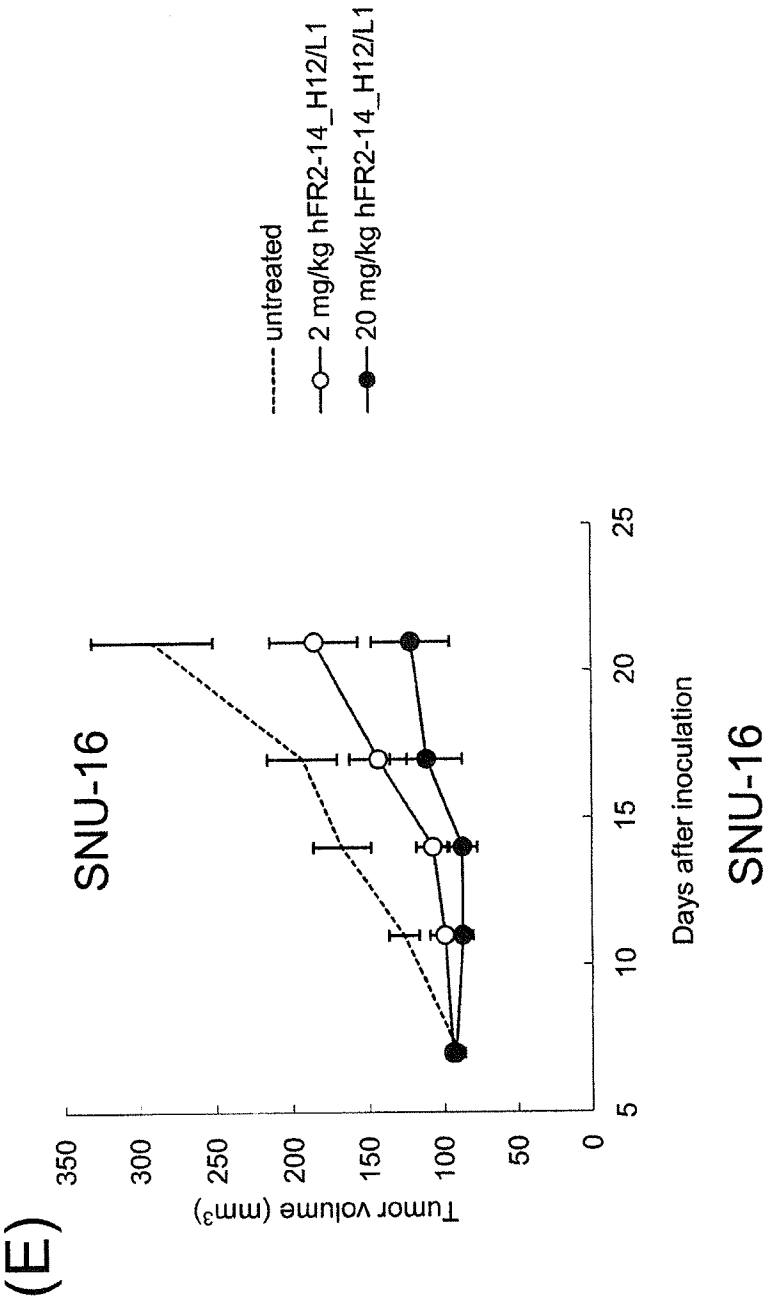

(E)
SNU-16
Tumor volume (mm3)
350
300
250
200
150
100
50
0
5
10
15
20
25
Days after inoculation
untreated
2 mg/kg hFR2-14_H12/L1
20 mg/kg hFR2-14_H12/L1
SNU-16

FIG. 135F

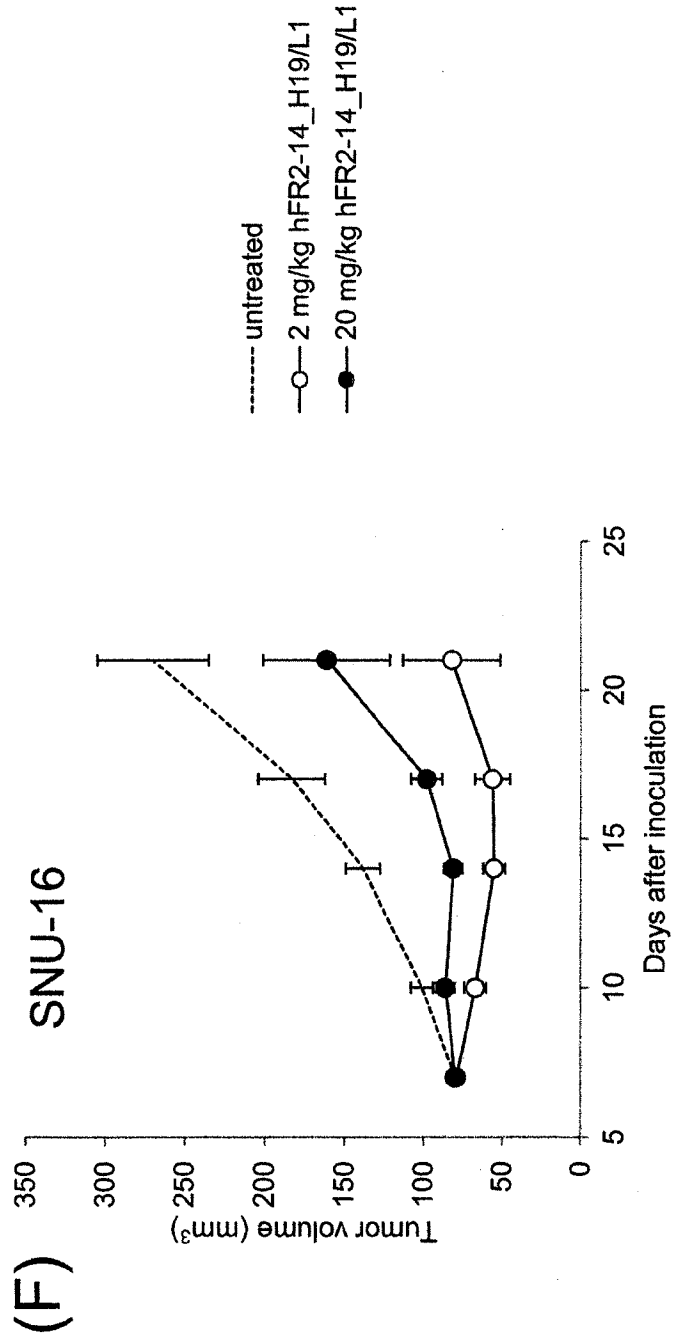

(F)
SNU-16
Tumor volume (mm3)
350
300
250
200
150
100
50
0
5
10
15
20
25
Days after inoculation
untreated
2 mg/kg hFR2-14_H19/L1
20 mg/kg hFR2-14_H19/L1

FIG. 136

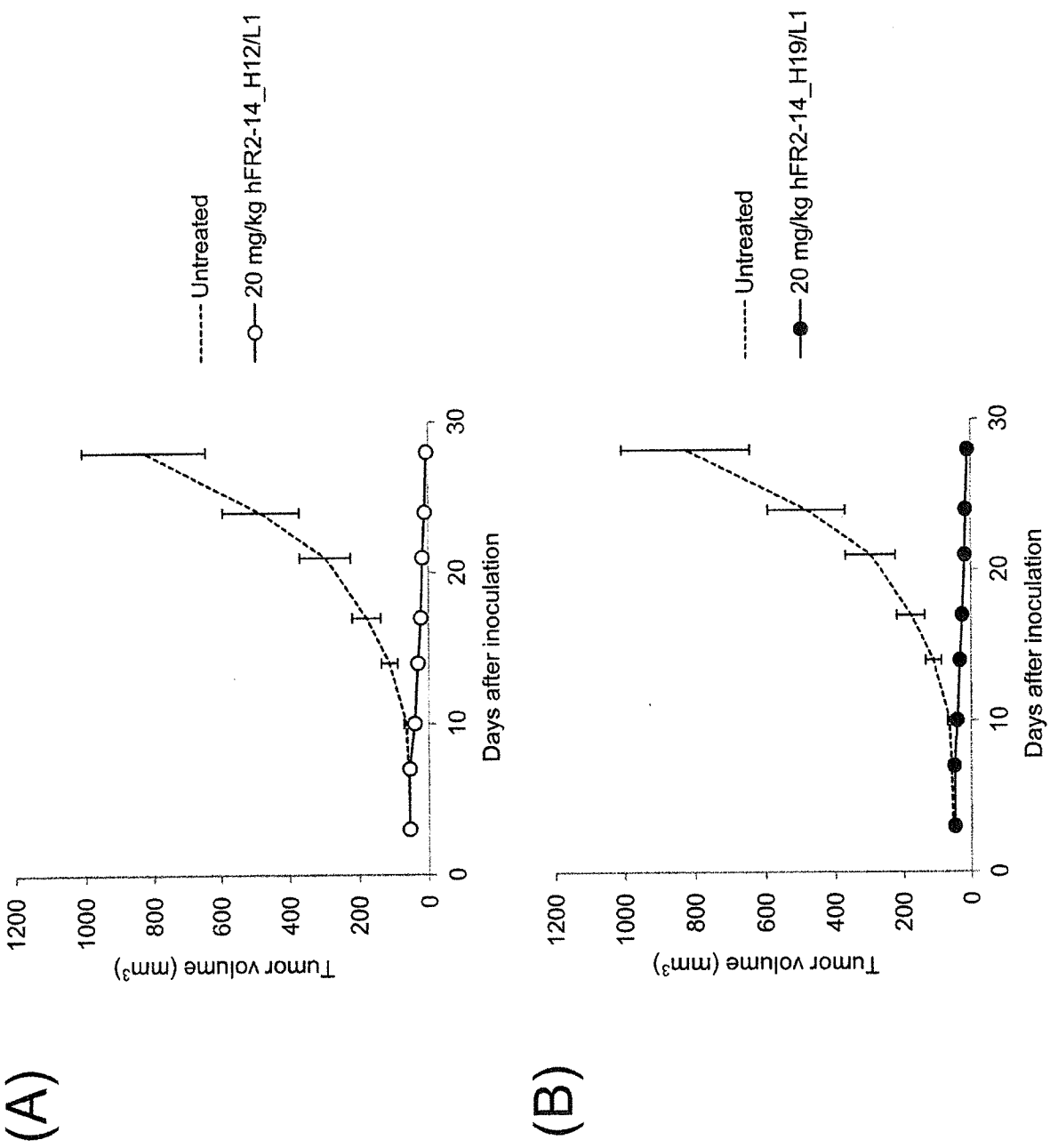

(A)
Untreated
20 mg/kg hFR2-14_H12/L1
Tumor volume (mm3)
1200
1000
800
600
400
200
0
0
10
20
30
Days after inoculation
(B)
Untreated
20 mg/kg hFR2-14_H19/L1
Tumor volume (mm3)
1200
1000
800
600
400
200
0
0
10
20
30
Days after inoculation

FIG. 137

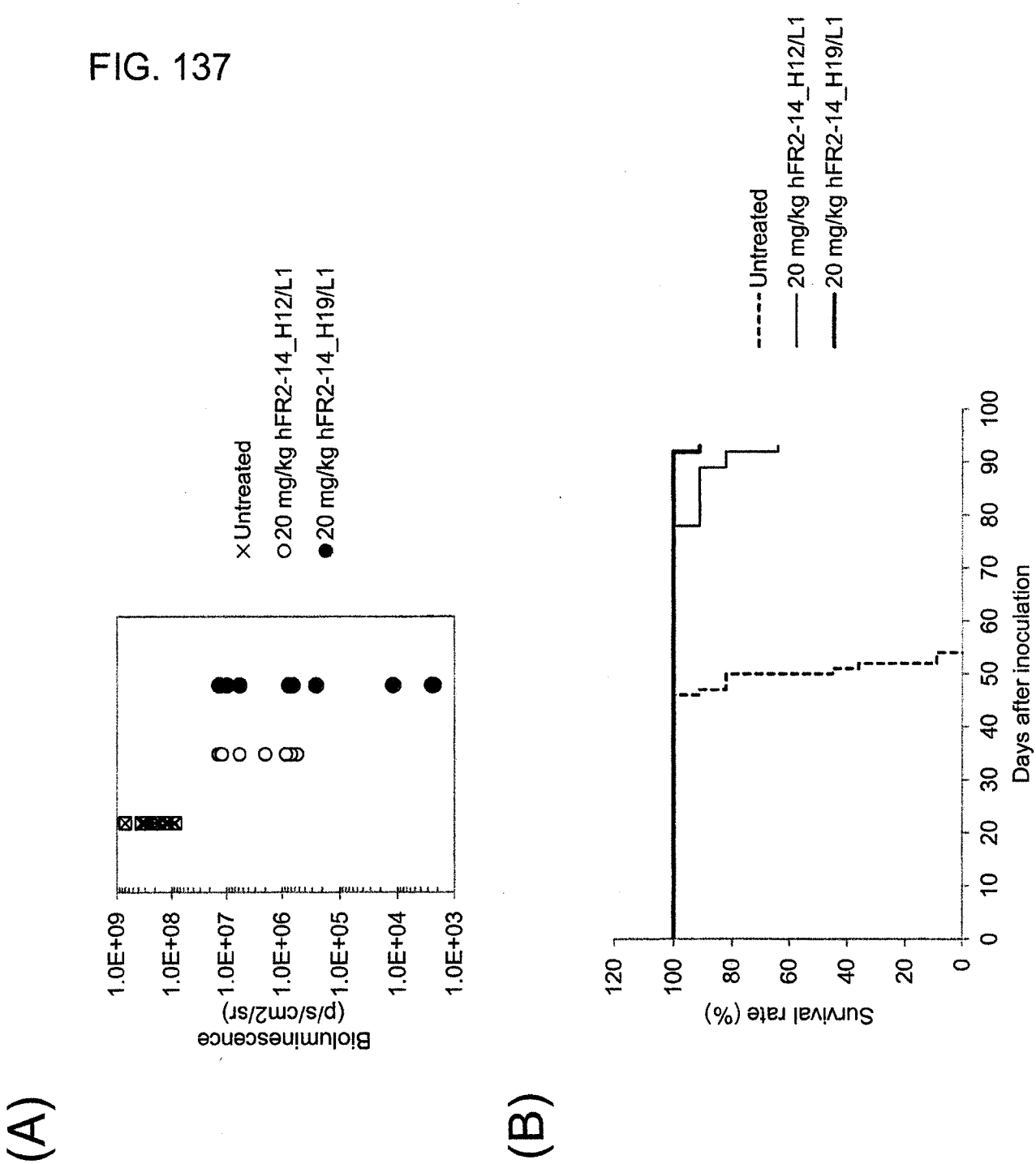

(A)
Bioluminescence (p/s/cm2/sr)
1.0E+09
1.0E+08
1.0E+07
1.0E+06
1.0E+05
1.0E+04
1.0E+03
×Untreated
○20 mg/kg hFR2-14_H12/L1
●20 mg/kg hFR2-14_H19/L1
(B)
Survival rate (%)
120
100
80
60
40
20
0
0
10
20
30
40
50
60
70
80
90
100
Days after inoculation
Untreated
20 mg/kg hFR2-14_H12/L1
20 mg/kg hFR2-14_H19/L1

FIG. 138

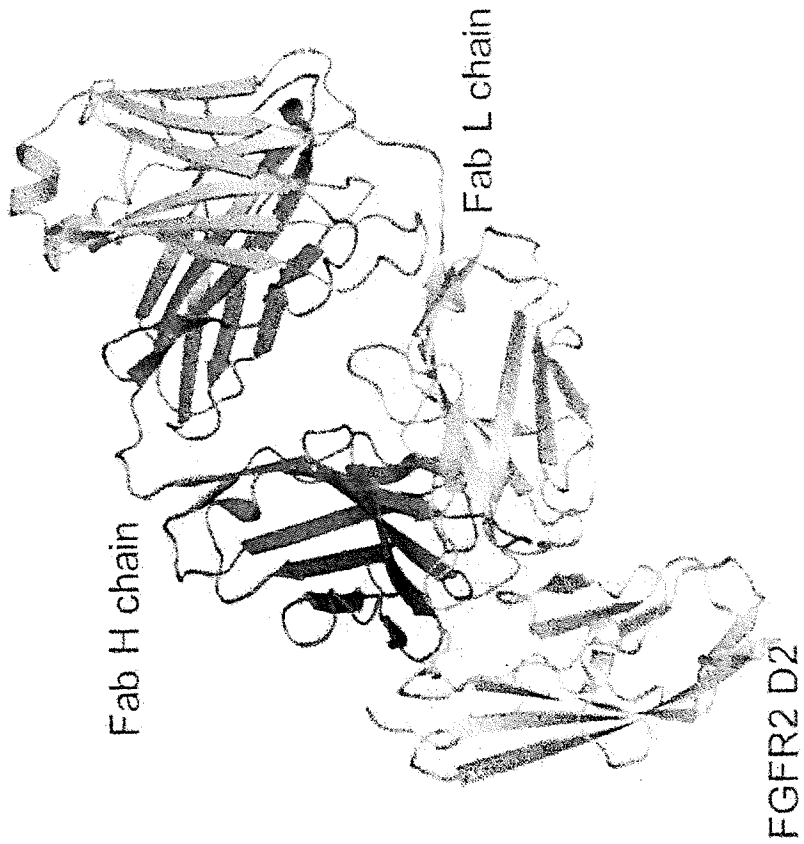


FIG. 139

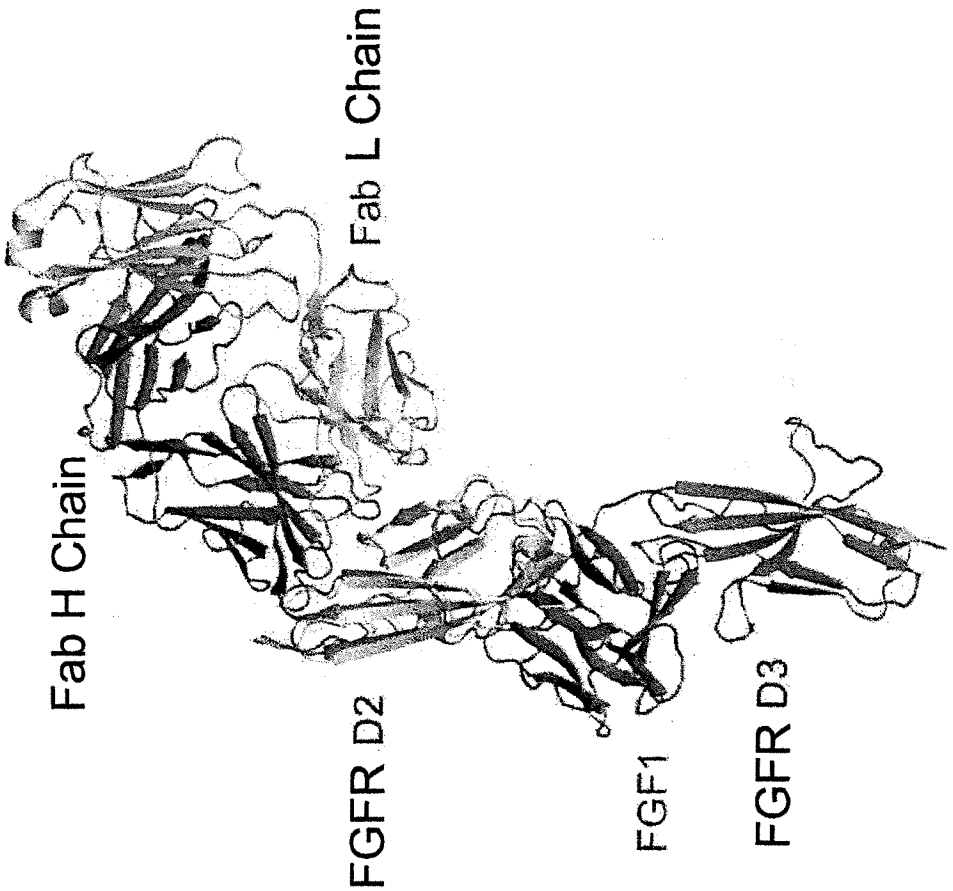


FIG. 140

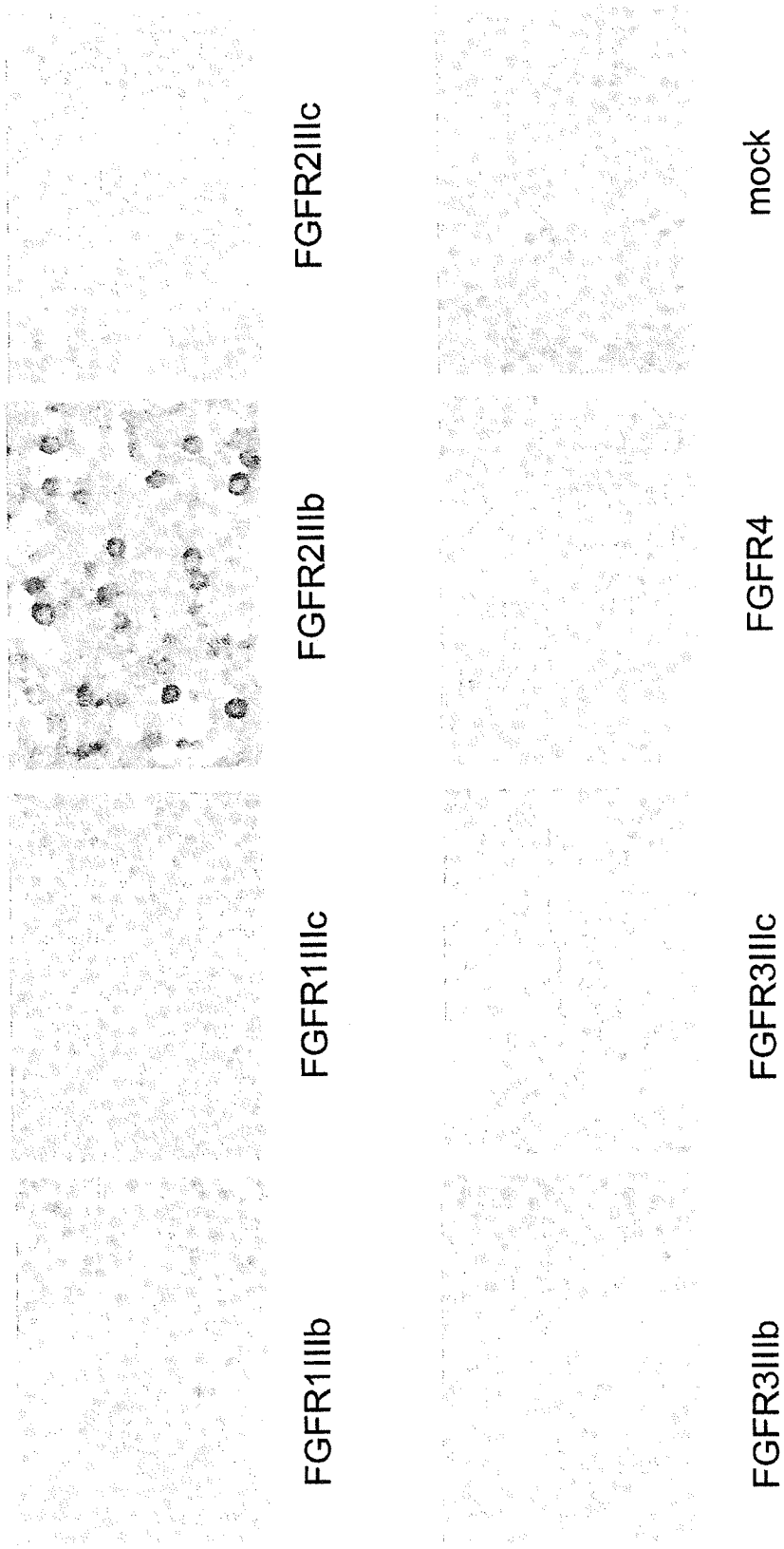

FGFR2IIIc
mock
FGFR2IIIb
FGFR4
FGFR1IIIc
FGFR3IIIc
FGFR1IIIb
FGFR3IIIb

FIG. 141

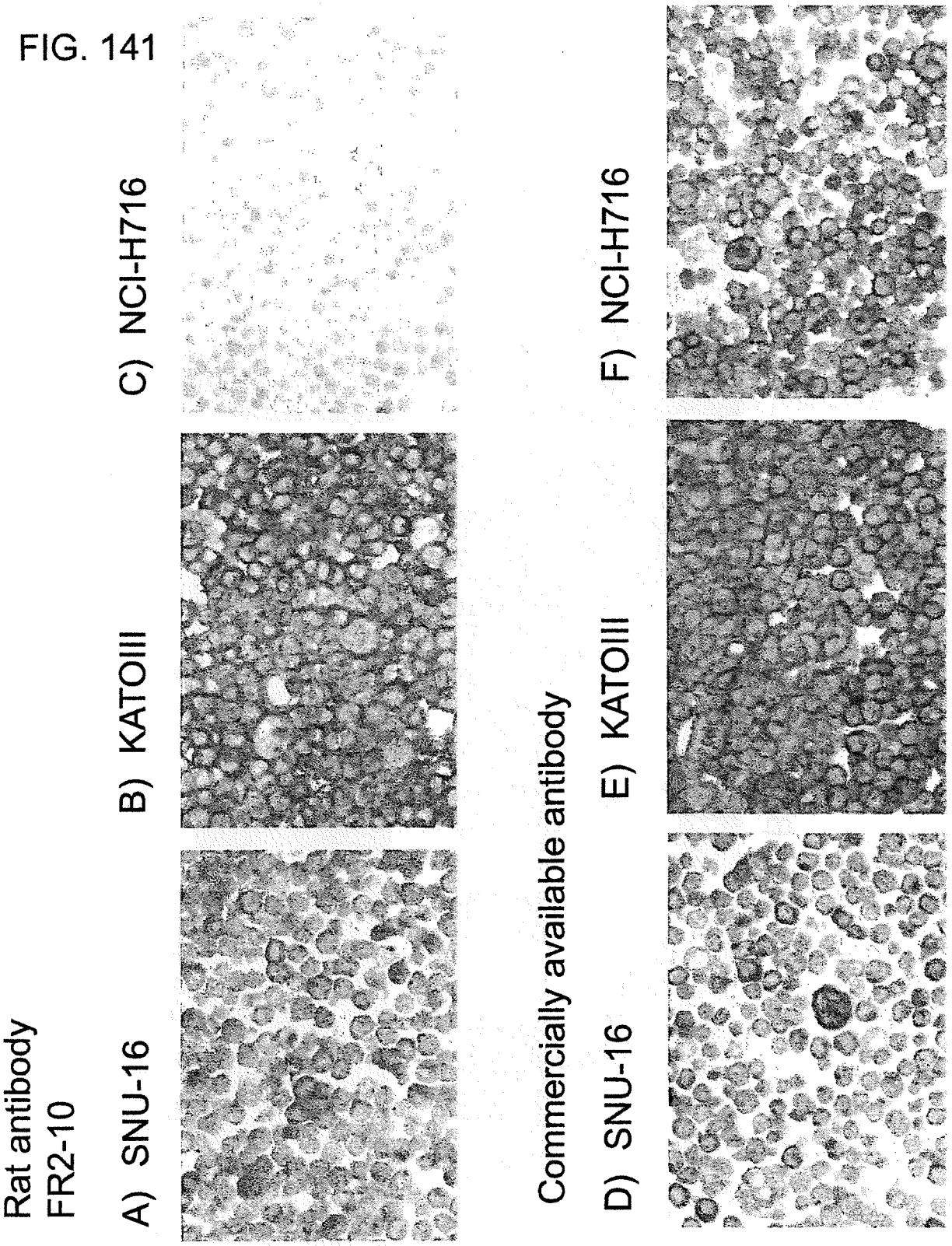

Rat antibody
FR2-10
A) SNU-16
B) KATOIII
C) NCI-H716
Commercially available antibody
D) SNU-16
E) KATOIII
F) NCI-H716

FIG. 142

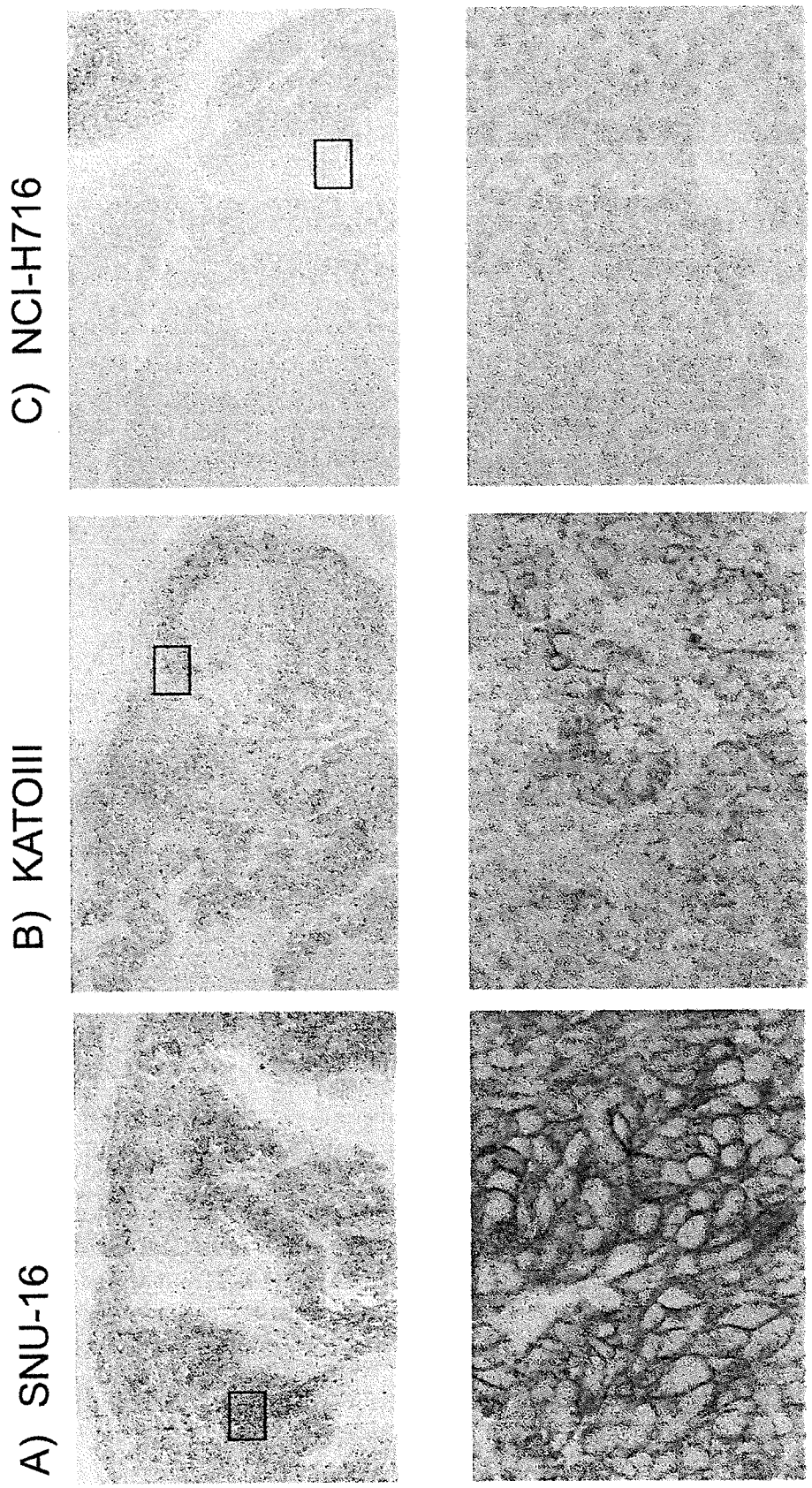
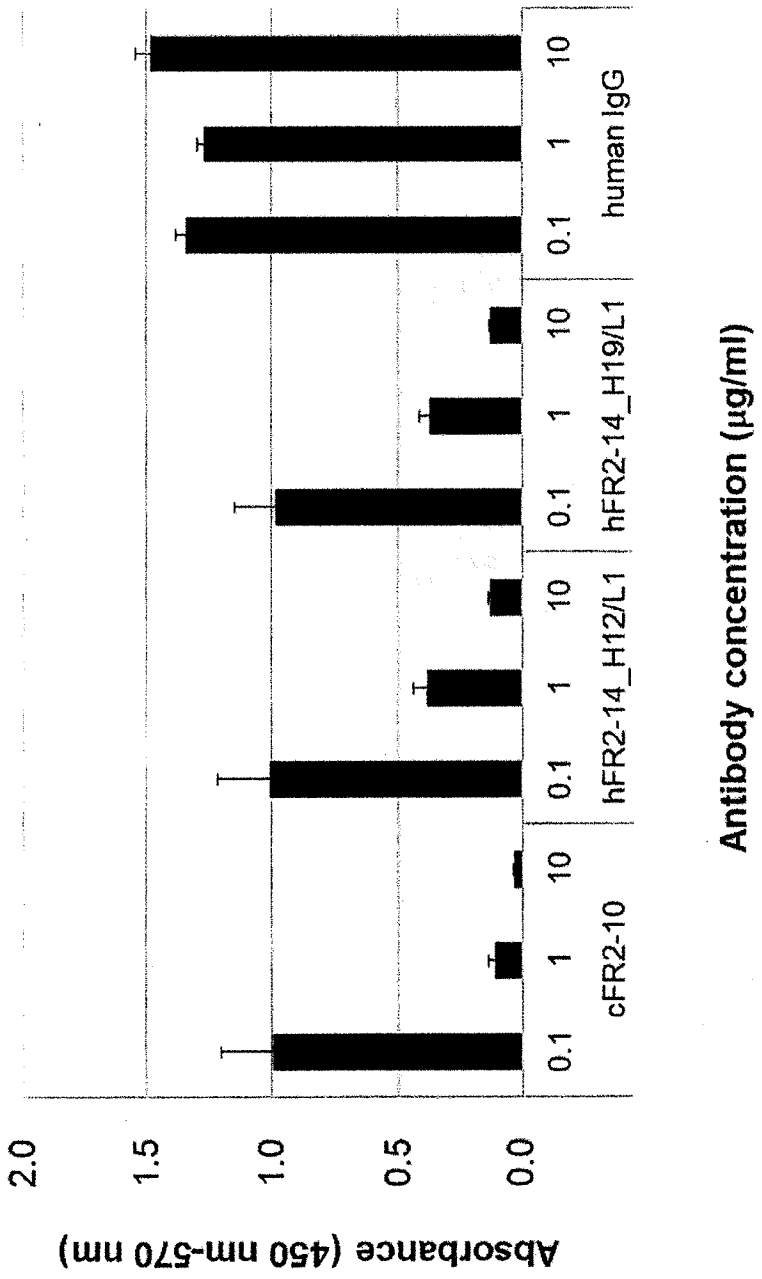


FIG. 143


Absorbance (450 nm-570 nm)
2.0
1.5
1.0
0.5
0.0
cFR2-10
hFR2-14_H12/L1
hFR2-14_H19/L1
human IgG
0.1
1
10
Antibody concentration (μg/ml)

SEQUENCE LISTING

<110> DAIICHI SANYKO CO., LTD.

<120> ANTI-FGFR2 ANTIBODY

<130> SG5039A

<160> 113

<170> PatentIn version 3.5

<210> 1
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<210> 2
<211> 13
<212> PRT
<213> Rattus norvegicus

<400> 2

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
1 5 10

<210> 3
<211> 5
<212> PRT
<213> Rattus norvegicus

<400> 3

Gln Val Lys Leu Leu
1 5

<210> 4
<211> 17
<212> PRT
<213> Rattus norvegicus

<400> 4

Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Glu

<210> 5
<211> 5
<212> PRT
<213> Rattus norvegicus

<400> 5

Gln Val Lys Leu Leu

1 5

<210> 6
<211> 17
<212> PRT
<213> Rattus norvegicus

<400> 6

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1 5 10 15

Glu

<210> 7
<211> 28
<212> PRT
<213> Artifitial Sequence

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1 5 10 15

Cys Ala Gly Thr Thr Cys Cys Ala Gly Gly Ala Gly
20 25

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<212> DNA
<213> Artifitial Sequence

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<210> 9
<211> 20
<212> DNA
<213> Artifitial Sequence

<400> 9
catatgatca gtgtcctctc 20

<210> 10
<211> 20
<212> DNA
<213> Artifitial Sequence

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atatgatcag tgtcctctcc 20

<210> 11
<211> 366
<212> DNA
<213> Rattus norvegicus

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<222> (1)..(366)

<400> 11

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                  10                  15

tct ctg aaa cta tcc tgt gta gcc tct gga ttc aga ttc aat gac ttt          96
Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Arg Phe Asn Asp Phe
            20                  25                  30

tgg atg acc tgg atc cgc cag gct cca ggg aag ggg ctg gag tgg gtt         144
Trp Met Thr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

gca tcc att act tat act ggt gat aac act tac tat gca ggc tct gtg         192
Ala Ser Ile Thr Tyr Thr Gly Asp Asn Thr Tyr Tyr Ala Gly Ser Val
    50                  55                  60

aag ggc cga atc act atc tcc aga gat aat gcg aag agc acc cta tac         240
Lys Gly Arg Ile Thr Ile Ser Arg Asp Asn Ala Lys Ser Thr Leu Tyr
65                  70                  75                  80

ctg caa atg aac agt ctg agg tct gag gac acg gcc act tat tac tgt         288
Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

aca aga gat gac tac gga gga tat agc ccc tac tat atg gat gcc tgg         336
Thr Arg Asp Asp Tyr Gly Gly Tyr Ser Pro Tyr Tyr Met Asp Ala Trp
            100                 105                 110

ggt caa gga act tca gtc act gtc tcc tca                                 366
Gly Gln Gly Thr Ser Val Thr Val Ser Ser
        115                 120
```

<210> 12
<211> 122
<212> PRT
<213> Rattus norvegicus

<400> 12

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                  10                  15

Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Arg Phe Asn Asp Phe
            20                  25                  30

Trp Met Thr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Ser Ile Thr Tyr Thr Gly Asp Asn Thr Tyr Tyr Ala Gly Ser Val
    50                  55                  60

Lys Gly Arg Ile Thr Ile Ser Arg Asp Asn Ala Lys Ser Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Thr Arg Asp Asp Tyr Gly Gly Tyr Ser Pro Tyr Tyr Met Asp Ala Trp
```

```
            100                 105                 110

Gly Gln Gly Thr Ser Val Thr Val Ser Ser
        115                 120


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<212>  DNA
<213>  Rattus norvegicus


<220>
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<222>  (1)..(354)

<400>  13
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Gln Val Lys Leu Leu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15

tca gtg aag ttg tcc tgc aag act tct ggt ttt acc ttc agc act agc          96
Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Thr Phe Ser Thr Ser
            20                  25                  30

tat atg agt tgg ttg aag cag gtg cct gga ccg agt att gag tgg att         144
Tyr Met Ser Trp Leu Lys Gln Val Pro Gly Pro Ser Ile Glu Trp Ile
        35                  40                  45

gga tgg att tat gct gga gat ggt ggt act aag tat aat cag aag ttc         192
Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn Gln Lys Phe
    50                  55                  60

aag ggc aag gcc aca ctg aca gta gac aaa tct tct agc aca gca tac         240
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

atg gat ctc agc agc ctg aca tct gag gac gct gca gtc tat ttt tgt         288
Met Asp Leu Ser Ser Leu Thr Ser Glu Asp Ala Ala Val Tyr Phe Cys
                85                  90                  95

gca acg gat ggt tat ggg gat tgg ttt gct tac tgg ggc caa ggc act         336
Ala Thr Asp Gly Tyr Gly Asp Trp Phe Ala Tyr Trp Gly Gln Gly Thr
            100                 105                 110

ctg gtc act gtc tct tca                                                 354
Leu Val Thr Val Ser Ser
        115


<210>  14
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<212>  PRT
<213>  Rattus norvegicus

<400>  14

Gln Val Lys Leu Leu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Thr Phe Ser Thr Ser
            20                  25                  30


Tyr Met Ser Trp Leu Lys Gln Val Pro Gly Pro Ser Ile Glu Trp Ile
        35                  40                  45
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Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met Asp Leu Ser Ser Leu Thr Ser Glu Asp Ala Ala Val Tyr Phe Cys
                85                  90                  95

Ala Thr Asp Gly Tyr Gly Asp Trp Phe Ala Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
```

<210> 15
<211> 354
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (1)..(354)

<400> 15

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Gln Val Lys Leu Leu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15

tca gtg aag ttg tcc tgc aag act tct ggt ttt aca ttc agc act agt          96
Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Thr Phe Ser Thr Ser
            20                  25                  30

tat atg agt tgg ttg aag cag gtg cct gga ccg agt act gag tgg att         144
Tyr Met Ser Trp Leu Lys Gln Val Pro Gly Pro Ser Thr Glu Trp Ile
        35                  40                  45

gga tgg att tat gct gga gat ggt ggt act aag tat aat cag aag ttc         192
Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn Gln Lys Phe
    50                  55                  60

aag ggc aag gcc aca ctg aca gta gac aaa ttt tct agc aca gca tac         240
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Phe Ser Ser Thr Ala Tyr
65                  70                  75                  80

atg gat ctc agc agc ctg aca tct gag gac gct gca gtc tat ttc tgt         288
Met Asp Leu Ser Ser Leu Thr Ser Glu Asp Ala Ala Val Tyr Phe Cys
                85                  90                  95

gca acg gat ggt tat ggg gat tgg ttt act tac tgg ggc caa ggc act         336
Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly Gln Gly Thr
            100                 105                 110

ctg gtc act gtc tct tca                                                 354
Leu Val Thr Val Ser Ser
        115
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<210> 16
<211> 118

<212> PRT
<213> Rattus norvegicus

<400> 16

Gln Val Lys Leu Leu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Thr Phe Ser Thr Ser
20 25 30

Tyr Met Ser Trp Leu Lys Gln Val Pro Gly Pro Ser Thr Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Phe Ser Ser Thr Ala Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Thr Ser Glu Asp Ala Ala Val Tyr Phe Cys
85 90 95

Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

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<210> 18
<211> 20
<212> DNA
<213> Artifitial Sequence

<400> 18
tccagttgct aactgttccg 20

<210> 19
<211> 19
<212> DNA
<213> Artifitial Sequence

<400> 19
cagtggtatc aacgcagag 19

<210> 20
<211> 327
<212> DNA
<213> Rattus norvegicus

<220>
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<400> 20
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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Phe Leu Gly
1 5 10 15

gac aga gtc act att act tgc cgg gca agt caa gac att gga aat tat 96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Tyr
20 25 30

tta aga tgg ttc cag cag aaa ccg ggg aaa tct cct agg ctt atg att 144
Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Arg Leu Met Ile
35 40 45

tat ggt gca acc aac ttg gca aat ggg gtc cca tca agg ttc agt ggc 192
Tyr Gly Ala Thr Asn Leu Ala Asn Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

agt agg tct ggg tca gat tat tct ctg acc atc aac aac ttg gag tct 240
Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Asn Asn Leu Glu Ser
65 70 75 80

gaa gac atg gct att tat tac tgt ctg aag cat aat gag tat cca ttc 288
Glu Asp Met Ala Ile Tyr Tyr Cys Leu Lys His Asn Glu Tyr Pro Phe
85 90 95

acg ttc ggc tca ggg acg aag ttg gaa ata aaa cgg gct 327
Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Ala
100 105

<210> 21
<211> 109
<212> PRT
<213> Rattus norvegicus

<400> 21

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Phe Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Tyr
20 25 30

Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Arg Leu Met Ile
35 40 45

Tyr Gly Ala Thr Asn Leu Ala Asn Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Asn Asn Leu Glu Ser
65 70 75 80

Glu Asp Met Ala Ile Tyr Tyr Cys Leu Lys His Asn Glu Tyr Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Ala

100 105

<210> 22
<211> 28
<212> DNA
<213> Artifitial Sequence

<400> 22
tacgtgctgt ctttgctgtc ctgatcag 28

<210> 23
<211> 330
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDA
<222> (1)..(330)

<220>
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<222> (1)..(330)

<400> 23
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Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

gaa act gtc acc atc gaa tgt cga gca agt gag gac att tac agt aat 96
Glu Thr Val Thr Ile Glu Cys Arg Ala Ser Glu Asp Ile Tyr Ser Asn
20 25 30

tta gcg tgg tat cag cag aaa cca ggg aac tct cct cag ctc ctg atc 144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ser Pro Gln Leu Leu Ile
35 40 45

tat gat gca aat atc ttg gca gat ggg gtc cca tca cgg ttc agt ggc 192
Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

agt ggg tct ggc aca cag tat tct cta aag ata aac agc ctg caa tct 240
Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65 70 75 80

gaa gat gtc gca agt tat ttc tgt caa cag tat aac aat tat cct ccg 288
Glu Asp Val Ala Ser Tyr Phe Cys Gln Gln Tyr Asn Asn Tyr Pro Pro
85 90 95

ttc acg ttt gga gtt ggg acc aag ctg gaa ctg aaa cgg gct 330
Phe Thr Phe Gly Val Gly Thr Lys Leu Glu Leu Lys Arg Ala
100 105 110

<210> 24
<211> 110
<212> PRT
<213> Rattus norvegicus

<400> 24

Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Glu Thr Val Thr Ile Glu Cys Arg Ala Ser Glu Asp Ile Tyr Ser Asn

```
          20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ser Pro Gln Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65                  70                  75                  80

Glu Asp Val Ala Ser Tyr Phe Cys Gln Gln Tyr Asn Asn Tyr Pro Pro
                85                  90                  95

Phe Thr Phe Gly Val Gly Thr Lys Leu Glu Leu Lys Arg Ala
            100                 105                 110
```

<210> 25
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<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (1)..(330)

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Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15

gaa act gtc acc atc gaa tgt cga gca agt gag gac ata tac agt aat          96
Glu Thr Val Thr Ile Glu Cys Arg Ala Ser Glu Asp Ile Tyr Ser Asn
            20                  25                  30

tta gcg tgg tat cag cag aaa cca ggg aac tct cct cag ctc ctg atc         144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ser Pro Gln Leu Leu Ile
        35                  40                  45

tat gat gca aat atc ctg gca gat ggg gtc cca tca cgg ttc agt ggc         192
Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

agt ggg tct ggc aca cag tat tct cta aag ata aac agc ctg caa tct         240
Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65                  70                  75                  80

gaa gat gtc gca agt tat ttc tgt caa cag tat aac aat tat cct ccg         288
Glu Asp Val Ala Ser Tyr Phe Cys Gln Gln Tyr Asn Asn Tyr Pro Pro
                85                  90                  95

ttc acg ttt gga gct ggg acc aag ctg gaa ctg aaa cgg gct                 330
Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala
            100                 105                 110
```

<210> 26
<211> 110
<212> PRT
<213> Rattus norvegicus

<400> 26

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1 5 10 15

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20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ser Pro Gln Leu Leu Ile
35 40 45

Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65 70 75 80

Glu Asp Val Ala Ser Tyr Phe Cys Gln Gln Tyr Asn Asn Tyr Pro Pro
85 90 95

Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala
100 105 110

<210> 27
<211> 449
<212> DNA
<213> Homo sapiens

<400> 27
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gtggatctcc ggcgcgtacg gcgatatcgt gatgattaaa cgtacggtgg ccgccccctc 120

cgtgttcatc ttcccccccct ccgacgagca gctgaagtcc ggcaccgcct ccgtggtgtg 180

cctgctgaat aacttctacc ccagagaggc caaggtgcag tggaaggtgg acaacgccct 240

gcagtccggg aactcccagg agagcgtgac cgagcaggac agcaaggaca gcacctacag 300

cctgagcagc accctgaccc tgagcaaagc cgactacgag aagcacaagg tgtacgcctg 360

cgaggtgacc caccagggcc tgagctcccc cgtcaccaag agcttcaaca gggggggagtg 420

ttaggggccc gtttaaacgg gggaggcta 449

<210> 28
<211> 30
<212> DNA
<213> Artifitial Sequence

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<210> 29
<211> 30
<212> DNA
<213> Artifitial Sequence

<400> 29

gctatggcag ggcctgccgc cccgacgttg 30

<210> 30
<211> 1132
<212> DNA
<213> Homo sapiens

<400> 30
gcctccggac tctagagcca ccatgaaaca cctgtggttc ttcctcctgc tggtggcagc 60

tcccagatgg gtgctgagcc aggtgcaatt gtgcaggcgg ttagctcagc ctccaccaag 120

ggcccaagcg tcttcccccc ggcaccctcc tccaagagca cctctggcgg cacagccgcc 180

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 240

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 300

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 360

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 420

aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc 480

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 540

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 600

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 660

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 720

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 780

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 840

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 900

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 960

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1020

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1080

tccctgtctc ccggcaaatg agatatcggg cccgtttaaa cgggggaggc ta 1132

<210> 31
<211> 702
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(702)

<400> 31
atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggc gcg tac ggc gac atc cag atg acc cag tct cca tct tcc ctg tct 96
Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

gca ttt ctg gga gac aga gtc act att act tgc cgg gca agt caa gac 144

```
Ala Phe Leu Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
        35                  40                  45

att gga aat tat tta aga tgg ttc cag cag aaa ccg ggg aaa tct cct        192
Ile Gly Asn Tyr Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro
    50                  55                  60

agg ctt atg att tat ggt gca acc aac ttg gca aat ggg gtc cca tca        240
Arg Leu Met Ile Tyr Gly Ala Thr Asn Leu Ala Asn Gly Val Pro Ser
65                  70                  75                  80

agg ttc agt ggc agt agg tct ggg tca gat tat tct ctg acc atc aac        288
Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Asn
                85                  90                  95

aac ttg gag tct gaa gac atg gct att tat tac tgt ctg aag cat aat        336
Asn Leu Glu Ser Glu Asp Met Ala Ile Tyr Tyr Cys Leu Lys His Asn
            100                 105                 110

gag tat cca ttc acg ttc ggc tca ggg acg aag ttg gaa ata aaa cgg        384
Glu Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
        115                 120                 125

gct gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc tcc gac gag cag        432
Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg aat aac ttc tac        480
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160

ccc aga gag gcc aag gtg cag tgg aag gtg gac aac gcc ctg cag tcc        528
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

ggg aac tcc cag gag agc gtg acc gag cag gac agc aag gac agc acc        576
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

tac agc ctg agc agc acc ctg acc ctg agc aaa gcc gac tac gag aag        624
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
        195                 200                 205

cac aag gtg tac gcc tgc gag gtg acc cac cag ggc ctg agc tcc ccc        672
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

gtc acc aag agc ttc aac agg ggg gag tgt                                702
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230
```

<210> 32
<211> 234
<212> PRT
<213> Artifitial Sequence

<400> 32

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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15

Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
            20                  25                  30

Ala Phe Leu Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
```

35 40 45

Ile Gly Asn Tyr Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro
50 55 60

Arg Leu Met Ile Tyr Gly Ala Thr Asn Leu Ala Asn Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Asn
85 90 95

Asn Leu Glu Ser Glu Asp Met Ala Ile Tyr Tyr Cys Leu Lys His Asn
100 105 110

Glu Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
115 120 125

Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 33
<211> 48
<212> DNA
<213> Artifitial Sequence

<400> 33
atctccggcg cgtacggcga catccagatg acccagtctc catcttcc 48

<210> 34
<211> 44
<212> DNA
<213> Artifitial Sequence

<400> 34
ggaggggcg gccacagccc gttttatttc caacttcgtc cctg 44

<210> 35
<211> 1413
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1413)

<400> 35
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc gag gtg cag ctg gtg gag tct ggg gga ggc ctg gtg cag 96
Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

cct gga agg tct ctg aaa cta tcc tgt gta gcc tct gga ttc aga ttc 144
Pro Gly Arg Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Arg Phe
35 40 45

aat gac ttt tgg atg acc tgg atc cgc cag gct cca ggg aag ggg ctg 192
Asn Asp Phe Trp Met Thr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

gag tgg gtt gca tcc att act tat act ggt gat aac act tac tat gca 240
Glu Trp Val Ala Ser Ile Thr Tyr Thr Gly Asp Asn Thr Tyr Tyr Ala
65 70 75 80

ggc tct gtg aag ggc cga atc act atc tcc aga gat aat gcg aag agc 288
Gly Ser Val Lys Gly Arg Ile Thr Ile Ser Arg Asp Asn Ala Lys Ser
85 90 95

acc cta tac ctg caa atg aac agt ctg agg tct gag gac acg gcc act 336
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Thr
100 105 110

tat tac tgt aca aga gat gac tac gga gga tat agc ccc tac tat atg 384
Tyr Tyr Cys Thr Arg Asp Asp Tyr Gly Gly Tyr Ser Pro Tyr Tyr Met
115 120 125

gat gcc tgg ggt caa gga act tca gtc act gtc agc tca gcc tcc acc 432
Asp Ala Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr
130 135 140

aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct 480
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145 150 155 160

ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa 528
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
165 170 175

ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac 576
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
180 185 190

acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc 624
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
195 200 205

gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc 672
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
210 215 220

```
aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag          720
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct          768
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag          816
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg          864
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac          912
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac          960
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac         1008
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc         1056
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg         1104
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag         1152
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac         1200
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag         1248
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc         1296
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca         1344
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc         1392
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

ctc tcc ctg tct ccc ggc aaa                                            1413
Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 36
<211> 471
<212> PRT

<213> Artifitial Sequence

<400> 36

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30

Pro Gly Arg Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Arg Phe
        35                  40                  45

Asn Asp Phe Trp Met Thr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Val Ala Ser Ile Thr Tyr Thr Gly Asp Asn Thr Tyr Tyr Ala
65                  70                  75                  80

Gly Ser Val Lys Gly Arg Ile Thr Ile Ser Arg Asp Asn Ala Lys Ser
                85                  90                  95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Thr
            100                 105                 110

Tyr Tyr Cys Thr Arg Asp Asp Tyr Gly Gly Tyr Ser Pro Tyr Tyr Met
        115                 120                 125

Asp Ala Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255
```

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
275 280 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
290 295 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305 310 315 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
340 345 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
355 360 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
370 375 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
420 425 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
435 440 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 37
<211> 47
<212> DNA
<213> Artifitial Sequence

<400> 37
ccagatgggt gctgagcgag gtgcagctgg tggagtctgg gggaggc 47

<210> 38
<211> 48
<212> DNA

<213> Artifitial Sequence

<400> 38
cttggtggag gctgagctga cagtgactga agttccttga ccccaggc 48

<210> 39
<211> 705
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(705)

<400> 39
atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggc gcg tac ggc gac atc cag atg aca cag tct cca gct tcc ctg tct 96
Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
20 25 30

gca tct ctg gga gaa act gtc acc atc gaa tgt cga gca agt gag gac 144
Ala Ser Leu Gly Glu Thr Val Thr Ile Glu Cys Arg Ala Ser Glu Asp
35 40 45

att tac agt aat tta gcg tgg tat cag cag aaa cca ggg aac tct cct 192
Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ser Pro
50 55 60

cag ctc ctg atc tat gat gca aat atc ttg gca gat ggg gtc cca tca 240
Gln Leu Leu Ile Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser
65 70 75 80

cgg ttc agt ggc agt ggg tct ggc aca cag tat tct cta aag ata aac 288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn
85 90 95

agc ctg caa tct gaa gat gtc gca agt tat ttc tgt caa cag tat aac 336
Ser Leu Gln Ser Glu Asp Val Ala Ser Tyr Phe Cys Gln Gln Tyr Asn
100 105 110

aat tat cct ccg ttc acg ttt gga gtt ggg acc aag ctg gaa ctg aaa 384
Asn Tyr Pro Pro Phe Thr Phe Gly Val Gly Thr Lys Leu Glu Leu Lys
115 120 125

cgg gct gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc tcc gac gag 432
Arg Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg aat aac ttc 480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

tac ccc aga gag gcc aag gtg cag tgg aag gtg gac aac gcc ctg cag 528
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

tcc ggg aac tcc cag gag agc gtg acc gag cag gac agc aag gac agc 576
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

acc tac agc ctg agc agc acc ctg acc ctg agc aaa gcc gac tac gag 624
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

```
aag cac aag gtg tac gcc tgc gag gtg acc cac cag ggc ctg agc tcc        672
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
    210                 215                 220

ccc gtc acc aag agc ttc aac agg ggg gag tgt                        705
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 40
<211> 235
<212> PRT
<213> Artifitial Sequence

<400> 40

```
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15

Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
            20                  25                  30

Ala Ser Leu Gly Glu Thr Val Thr Ile Glu Cys Arg Ala Ser Glu Asp
        35                  40                  45

Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ser Pro
    50                  55                  60

Gln Leu Leu Ile Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn
                85                  90                  95

Ser Leu Gln Ser Glu Asp Val Ala Ser Tyr Phe Cys Gln Gln Tyr Asn
            100                 105                 110

Asn Tyr Pro Pro Phe Thr Phe Gly Val Gly Thr Lys Leu Glu Leu Lys
        115                 120                 125

Arg Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
    130                 135                 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
        195                 200                 205
```

```
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
    210                 215                 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 41
<211> 48
<212> DNA
<213> Artifitial Sequence

<400> 41
atctccggcg cgtacggcga catccagatg acacagtctc cagcttcc 48

<210> 42
<211> 45
<212> DNA
<213> Artifitial Sequence

<400> 42
ggaggggcg gccacagccc gtttcagttc cagcttggtc ccaac 45

<210> 43
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 43

```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc cag gtt aag ctg ctg cag tct ggg gct gag ctg gta aaa          96
Val Leu Ser Gln Val Lys Leu Leu Gln Ser Gly Ala Glu Leu Val Lys
            20                  25                  30

cct ggt gct tca gtg aag ttg tcc tgc aag act tct ggt ttt acc ttc         144
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Thr Phe
        35                  40                  45

agc act agc tat atg agt tgg ttg aag cag gtg cct gga ccg agt att         192
Ser Thr Ser Tyr Met Ser Trp Leu Lys Gln Val Pro Gly Pro Ser Ile
    50                  55                  60

gag tgg att gga tgg att tat gct gga gat ggt ggt act aag tat aat         240
Glu Trp Ile Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aag ttc aag ggc aag gcc aca ctg aca gta gac aaa tct tct agc         288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
                85                  90                  95

aca gca tac atg gat ctc agc agc ctg aca tct gag gac gct gca gtc         336
Thr Ala Tyr Met Asp Leu Ser Ser Leu Thr Ser Glu Asp Ala Ala Val
            100                 105                 110

tat ttt tgt gca acg gat ggt tat ggg gat tgg ttt gct tac tgg ggc         384
Tyr Phe Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Ala Tyr Trp Gly
```

```
        115                 120                 125

caa ggc act ctg gtc act gtc agc tca gcc tcc acc aag ggc cca agc        432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc        480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg        528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct        576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg        624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac        672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt        720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg        768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg        816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac        864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg        912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac        960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc       1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc       1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg       1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc       1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag       1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
```

```
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc      1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                          1401
Pro Gly Lys
465
```

<210> 44
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 44

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Lys Leu Leu Gln Ser Gly Ala Glu Leu Val Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Ser Tyr Met Ser Trp Leu Lys Gln Val Pro Gly Pro Ser Ile
    50                  55                  60

Glu Trp Ile Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
                85                  90                  95

Thr Ala Tyr Met Asp Leu Ser Ser Leu Thr Ser Glu Asp Ala Ala Val
            100                 105                 110

Tyr Phe Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Ala Tyr Trp Gly
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160
```

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

```
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

Pro Gly Lys
465
```

<210> 45
<211> 47
<212> DNA
<213> Artifitial Sequence

<400> 45
ccagatgggt gctgagccag gttaagctgc tgcagtctgg ggctgag 47

<210> 46
<211> 46
<212> DNA
<213> Artifitial Sequence

<400> 46
cttggtggag gctgagctga cagtgaccag agtgccttgg ccccag 46

<210> 47
<211> 705
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(705)

<400> 47

```
atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc   48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15

ggc gcg tac ggc gac atc cag atg aca cag tct cca gct tcc ctg tct   96
Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
            20                  25                  30

gca tct ctg gga gaa act gtc acc atc gaa tgt cga gca agt gag gac  144
Ala Ser Leu Gly Glu Thr Val Thr Ile Glu Cys Arg Ala Ser Glu Asp
        35                  40                  45

ata tac agt aat tta gcg tgg tat cag cag aaa cca ggg aac tct cct  192
Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ser Pro
    50                  55                  60

cag ctc ctg atc tat gat gca aat atc ctg gca gat ggg gtc cca tca  240
Gln Leu Leu Ile Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser
65                  70                  75                  80

cgg ttc agt ggc agt ggg tct ggc aca cag tat tct cta aag ata aac  288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn
                85                  90                  95

agc ctg caa tct gaa gat gtc gca agt tat ttc tgt caa cag tat aac  336
```

```
Ser Leu Gln Ser Glu Asp Val Ala Ser Tyr Phe Cys Gln Gln Tyr Asn
            100                 105                 110

aat tat cct ccg ttc acg ttt gga gct ggg acc aag ctg gaa ctg aaa          384
Asn Tyr Pro Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
        115                 120                 125

cgg gct gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc tcc gac gag          432
Arg Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
    130                 135                 140

cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg aat aac ttc          480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160

tac ccc aga gag gcc aag gtg cag tgg aag gtg gac aac gcc ctg cag          528
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175

tcc ggg aac tcc cag gag agc gtg acc gag cag gac agc aag gac agc          576
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190

acc tac agc ctg agc agc acc ctg acc ctg agc aaa gcc gac tac gag          624
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
        195                 200                 205

aag cac aag gtg tac gcc tgc gag gtg acc cac cag ggc ctg agc tcc          672
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
    210                 215                 220

ccc gtc acc aag agc ttc aac agg ggg gag tgt                              705
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210>  48
<211>  235
<212>  PRT
<213>  Artifitial Sequence

<400>  48

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                   10                  15

Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
            20                  25                  30

Ala Ser Leu Gly Glu Thr Val Thr Ile Glu Cys Arg Ala Ser Glu Asp
        35                  40                  45

Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ser Pro
    50                  55                  60

Gln Leu Leu Ile Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser
65                  70                  75                  80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn
                85                  90                  95

Ser Leu Gln Ser Glu Asp Val Ala Ser Tyr Phe Cys Gln Gln Tyr Asn
```

```
            100                 105                 110

Asn Tyr Pro Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
        115                 120                 125

Arg Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
    130                 135                 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
        195                 200                 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
    210                 215                 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 49
<211> 45
<212> DNA
<213> Artifitial Sequence

<400> 49
ggaggggcg gccacagccc gtttcagttc cagcttggtc ccagc 45

<210> 50
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 50
```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc cag gtt aag ctg ctg cag tct ggg gct gag ctg gta aaa          96
Val Leu Ser Gln Val Lys Leu Leu Gln Ser Gly Ala Glu Leu Val Lys
            20                  25                  30

cct ggt gct tca gtg aag ttg tcc tgc aag act tct ggt ttt aca ttc         144
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Thr Phe
        35                  40                  45

agc act agt tat atg agt tgg ttg aag cag gtg cct gga ccg agt act         192
```

```
Ser Thr Ser Tyr Met Ser Trp Leu Lys Gln Val Pro Gly Pro Ser Thr
    50                  55                  60

gag tgg att gga tgg att tat gct gga gat ggt ggt act aag tat aat      240
Glu Trp Ile Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aag ttc aag ggc aag gcc aca ctg aca gta gac aaa ttt tct agc      288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Phe Ser Ser
                85                  90                  95

aca gca tac atg gat ctc agc agc ctg aca tct gag gac gct gca gtc      336
Thr Ala Tyr Met Asp Leu Ser Ser Leu Thr Ser Glu Asp Ala Ala Val
            100                 105                 110

tat ttc tgt gca acg gat ggt tat ggg gat tgg ttt act tac tgg ggc      384
Tyr Phe Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

caa ggc act ctg gtc act gtc agc tca gcc tcc acc aag ggc cca agc      432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc      480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg      528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct      576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg      624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg      768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg      816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac      960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc     1008
```

```
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc      1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg      1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc      1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag      1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc      1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                         1401
Pro Gly Lys
465
```

<210> 51
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 51

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Lys Leu Leu Gln Ser Gly Ala Glu Leu Val Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Ser Tyr Met Ser Trp Leu Lys Gln Val Pro Gly Pro Ser Thr
    50                  55                  60

Glu Trp Ile Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Phe Ser Ser
```

85 90 95

Thr Ala Tyr Met Asp Leu Ser Ser Leu Thr Ser Glu Asp Ala Ala Val
100 105 110

Tyr Phe Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 52
<211> 5
<212> PRT
<213> Rattus norvegicus

<400> 52

Asp Phe Trp Met Thr
1 5

<210> 53
<211> 17
<212> PRT
<213> Rattus norvegicus

<400> 53

Ser Ile Thr Tyr Thr Gly Asp Asn Thr Tyr Tyr Ala Gly Ser Val Lys
1 5 10 15

Gly

<210> 54
<211> 13
<212> PRT
<213> Rattus norvegicus

<400> 54

Asp Asp Tyr Gly Gly Tyr Ser Pro Tyr Tyr Met Asp Ala
1 5 10

<210> 55
<211> 5
<212> PRT
<213> Rattus norvegicus

<400> 55

Thr Ser Tyr Met Ser
1 5

<210> 56
<211> 17
<212> PRT
<213> Rattus norvegicus

<400> 56

Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 57
<211> 9
<212> PRT
<213> Rattus norvegicus

<400> 57

Asp Gly Tyr Gly Asp Trp Phe Ala Tyr
1 5

<210> 58
<211> 5
<212> PRT
<213> Rattus norvegicus

<400> 58

Thr Ser Tyr Met Ser
1 5

<210> 59
<211> 17
<212> PRT
<213> Rattus norvegicus

<400> 59

Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 60
<211> 9
<212> PRT
<213> Rattus norvegicus

<400> 60

Asp Gly Tyr Gly Asp Trp Phe Thr Tyr
1 5

<210> 61
<211> 11
<212> PRT
<213> Rattus norvegicus

<400> 61

Arg Ala Ser Gln Asp Ile Gly Asn Tyr Leu Arg
1 5 10

<210> 62
<211> 7
<212> PRT
<213> Rattus norvegicus

<400> 62

Gly Ala Thr Asn Leu Ala Asn
1 5

<210> 63
<211> 9
<212> PRT
<213> Rattus norvegicus

<400> 63

Leu Lys His Asn Glu Tyr Pro Phe Thr
1 5

<210> 64
<211> 11
<212> PRT
<213> Rattus norvegicus

<400> 64

Arg Ala Ser Glu Asp Ile Tyr Ser Asn Leu Ala
1 5 10

<210> 65
<211> 7
<212> PRT
<213> Rattus norvegicus

<400> 65

Asp Ala Asn Ile Leu Ala Asp
1 5

<210> 66
<211> 10
<212> PRT
<213> Rattus norvegicus

<400> 66

```
Gln Gln Tyr Asn Asn Tyr Pro Pro Phe Thr
1               5                   10


<210>  67
<211>  11
<212>  PRT
<213>  Rattus norvegicus

<400>  67

Arg Ala Ser Glu Asp Ile Tyr Ser Asn Leu Ala
1               5                   10


<210>  68
<211>  7
<212>  PRT
<213>  Rattus norvegicus

<400>  68

Asp Ala Asn Ile Leu Ala Asp
1               5


<210>  69
<211>  10
<212>  PRT
<213>  Rattus norvegicus

<400>  69

Gln Gln Tyr Asn Asn Tyr Pro Pro Phe Thr
1               5                   10


<210>  70
<211>  822
<212>  PRT
<213>  Homo sapiens

<400>  70

Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
1               5                   10                  15


Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
            20                  25                  30


Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
        35                  40                  45


Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
    50                  55                  60


Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65                  70                  75                  80


Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
                85                  90                  95
```

```
Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
            100                 105                 110

Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
        115                 120                 125

Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
    130                 135                 140

Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145                 150                 155                 160

Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
                165                 170                 175

Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
            180                 185                 190

Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
        195                 200                 205

Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
    210                 215                 220

Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225                 230                 235                 240

Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
                245                 250                 255

Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
            260                 265                 270

Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
        275                 280                 285

Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
    290                 295                 300

Gly Leu Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser
305                 310                 315                 320

Asn Ala Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly
                325                 330                 335

Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser
            340                 345                 350

Ala Trp Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys
        355                 360                 365
```

```
Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile
    370                 375                 380

Gly Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg
385                 390                 395                 400

Met Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val
                405                 410                 415

His Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser
            420                 425                 430

Ala Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile
        435                 440                 445

Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val
    450                 455                 460

Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp
465                 470                 475                 480

Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val
                485                 490                 495

Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala
            500                 505                 510

Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp
        515                 520                 525

Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys
    530                 535                 540

His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro
545                 550                 555                 560

Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr
                565                 570                 575

Leu Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn
            580                 585                 590

Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr
        595                 600                 605

Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile
    610                 615                 620

His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val
625                 630                 635                 640
```

Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp
645 650 655

Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala
660 665 670

Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp
675 680 685

Ser Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro
690 695 700

Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly
705 710 715 720

His Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met
725 730 735

Met Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys
740 745 750

Gln Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu
755 760 765

Glu Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr
770 775 780

Pro Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser
785 790 795 800

Pro Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile
805 810 815

Asn Gly Ser Val Lys Thr
820

<210> 71
<211> 821
<212> PRT
<213> Homo sapiens

<400> 71

Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
1 5 10 15

Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
20 25 30

Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
35 40 45

Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu

50 55 60

Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65 70 75 80

Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
85 90 95

Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
100 105 110

Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
115 120 125

Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
130 135 140

Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145 150 155 160

Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
165 170 175

Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
180 185 190

Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
195 200 205

Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
210 215 220

Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225 230 235 240

Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
245 250 255

Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
260 265 270

Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
275 280 285

Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
290 295 300

Gly Leu Pro Tyr Leu Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr
305 310 315 320

Asp Lys Glu Ile Glu Val Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp

325 330 335

Ala Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe
340 345 350

His Ser Ala Trp Leu Thr Val Leu Pro Ala Pro Gly Arg Glu Lys Glu
355 360 365

Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly
370 375 380

Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met
385 390 395 400

Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His
405 410 415

Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala
420 425 430

Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr
435 440 445

Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser
450 455 460

Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys
465 470 475 480

Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val
485 490 495

Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val
500 505 510

Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu
515 520 525

Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His
530 535 540

Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu
545 550 555 560

Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu
565 570 575

Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg
580 585 590

Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr

595 600 605

Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His
610 615 620

Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met
625 630 635 640

Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr
645 650 655

Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro
660 665 670

Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser
675 680 685

Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr
690 695 700

Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His
705 710 715 720

Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met
725 730 735

Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln
740 745 750

Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu
755 760 765

Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro
770 775 780

Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro
785 790 795 800

Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn
805 810 815

Gly Ser Val Lys Thr
820

<210> 72
<211> 705
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(705)

<400> 72

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atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc          48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                  10                  15

ggc gcg tac ggc gac atc cag atg acc cag agc ccc agc agc ctg agc          96
Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
            20                  25                  30

gcc agc gtg ggc gac aga gtg acc atc acc tgt cgg gcc agc gag gac         144
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp
        35                  40                  45

atc tac agc aac ctg gcc tgg tat cag cag aag ccc ggc aag agc ccc         192
Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro
    50                  55                  60

cag ctg ctg atc tac gac gcc aac atc ctg gcc gac ggc gtg ccc agc         240
Gln Leu Leu Ile Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser
65                  70                  75                  80

aga ttc agc ggc agc ggc tcc ggc acc gac tac acc ctg acc atc tcc         288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
                85                  90                  95

agc ctg cag ccc gag gac ttc gcc acc tac tac tgc cag cag tac aac         336
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn
            100                 105                 110

aac tac ccc cca ttc acc ttc ggc cag ggc acc aag gtg gaa atc aag         384
Asn Tyr Pro Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc tcc gac gag         432
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
    130                 135                 140

cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg aat aac ttc         480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160

tac ccc aga gag gcc aag gtg cag tgg aag gtg gac aac gcc ctg cag         528
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175

tcc ggg aac tcc cag gag agc gtg acc gag cag gac agc aag gac agc         576
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190

acc tac agc ctg agc agc acc ctg acc ctg agc aaa gcc gac tac gag         624
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
        195                 200                 205

aag cac aag gtg tac gcc tgc gag gtg acc cac cag ggc ctg agc tcc         672
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
    210                 215                 220

ccc gtc acc aag agc ttc aac agg ggg gag tgt                             705
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 73
<211> 235
<212> PRT
<213> Artifitial Sequence

<400> 73

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp
35 40 45

Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro
50 55 60

Gln Leu Leu Ile Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn
100 105 110

Asn Tyr Pro Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 74
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 74

```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc cag gga ctg         192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac         240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc         288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg         336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac ggc tac ggc gac tgg ttc aca tac tgg ggc         384
Tyr Tyr Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc         432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc         480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg         528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct         576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg         624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac         672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt         720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg         768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255
```

```
gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg          816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac          864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg          912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac          960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc         1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc         1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg         1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc         1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag         1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc         1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg         1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg         1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct         1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                             1401
Pro Gly Lys
465
```

<210> 75
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 75

```
Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15
```

```
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285
```

```
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

Pro Gly Lys
465
```

<210> 76
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 76

```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30
```

```
cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc          144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc cag gga ctg          192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac          240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gcc gac aag agc acc agc          288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Ala Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg          336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac ggc tac ggc gac tgg ttc aca tac tgg ggc          384
Tyr Tyr Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc          432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc          480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg          528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct          576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg          624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac          672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt          720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg          768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg          816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac          864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg          912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300
```

```
cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac          960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc         1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc         1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg         1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc         1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag         1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc         1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg         1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg         1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct         1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                             1401
Pro Gly Lys
465
```

<210> 77
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 77

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60
```

```
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Ala Asp Lys Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335
```

```
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

Pro Gly Lys
465
```

<210> 78
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 78

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atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc         192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac         240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc         288
```

```
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg        336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac ggc tac ggc gac tgg ttc aca tac tgg ggc        384
Tyr Tyr Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc        432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc        480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg        528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct        576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg        624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac        672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt        720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg        768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg        816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac        864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg        912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac        960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc       1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc       1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg       1104
```

```
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc      1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag      1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc      1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                          1401
Pro Gly Lys
465
```

<210> 79
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 79

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
```

```
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
```

385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 80
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 80
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa 96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
35 40 45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc atc 192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Ile
50 55 60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac 240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc 288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg 336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

tac tac tgc gcc acc gac ggc tac ggc gac tgg ttc gcc tac tgg ggc 384
Tyr Tyr Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Ala Tyr Trp Gly
115 120 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc 432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser

```
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc        480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg        528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct        576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg        624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac        672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt        720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg        768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg        816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac        864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg        912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac        960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc       1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc       1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg       1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc       1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag       1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc       1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
```

```
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                          1401
Pro Gly Lys
465
```

<210> 81
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 81

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Ile
    50                  55                  60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Ala Tyr Trp Gly
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175
```

```
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445
```

```
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

Pro Gly Lys
465
```

<210> 82
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 82

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atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc         192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac         240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc         288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg         336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gag ggc tac ggc gac tgg ttc aca tac tgg ggc         384
Tyr Tyr Cys Ala Thr Glu Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc         432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc         480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg         528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct         576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190
```

```
gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg        624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac        672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt        720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg        768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg        816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac        864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg        912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac        960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc       1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc       1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg       1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc       1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag       1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc       1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg       1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg       1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct       1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460
```

ccc ggc aaa
Pro Gly Lys
465

<210> 83
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 83

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
35 40 45

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Thr Glu Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 84
<211> 1401
<212> DNA

<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 84

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atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc         192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac         240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc         288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg         336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac gcc tac ggc gac tgg ttc aca tac tgg ggc         384
Tyr Tyr Cys Ala Thr Asp Ala Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc         432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc         480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg         528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct         576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg         624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac         672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt         720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240
```

```
gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg        768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg        816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac        864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg        912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac        960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc       1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc       1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg       1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc       1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag       1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc       1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg       1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg       1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct       1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                           1401
Pro Gly Lys
465
```

<210> 85
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 85

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
35 40 45

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Thr Asp Ala Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

```
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

Pro Gly Lys
465
```

<210> 86
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 86

```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg        48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa        96
```

```
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc      144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc      192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac      240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc      288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg      336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac gag tac ggc gac tgg ttc aca tac tgg ggc      384
Tyr Tyr Cys Ala Thr Asp Glu Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc      432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc      480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg      528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct      576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg      624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg      768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg      816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
```

```
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac        960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc       1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc       1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg       1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc       1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag       1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc       1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg       1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg       1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct       1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                           1401
Pro Gly Lys
465
```

<210> 87
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 87

```
Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
```

50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Thr Asp Glu Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

```
                325                 330                 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

Pro Gly Lys
465
```

<210> 88
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 88

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atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc         192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac         240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
```

```
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc      288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg      336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac ttc tac ggc gac tgg ttc aca tac tgg ggc      384
Tyr Tyr Cys Ala Thr Asp Phe Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc      432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc      480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg      528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct      576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg      624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg      768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg      816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac      960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc     1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc     1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
```

```
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg      1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc      1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag      1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc      1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                          1401
Pro Gly Lys
465
```

<210> 89
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 89

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110
```

```
Tyr Tyr Cys Ala Thr Asp Phe Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380
```

```
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

Pro Gly Lys
465
```

<210> 90
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 90

```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc         192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac         240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc         288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg         336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac cac tac ggc gac tgg ttc aca tac tgg ggc         384
Tyr Tyr Cys Ala Thr Asp His Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125
```

```
cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc        432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc        480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg        528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct        576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg        624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac        672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt        720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg        768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg        816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac        864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg        912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac        960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc       1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc       1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg       1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc       1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag       1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400
```

```
tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc      1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                          1401
Pro Gly Lys
465
```

<210> 91
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 91

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Asp His Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160
```

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

```
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

Pro Gly Lys
465
```

<210> 92
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 92

```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc         192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac         240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc         288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg         336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac atc tac ggc gac tgg ttc aca tac tgg ggc         384
Tyr Tyr Cys Ala Thr Asp Ile Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc         432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc         480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg         528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175
```

```
agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct        576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg        624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac        672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt        720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg        768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg        816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac        864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg        912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac        960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc       1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc       1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg       1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc       1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag       1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc       1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg       1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg       1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445
```

```
cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                        1401
Pro Gly Lys
465
```

<210> 93
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 93

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Asp Ile Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205
```

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 94
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 94

```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc         192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac         240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc         288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg         336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac aag tac ggc gac tgg ttc aca tac tgg ggc         384
Tyr Tyr Cys Ala Thr Asp Lys Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc         432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc         480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg         528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct         576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg         624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac         672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt         720
```

```
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg      768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg      816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac      960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc     1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc     1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg     1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc     1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag     1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc     1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg     1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg     1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct     1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                        1401
Pro Gly Lys
465
```

<210> 95
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 95

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Asp Lys Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
```

260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 96
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 96
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp

```
1               5                  10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc         192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac         240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc         288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg         336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac ctg tac ggc gac tgg ttc aca tac tgg ggc         384
Tyr Tyr Cys Ala Thr Asp Leu Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc         432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc         480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg         528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct         576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg         624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac         672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt         720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg         768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg         816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac         864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
```

```
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg        912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac        960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc       1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc       1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg       1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc       1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag       1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc       1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg       1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg       1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct       1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                           1401
Pro Gly Lys
465
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<210> 97
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 97

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45
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Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Thr Asp Leu Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

```
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

Pro Gly Lys
465
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<210> 98
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 98

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atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc         192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60
```

```
gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac        240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc        288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg        336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac atg tac ggc gac tgg ttc aca tac tgg ggc        384
Tyr Tyr Cys Ala Thr Asp Met Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc        432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc        480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg        528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct        576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg        624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac        672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt        720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg        768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg        816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac        864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg        912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac        960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc       1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335
```

```
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc      1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg      1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc      1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag      1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc      1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                         1401
Pro Gly Lys
465
```

<210> 99
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 99

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95
```

```
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Asp Met Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365
```

```
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

Pro Gly Lys
465
```

<210> 100
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 100

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atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc         192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac         240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc         288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg         336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110
```

```
tac tac tgc gcc acc gac cag tac ggc gac tgg ttc aca tac tgg ggc        384
Tyr Tyr Cys Ala Thr Asp Gln Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc        432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc        480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg        528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct        576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg        624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac        672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt        720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg        768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg        816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac        864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg        912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac        960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc       1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc       1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg       1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc       1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380
```

```
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag      1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc      1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                          1401
Pro Gly Lys
465
```

<210> 101
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 101

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Asp Gln Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140
```

```
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415
```

```
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

Pro Gly Lys
465
```

<210> 102
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 102

```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc         192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac         240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc         288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg         336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac cgg tac ggc gac tgg ttc aca tac tgg ggc         384
Tyr Tyr Cys Ala Thr Asp Arg Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc         432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc         480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg         528
```

```
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct  576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg  624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac  672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt  720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg  768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg  816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac  864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg  912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac  960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg 1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc 1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc 1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg 1344
```

```
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                          1401
Pro Gly Lys
465
```

<210> 103
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 103

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Asp Arg Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
```

```
        195                 200                 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

Pro Gly Lys
```

465

<210> 104
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 104

```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc         192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac         240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc         288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg         336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac gtg tac ggc gac tgg ttc aca tac tgg ggc         384
Tyr Tyr Cys Ala Thr Asp Val Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc         432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc         480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg         528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct         576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg         624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac         672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
```

```
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt        720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg        768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg        816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac        864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg        912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac        960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc       1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc       1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg       1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc       1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag       1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc       1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg       1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg       1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct       1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                           1401
Pro Gly Lys
465
```

<210> 105

<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 105

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
35 40 45

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Thr Asp Val Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

```
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

Pro Gly Lys
465
```

<210> 106
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 106

```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc         192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac         240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc         288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg         336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac tgg tac ggc gac tgg ttc aca tac tgg ggc         384
Tyr Tyr Cys Ala Thr Asp Trp Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc         432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc         480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg         528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct         576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg         624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac         672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt         720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg         768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg         816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270
```

```
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac        864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg        912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac        960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc       1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc       1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg       1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc       1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag       1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc       1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg       1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg       1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct       1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                           1401
Pro Gly Lys
465
```

<210> 107
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 107

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Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30
```

```
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Asp Trp Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300
```

```
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

Pro Gly Lys
465
```

<210> 108
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 108

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atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg          48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa          96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc         144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45
```

```
agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc      192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac      240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc      288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg      336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac tac tac ggc gac tgg ttc aca tac tgg ggc      384
Tyr Tyr Cys Ala Thr Asp Tyr Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc      432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc      480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg      528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct      576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg      624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg      768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg      816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac      960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320
```

```
cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc        1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc        1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg        1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc        1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag        1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc        1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg        1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg        1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct        1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                            1401
Pro Gly Lys
465
```

<210> 109
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 109

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80
```

```
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Asp Tyr Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350
```

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 110
<211> 39
<212> DNA
<213> Artifitial Sequence

<400> 110
ggcagagtga ccctgaccgc cgacaagagc accagcacc 39

<210> 111
<211> 39
<212> DNA
<213> Artifitial Sequence

<400> 111
ggtgctggtg ctcttgtcgg cggtcagggt cactctgcc 39

<210> 112
<211> 39
<212> DNA
<213> Artifitial Sequence

<400> 112
ggtgctggtg ctcttgtcgg cggtcagggt cactctgcc 39

<210> 113
<211> 42
<212> DNA
<213> Artifitial Sequence

<400> 113
cgcaagcttg tcgactcaaa caacatccag atgataggta tg 42